

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: September 2, 2006, 06:47:12 ; Search time 199 Seconds  
(without alignments)  
2242.428 Million cell updates/sec

Title: US-10-519-135-2

Perfect score: 5043

Sequence: 1 MAFRIYVGLFGLCLSLVA.....SASDAQPLRFQGVQVQNSSE 976

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A\_Geneseq\_8: \*  
1: geneseqp1980s: \*  
2: geneseqp1990s: \*  
3: geneseqp2000s: \*  
4: geneseqp2001s: \*  
5: geneseqp2002s: \*  
6: geneseqp2003as: \*  
7: geneseqp2003bs: \*  
8: geneseqp2004s: \*  
9: geneseqp2005s: \*  
10: geneseqp2006s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5043	100.0	976	2	AAW13408 Arabidops
2	5043	100.0	976	5	ABB91884 Arabidops
3	5043	100.0	976	8	AD132614 Thale cre
4	5043	100.0	976	8	AED28149 Arabidops
5	3602.5	71.4	838	8	ADX95769 Plant ful
6	3372.5	66.9	921	8	AD132618 Sorghum t
7	3372.5	66.9	921	8	ADU94448 Oll-assoc
8	3167	62.8	614	9	AED28151 Arabidops
9	3113	61.7	999	8	AD132616 Rice tran
10	3091.5	61.3	966	5	ABB93915 Arabidops
11	3091.5	61.3	966	8	AD132622 Thale cre
12	3089.5	61.3	966	9	AED28155 Arabidops
13	3079.5	61.1	966	9	AED28153 Arabidops
14	3059	60.7	932	5	ABB93386 Arabidops
15	3059	60.7	932	8	AD132620 Thale cre
16	2791	55.3	764	8	ADX95784 Plant ful
17	2482	49.2	675	8	AD132657 Maize tra
18	2384.5	47.3	578	8	ADU76417 Plant ful
19	2322.5	46.1	611	9	AED28234 Rice ERRC
20	2259.5	44.8	613	9	AED28233 Rice ERRC
21	2236.5	44.3	541	8	ADU74616 Plant ful
22	2215	43.9	713	8	ADX95337 Plant ful
23	2010	39.9	621	9	AED28235 Rice ERRC

24	1968.5	39.0	619	9	AED28159 Arabidops
25	1956.5	38.8	616	9	AED28157 Arabidops
26	1596	31.6	458	8	ADU91124 Plant ful
27	1568	31.1	502	3	ABB25570 Pinus rad
28	1543	30.6	426	8	ADX96775 Pinus rad
29	1504.5	29.8	1124	5	ABB91986 Arabidops
30	1489	29.5	1109	7	ABB93939 Arabidops
31	1480.5	29.4	1109	7	ABM6574 Rice abio
32	1446	28.7	1109	8	ADU50374 Oll-assoc
33	1442	28.6	1109	8	ABB93705 Arabidops
34	1441	28.6	1109	8	ADU49192 Oll-assoc
35	1432.5	28.4	998	3	ABB25556 Pinus rad
36	1417.5	28.1	448	8	AD132632 Bread whe
37	1412.5	28.0	1133	5	ABB91038 Arabidops
38	1410.5	28.0	1003	4	AAW52369 Receptor
39	1410.5	28.0	1003	5	ABB93956 Arabidops
40	1404.5	27.9	998	3	ABB25520 Pinus rad
41	1397	27.7	1123	3	AAW52565 Arabidops
42	1393.5	27.6	1192	6	ABB25569 Pinus rad
43	1373.5	27.1	1002	3	ABB82564 Arabidops
44	1368.5	27.1	1002	3	AAW38741 Arabidops
45	1368.5	27.1	1002	5	ABB92602 Arabidops

## ALIGNMENTS

RESULT 1  
AAW13408  
ID AAW13408 standard; protein; 976 AA.  
XX  
AC AAW13408;  
XX  
DT 10-JUN-1997 (first entry)  
XX  
DE Arabidopsis thaliana plant morphogenesis regulatory protein.  
XX  
KW Plant, morphogenesis; regulation; short; stem; alteration; inflorescence;  
KW extraneous; gene; expression; transformation; increase; control; form;  
KW length.  
XX  
OS Arabidopsis thaliana.  
XX  
PN JP09056382-A.  
XX  
PD 04-MAR-1997.  
XX  
PF 24-AUG-1995; 95JP-00216187.  
XX  
PR 24-AUG-1995; 95JP-00216187.  
XX  
PA (CHIK-) ZH CHIKYU KANKYO SANGYO GIITSU KENKYU.  
PA (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.  
DR WPI; 1997-206629/19.  
DR N-PSDB; AAT62124.  
XX  
PT DNA encoding plant morphogenesis regulatory protein - useful to yield  
PT plants with short stems or altered inflorescence.  
XX  
PS Claim 1; Page 6-10; 17pp; Japanese.  
XX  
CC The present sequence is an Arabidopsis thaliana plant morphogenesis  
CC regulatory protein (MRP), which can be used to yield a plant with, e.g.  
CC short stems or altered inflorescence. The MRP acts on a plant at a  
CC specific site for a specific period, and can therefore be used to  
CC regulate extraneous gene expression in a plant. The MRP's cDNA or genomic  
CC DNA can be used to transform a plant to increase its MRP expression, and  
CC therefore control the form (particularly stem length) of the plant  
XX  
SQ Sequence 976 AA;  
Query Match 100.0%; Score 5043; DB 2; Length 976;

Best Local Similarity 100.0%; Pred. No. 0;  
Matches 976; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MALFRDVLVLLGFCLSLVATVTSSEGAATLLEIKSFQDVNNVLYDMTSSPSSDYCWMRG 60
DB 1 MALFRDVLVLLGFCLSLVATVTSSEGAATLLEIKSFQDVNNVLYDMTSSPSSDYCWMRG 60
QY VSCENVTFNVALNLSDNLNDEGEISPAIGDKSLSIDLRGNRLSGQIPDEIGCCSLQN 120
DB 61 VSCENVTFNVALNLSDNLNDEGEISPAIGDKSLSIDLRGNRLSGQIPDEIGCCSLQN 120
QY 121 LDISFNLSGDIPPSISKQLQEQILKNNQIGPISSTLSQIPNLKIIDLQNKLSGEI 180
DB 121 LDISFNLSGDIPPSISKQLQEQILKNNQIGPISSTLSQIPNLKIIDLQNKLSGEI 180
QY 181 PRLIYMEVQYGLRGNNLVGNISPDLCQLTGLMFDVRNNSLTGSIPTETIGNCTAFQV 240
DB 181 PRLIYMEVQYGLRGNNLVGNISPDLCQLTGLMFDVRNNSLTGSIPTETIGNCTAFQV 240
QY 241 LDISYNQLTGEIPPDIGFLQVATLSLQGNQLSGKIPSVIGLMQALAVLDLSGNLSSGIP 300
DB 241 LDISYNQLTGEIPPDIGFLQVATLSLQGNQLSGKIPSVIGLMQALAVLDLSGNLSSGIP 300
QY 301 PILGNLTFTTEKLYLHNSKLTGSIPELGNNSKLYLELNDNHLTGHIPEELGKLTDLFDL 360
DB 301 PILGNLTFTTEKLYLHNSKLTGSIPELGNNSKLYLELNDNHLTGHIPEELGKLTDLFDL 360
QY 361 NVANNDEEGPDPDLSSCTNLNSLVNHNKFSGTIPPAFOKLESMTYLNLSNNIKGPIR 420
DB 361 NVANNDEEGPDPDLSSCTNLNSLVNHNKFSGTIPPAFOKLESMTYLNLSNNIKGPIR 420
QY 421 VELSRIGNLDTLDLSNNKINGIIPSSLGDEHLKNNLSRNHITGVVPGDFGNLSIMEI 480
DB 421 VELSRIGNLDTLDLSNNKINGIIPSSLGDEHLKNNLSRNHITGVVPGDFGNLSIMEI 480
QY 481 DLSNNDISGPIPEELNQLQNTILRLENNNTGVVSGLANCLSTVNVSHNNVGDIPK 540
DB 481 DLSNNDISGPIPEELNQLQNTILRLENNNTGVVSGLANCLSTVNVSHNNVGDIPK 540
QY 541 NNNNSRSPSPSFGNPGLCGSMWNSPCHDSRRTVRSIRAIIGIAGIIVILLMVLIA 600
DB 541 NNNNSRSPSPSFGNPGLCGSMWNSPCHDSRRTVRSIRAIIGIAGIIVILLMVLIA 600
QY 601 ACRPHNPPLFDGSLDKPVYTSPEKLVILHNNMALHYEDIMRMTENLSEKXIIGHGASS 660
DB 601 ACRPHNPPLFDGSLDKPVYTSPEKLVILHNNMALHYEDIMRMTENLSEKXIIGHGASS 660
QY 661 TVYKCVLKNCKPVAIKRLYSHNPQSMKQFETELMSSIKGRNLSIQAVSLSHLSLLF 720
DB 661 TVYKCVLKNCKPVAIKRLYSHNPQSMKQFETELMSSIKGRNLSIQAVSLSHLSLLF 720
QY 721 YDYLENGSLMDLHGPTKKKTLDMDTRLKIAYGAAQGLAYHHDCSPRIIHRDVKSSNLL 780
DB 721 YDYLENGSLMDLHGPTKKKTLDMDTRLKIAYGAAQGLAYHHDCSPRIIHRDVKSSNLL 780
QY 781 LDKDLRLRLTDGFIKSLCVSKSHTSTYVMGTIGYIDPEVARTSRLTEKSDVVSYGIVLL 840
DB 781 LDKDLRLRLTDGFIKSLCVSKSHTSTYVMGTIGYIDPEVARTSRLTEKSDVVSYGIVLL 840
QY 841 ELLTRRAVAVDESNLHLIMSKTGNNEVEMADPDITSTCKDLGVKKVFOALALCTKRQ 900
DB 841 ELLTRRAVAVDESNLHLIMSKTGNNEVEMADPDITSTCKDLGVKKVFOALALCTKRQ 900
QY 901 PNDRPTMHQVTRVYSGFMLSQPPAATDTSATLAGSCYVDEYANLKTPHSVNCSMSASD 960
DB 901 PNDRPTMHQVTRVYSGFMLSQPPAATDTSATLAGSCYVDEYANLKTPHSVNCSMSASD 960
QY 961 AOLFLRFGQVISONSE 976
DB 961 AOLFLRFGQVISONSE 976
```

RESULT 2

ABB91884  
ID ABB91884 standard; protein; 976 AA.

AC ABB91884;

DT 31-MAY-2002 (first entry)

DE Herbicidally active polypeptide SEQ ID NO 1095.

KW Herbicidal; plant; agriculture; herbicide.

OS Arabidopsis thaliana.

PN W0200210210-A2.

PD 07-FEB-2002.

PF 28-AUG-2001; 2001WO-EP009892.

PR 28-AUG-2001; 2001WO-EP009892.

PA (FARB ) BAYER AG.

PI Tietjen K, Weidner M;

DR WPI; 2002-269010/31.

PT Identifying plant target proteins for herbicidally active compounds,  
comprising aligning and comparing nucleic acid or amino acid sequences  
from plant with nucleic acid or amino acid sequences from non-plant  
organisms.

PS Claim 5; SEQ ID NO 1095; 261pp + Sequence Listing; English.

CC The invention relates to identifying target proteins (ABB90790-ABB94016)  
for herbicidally active compounds, comprising aligning and comparing  
nucleic acid or amino acid sequences from plant with nucleic acid or  
amino acid sequences from non-plant organisms using suitable search  
parameters, where plant sequences having an E-value greater by a factor  
of 3 than the E-value of most similar non-plant sequences are selected.  
CC The polypeptides or nucleic acids encoding them are useful for  
identifying modulators. The identified modulators are useful as  
herbicides

CC Sequence 976 AA;

Query Match 100.0%; Score 5043; DB 5; Length 976;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 976; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MALFRDVLVLLGFCLSLVATVTSSEGAATLLEIKSFQDVNNVLYDMTSSPSSDYCWMRG 60
DB 1 MALFRDVLVLLGFCLSLVATVTSSEGAATLLEIKSFQDVNNVLYDMTSSPSSDYCWMRG 60
QY VSCENVTFNVALNLSDNLNDEGEISPAIGDKSLSIDLRGNRLSGQIPDEIGCCSLQN 120
DB 61 VSCENVTFNVALNLSDNLNDEGEISPAIGDKSLSIDLRGNRLSGQIPDEIGCCSLQN 120
QY 121 LDISFNLSGDIPPSISKQLQEQILKNNQIGPISSTLSQIPNLKIIDLQNKLSGEI 180
DB 121 LDISFNLSGDIPPSISKQLQEQILKNNQIGPISSTLSQIPNLKIIDLQNKLSGEI 180
QY 181 PRLIYMEVQYGLRGNNLVGNISPDLCQLTGLMFDVRNNSLTGSIPTETIGNCTAFQV 240
DB 181 PRLIYMEVQYGLRGNNLVGNISPDLCQLTGLMFDVRNNSLTGSIPTETIGNCTAFQV 240
QY 241 LDISYNQLTGEIPPDIGFLQVATLSLQGNQLSGKIPSVIGLMQALAVLDLSGNLSSGIP 300
DB 241 LDISYNQLTGEIPPDIGFLQVATLSLQGNQLSGKIPSVIGLMQALAVLDLSGNLSSGIP 300
QY 301 PILGNLTFTTEKLYLHNSKLTGSIPELGNNSKLYLELNDNHLTGHIPEELGKLTDLFDL 360
DB 301 PILGNLTFTTEKLYLHNSKLTGSIPELGNNSKLYLELNDNHLTGHIPEELGKLTDLFDL 360
```

```

QY 361 NVANNDEGPDPHLSCTNLNSLVNHNKSGTIPRAFOKLESMTYLNLSNNIKGP 420
XX |||||
DB 361 NVANNDEGPDPHLSCTNLNSLVNHNKSGTIPRAFOKLESMTYLNLSNNIKGP 420
QY 421 VELSRIGNDTDLNSNNKINGIIPSSLGDEHLLKNNLSRNHITGVVPGDFGNLSIMEI 480
XX |||||
DB 421 VELSRIGNDTDLNSNNKINGIIPSSLGDEHLLKNNLSRNHITGVVPGDFGNLSIMEI 480
QY 481 DLSNNDISGPIPEELNOLONIILRLNENNLTVGVSLANCLSLTVLVNHNHVGDIK 540
XX |||||
DB 481 DLSNNDISGPIPEELNOLONIILRLNENNLTVGVSLANCLSLTVLVNHNHVGDIK 540
QY 541 NNNFSRFPSPDFGNGSLGSMWNSPCHDSRRTVRVVISRAAIIIGAIIGLVLLAVLIA 600
XX |||||
DB 541 NNNFSRFPSPDFGNGSLGSMWNSPCHDSRRTVRVVISRAAIIIGAIIGLVLLAVLIA 600
QY 601 ACRPHNPPEPLDGLDKPVYVSTPKLVILHMMNALHYVEDIMMNTENLSEKYYIIGHGASS 660
XX |||||
DB 601 ACRPHNPPEPLDGLDKPVYVSTPKLVILHMMNALHYVEDIMMNTENLSEKYYIIGHGASS 660
QY 661 TVYKCVLKNCKPAVKRLYSNPOSKQFTELEMLSSIGHRLVLSIQAYSLSHLSGLLF 720
XX |||||
DB 661 TVYKCVLKNCKPAVKRLYSNPOSKQFTELEMLSSIGHRLVLSIQAYSLSHLSGLLF 720
QY 721 YDYLENGSLMDLHGPTKKKTLDMDRKLTAAGAAGLAVLHHDGSPRIIHRVKSNTL 780
XX |||||
DB 721 YDYLENGSLMDLHGPTKKKTLDMDRKLTAAGAAGLAVLHHDGSPRIIHRVKSNTL 780
QY 781 LDKLEBARLDFGIASLGVSKSHTSYVVGITGYIDPEYARTSRULEKSDVYSYGVLL 840
XX |||||
DB 781 LDKLEBARLDFGIASLGVSKSHTSYVVGITGYIDPEYARTSRULEKSDVYSYGVLL 840
QY 841 ELLTRKAVADESNLHLLIMSKTGNNEVMADPDITSTCKDGVVKKYVQLALLCTKRQ 900
XX |||||
DB 841 ELLTRKAVADESNLHLLIMSKTGNNEVMADPDITSTCKDGVVKKYVQLALLCTKRQ 900
QY 901 PNDPRTMHQVTRVLGSPMLSEOPPAATDTSATLAGSCYVDEVYANLKTPHSVNCSMSASP 960
XX |||||
DB 901 PNDPRTMHQVTRVLGSPMLSEOPPAATDTSATLAGSCYVDEVYANLKTPHSVNCSMSASP 960
QY 961 AQLFLRFGOVISONSE 976
XX |||||
DB 961 AQLFLRFGOVISONSE 976

```

## RESULT 3

AD132614  
ID AD132614 standard; protein; 976 AA.

XX AD132614;

XX 22-APR-2004 (first entry)

DE Thale cress transpiration efficiency-related ERECTA protein.

KM plant; transpiration efficiency; ERECTA; breeding; genetic engineering;

KW thale cress; chromosome 2.

XX Arabidopsis thaliana.

XX OS MO2004005555-A1.

XX PD 15-JAN-2004.

XX PF 02-JUL-2003; 2003WO-AU000854.

XX PR 02-JUL-2002; 2002AU-00003339.

XX PA (AUSU) UNIV AUSTRALIAN NAT.

XX PI Masle J, Farquhar GD, Gilmore SR;

```

DR WPI; 2004-091390/09.
DR N-PSDB; AD132613.
XX
PT Selecting plant having enhanced transpiration efficiency, useful for
PT producing plants with enhanced transcription efficiency comprising
PT selecting plant expressing a genetic marker linked to the ERECTA locus in
PT the genome of the plant.
XX
PS Claim 4; SEQ ID NO 2; 209pp; English.
XX
CC The invention relates to a novel method for selecting a plant having
CC enhanced transpiration efficiency comprising detecting a genetic marker
CC for transpiration efficiency, where the marker comprises a nucleotide
CC sequence linked genetically to an ERECTA locus in the genome of the plant
CC and selecting a plant that comprises or expresses the genetic marker. The
CC method of the invention may be useful for selecting a plant having
CC enhanced transpiration efficiency. The isolated ERECTA gene or allelic
CC variant or protein-encoding region may be useful in the preparation of a
CC genetic construct for modulating the transpiration efficiency of a plant.
CC Furthermore, the ERECTA genes may be useful for producing plants having
CC enhanced transpiration efficiency by both traditional plant breeding and
CC genetic engineering approaches. The current sequence is that of the thale
CC cress ERECTA protein of the invention which is encoded by DNA located on
CC chromosome 2.
XX
SQ Sequence 976 AA:
Query Match 100.0%; Score 5043; DB 8; Length 976;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 976; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALFRDIVLGFPCLSIVATVSEGAITLTKKSKFQVNNVLYDMTSSPSDDCYWVG 60
DB 1 MALFRDIVLGFPCLSIVATVSEGAITLTKKSKFQVNNVLYDMTSSPSDDCYWVG 60
QY 61 VSCENTFVNVALNLSLMDLMDGEISPAIDKSLSIDLRGNRLSGQIPDEIGDCSLON 120
DB 61 VSCENTFVNVALNLSLMDLMDGEISPAIDKSLSIDLRGNRLSGQIPDEIGDCSLON 120
QY 121 LDISFNEBSGDIPFSISKLEQLILKNNQLIGPISPTLSQIPNKLIDLAONKISGEI 180
DB 121 LDISFNEBSGDIPFSISKLEQLILKNNQLIGPISPTLSQIPNKLIDLAONKISGEI 180
QY 181 PRLIYNEVLYQYGLRGNLVGNISPDLCOLTGMLFEDVRNNSLTGSIPTIGNCTAFQV 240
DB 181 PRLIYNEVLYQYGLRGNLVGNISPDLCOLTGMLFEDVRNNSLTGSIPTIGNCTAFQV 240
QY 241 LDISYNQLTGEIPFDIGFLOVATLSLQGNQLSGKIPSVIGLQALAVLDLSGNLSGSIP 300
DB 241 LDISYNQLTGEIPFDIGFLOVATLSLQGNQLSGKIPSVIGLQALAVLDLSGNLSGSIP 300
QY 301 PIIGNLTFTBEKLYLHNSKLTGSIPELGNMSKLYHLELNDNHLTGHIPELGLKTLDFDL 360
DB 301 PIIGNLTFTBEKLYLHNSKLTGSIPELGNMSKLYHLELNDNHLTGHIPELGLKTLDFDL 360
QY 361 NVANNDEGPDPHLSCTNLNSLVNHNKSGTIPRAFOKLESMTYLNLSNNIKGP 420
DB 361 NVANNDEGPDPHLSCTNLNSLVNHNKSGTIPRAFOKLESMTYLNLSNNIKGP 420
QY 421 VELSRIGNDTDLNSNNKINGIIPSSLGDEHLLKNNLSRNHITGVVPGDFGNLSIMEI 480
DB 421 VELSRIGNDTDLNSNNKINGIIPSSLGDEHLLKNNLSRNHITGVVPGDFGNLSIMEI 480
QY 481 DLSNNDISGPIPEELNOLONIILRLNENNLTVGVSLANCLSLTVLVNHNHVGDIK 540
DB 481 DLSNNDISGPIPEELNOLONIILRLNENNLTVGVSLANCLSLTVLVNHNHVGDIK 540
QY 541 NNNFSRFPSPDFGNGSLGSMWNSPCHDSRRTVRVVISRAAIIIGAIIGLVLLAVLIA 600
DB 541 NNNFSRFPSPDFGNGSLGSMWNSPCHDSRRTVRVVISRAAIIIGAIIGLVLLAVLIA 600
QY 601 ACRPHNPPEPLDGLDKPVYVSTPKLVILHMMNALHYVEDIMMNTENLSEKYYIIGHGASS 660
DB 601 ACRPHNPPEPLDGLDKPVYVSTPKLVILHMMNALHYVEDIMMNTENLSEKYYIIGHGASS 660

```

Db 601 ACRPHNPPEFLDGLDKPVTYSTPKLVILHMNALHVEDIMMTENLSEKYYIIGHGASS 660  
QY 661 TVYKCVLKNCKPVAIKRLYSHPNPOSMKQFETELMSSIKHRNLVSLQAVSLHLSGLF 720  
Db 661 TVYKCVLKNCKPVAIKRLYSHPNPOSMKQFETELMSSIKHRNLVSLQAVSLHLSGLF 720  
QY 721 YDYLENGSLWDLHGPTKKKTLDMDTRLKIAYGAAQGLAYLHHDSPRIIHRDVKSNNIL 780  
Db 721 YDYLENGSLWDLHGPTKKKTLDMDTRLKIAYGAAQGLAYLHHDSPRIIHRDVKSNNIL 780  
QY 781 LDKDLEARLTDGFIAGSLCVSKSHSTYVNGTIGYIDPEYARTSRLTEKSDVSYGIVLL 840  
Db 781 LDKDLEARLTDGFIAGSLCVSKSHSTYVNGTIGYIDPEYARTSRLTEKSDVSYGIVLL 840  
QY 841 ELITRRKAVDDESNLHLIMSKTGNNEVMEADPDITSTCKDGLGVKKVQALALCTKRQ 900  
Db 841 ELITRRKAVDDESNLHLIMSKTGNNEVMEADPDITSTCKDGLGVKKVQALALCTKRQ 900  
QY 901 PNDRPTMHQVTRVLGFMLESEQPPAATDTSATLAGSCYDEYANLKTPHSVNCSMSASD 960  
Db 901 PNDRPTMHQVTRVLGFMLESEQPPAATDTSATLAGSCYDEYANLKTPHSVNCSMSASD 960  
QY 961 AOLFLREGQVISONSE 976  
Db 961 AOLFLREGQVISONSE 976

RESULT 4  
AED28149 standard; protein: 976 AA.  
ID AED28149;

DT 01-DEC-2005 (first entry)

XX Arabidopsis thaliana ERECTA protein.

XX Plant growth regulation; transgenic plant; crop improvement; ERECTA.

XX Arabidopsis thaliana.

PN US2005223428-A1.

PD 06-OCT-2005.

PF 30-DEC-2004; 2004US-00027304.

PR 01-APR-2004; 2004US-0558529P.

PA (TORI/) TORII K U.

PA (SHPA/) SHPAK E D.

PI Torii KU, Shpak ED;

XX WPI; 2005-675788/69.

DR N-PSDB; AED28148.

XX Modulating plant height and organ shape comprises expressing, in plants, a transgene encoding an ERECTA-like protein lacking an active kinase domain.

PT a transgene encoding an ERECTA-like protein lacking an active kinase domain.

XX Claim 3; SEQ ID NO 2; 722p; English.

CC The present invention relates to a method for modulating plant height and organ shape. The method involves expressing a transgene in a plant, where the transgene encodes an ERECTA-like protein lacking an active kinase domain and where expression of the transgene modulates plant height or organ shape. ERECTA protein contains leucine-rich repeat receptor-like kinase (LRR-RLK) with 20 consecutive leucine-rich repeats (LRR) and functional Ser/Thr kinase activity. The invention is useful for producing transgenic plant and for enhancing the yield of a crop plant. The present sequence is the Arabidopsis thaliana ERECTA protein.

SQ Sequence 976 AA:

Query Match 100.0%; Score 5043; DB 9; Length 976;  
Best Local Similarity 100.0%; Pred. No.0;  
Matches 976; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALFRDIYLLGFPLCSLVATVTSSEGAATLLEIKSKFKDVNNVLYDMTSSPSDDYCVWRG 60  
Db 1 MALFRDIYLLGFPLCSLVATVTSSEGAATLLEIKSKFKDVNNVLYDMTSSPSDDYCVWRG 60  
QY 61 VSCENYTFNNVALNLSLDNLMDGISPAIGDKSLSLSDLRGNLSGQIPREIDCSSLQV 120  
Db 61 VSCENYTFNNVALNLSLDNLMDGISPAIGDKSLSLSDLRGNLSGQIPREIDCSSLQV 120  
QY 121 LDLSFNLSDIDPFSSISKQLEQLILKNNQLGPIPSLTSQIPNLKILDLAONKLSGEI 180  
Db 121 LDLSFNLSDIDPFSSISKQLEQLILKNNQLGPIPSLTSQIPNLKILDLAONKLSGEI 180  
QY 181 PRLIYNEVLYGLKGNLVGNISPDLCQTLGMYFDVRNNSLTGSIPEITGNCTAFQV 240  
Db 181 PRLIYNEVLYGLKGNLVGNISPDLCQTLGMYFDVRNNSLTGSIPEITGNCTAFQV 240  
QY 241 LDLSYNQLTGEIPFDIGFLOVATLSIQGNLSGKIFSVIGMQLAVLDLSGNLSGSIP 300  
Db 241 LDLSYNQLTGEIPFDIGFLOVATLSIQGNLSGKIFSVIGMQLAVLDLSGNLSGSIP 300  
QY 301 PILGNLTFTFEKLYLHNSKLTGSIPEELGNMSKLYLELDNDNLTHIIPPELAGKLTDLFDL 360  
Db 301 PILGNLTFTFEKLYLHNSKLTGSIPEELGNMSKLYLELDNDNLTHIIPPELAGKLTDLFDL 360  
QY 361 NVANNDLEGPIDPHLSSCTNLNSLVNHNKFSCTIPRAQFLESMTYLNLSNNIKGPI 420  
Db 361 NVANNDLEGPIDPHLSSCTNLNSLVNHNKFSCTIPRAQFLESMTYLNLSNNIKGPI 420  
QY 421 VELSRIGNDLTDLNNKINGITPSSLDLEHLKNNLSNNHTGVVPDGGFLRSIMEI 480  
Db 421 VELSRIGNDLTDLNNKINGITPSSLDLEHLKNNLSNNHTGVVPDGGFLRSIMEI 480  
QY 481 DLSNNDISGPIPEELNQLQNIILRLNENNLGTNGVSLANCLSTVLYNSHNNLVGDIPK 540  
Db 481 DLSNNDISGPIPEELNQLQNIILRLNENNLGTNGVSLANCLSTVLYNSHNNLVGDIPK 540  
QY 541 NNNFSRSPDSFTGNPGLCGSWLNSPCHDSRTVRVVISRAAILGIALIGLVILLMVLIA 600  
Db 541 NNNFSRSPDSFTGNPGLCGSWLNSPCHDSRTVRVVISRAAILGIALIGLVILLMVLIA 600  
QY 601 ACRPHNPPEFLDGLDKPVTYSTPKLVILHMNALHVEDIMMTENLSEKYYIIGHGASS 660  
Db 601 ACRPHNPPEFLDGLDKPVTYSTPKLVILHMNALHVEDIMMTENLSEKYYIIGHGASS 660  
QY 661 TVYKCVLKNCKPVAIKRLYSHPNPOSMKQFETELMSSIKHRNLVSLQAVSLHLSGLF 720  
Db 661 TVYKCVLKNCKPVAIKRLYSHPNPOSMKQFETELMSSIKHRNLVSLQAVSLHLSGLF 720  
QY 721 YDYLENGSLWDLHGPTKKKTLDMDTRLKIAYGAAQGLAYLHHDSPRIIHRDVKSNNIL 780  
Db 721 YDYLENGSLWDLHGPTKKKTLDMDTRLKIAYGAAQGLAYLHHDSPRIIHRDVKSNNIL 780  
QY 781 LDKDLEARLTDGFIAGSLCVSKSHSTYVNGTIGYIDPEYARTSRLTEKSDVSYGIVLL 840  
Db 781 LDKDLEARLTDGFIAGSLCVSKSHSTYVNGTIGYIDPEYARTSRLTEKSDVSYGIVLL 840  
QY 841 ELITRRKAVDDESNLHLIMSKTGNNEVMEADPDITSTCKDGLGVKKVQALALCTKRQ 900  
Db 841 ELITRRKAVDDESNLHLIMSKTGNNEVMEADPDITSTCKDGLGVKKVQALALCTKRQ 900  
QY 901 PNDRPTMHQVTRVLGFMLESEQPPAATDTSATLAGSCYDEYANLKTPHSVNCSMSASD 960  
Db 901 PNDRPTMHQVTRVLGFMLESEQPPAATDTSATLAGSCYDEYANLKTPHSVNCSMSASD 960  
QY 961 AOLFLREGQVISONSE 976  
Db 961 AOLFLREGQVISONSE 976



XX	RESULT 5	
XX	ID ADX95769	
XX	ID ADX95769 standard; protein; 838 AA.	
XX	AC ADX95769;	
XX	DT 21-APR-2005 (first entry)	
XX	DE Plant full length insert polypeptide seqid 58433.	
XX	KM plant protectant; plant growth regulant; gene therapy; plant;	
XX	KM recombinant DNA construct; physical array; plant breeding marker;	
XX	KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;	
XX	KM extreme osmotic condition; pathogen tolerance; pest tolerance;	
XX	KM growth rate; cell cycle pathway; disease resistance;	
XX	KM galactomannan production; lignin production; plant growth regulator;	
XX	KM yield; plant growth; plant development; seed oil; protein yield;	
XX	KM protein content.	
XX	OS Unidentified.	
XX	PN US2004034888-A1.	
XX	XX	
XX	PD 19-FEB-2004.	
XX	PF 28-APR-2003; 2003US-00425114.	
XX	PR 06-MAY-1999; 98US-00304517.	
XX	PR 05-NOV-2001; 2001US-00985678.	
XX	PA (LNUJ/) LNU J.	
XX	PA (ZHOU/) ZHOU Y.	
XX	PA (KOVA/) KOVALIC D K.	
XX	PA (SCRE/) SCREEN S E.	
XX	PA (TABBA/) TABASKA J E.	
XX	PA (CAOY/) CAO Y.	
XX	PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;	
XX	DR WPI; 2004-180133/17.	
XX	PT New recombinant DNA construct, useful for improving plant tolerance to	
XX	PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or	
XX	PT pests, for conferring increased resistance to plant disease, or for	
XX	PT improving yield.	
XX	PS Claim 1; SEQ ID NO 58433; 15pp; English.	
XX	XX	
XX	XX The invention describes a recombinant DNA construct comprising a	
XX	XX polynucleotide consisting of a sequence encoding an amino acid sequence	
XX	XX available in electronic form from the US patent office at	
XX	XX ftp://seeddata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide	
XX	XX of the invention are also useful in physical arrays of molecules and as	
XX	XX plant breeding markers. The recombinant DNA construct is useful for	
XX	XX improving plant tolerance to cold, heat, drought, herbicides, extreme	
XX	XX osmotic conditions, pathogens or pests, for manipulating growth rate in	
XX	XX plant cells by modification of the cell cycle pathway, for conferring	
XX	XX increased resistance to plant disease, for producing galactomannan,	
XX	XX lignin or plant growth regulators, for increasing the rate of homologous	
XX	XX recombination in plants, for improving yield by modification of	
XX	XX photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake	
XX	XX or by providing improved plant growth and development under at least one	
XX	XX stress condition or for modifying seed oil or protein yield and/or	
XX	XX content. This is the amino acid sequence of a plant full length insert	
XX	XX polypeptide that can be used in the recombinant DNA construct of the	
XX	XX invention.	
XX	XX	
XX	XX Sequence 838 AA;	
XX	XX	
XX	Query Match 71.4%; Score 3602.5; DB 8; Length 838;	
XX	Best Local Similarity 82.0%; Ptd No. 4,1e-372;	

[illegible]

[illegible]

```

Db 402 DLSGNMTGPJBSISGSLEHLRLNLKNGVLGFIIPAFGNLRSWMEIDSYNHLGGILP 461
Qy 493 EELNQLQNIILRLENNLI.TGNVGLANCLSTVLNVSNNLVGDIPKNNESFSPDSF 552
Db 462 QLEMLQNI.LML.-----LNVSYNNLAGV.PADNNFTFSPDSF 498
Qy 553 IGNPG.CGSWMS.PCHDSRRYRVSISRPA.LIGLIGLVL.LWVL.LAACPHNPPFLD 612
Db 499 LGNPG.CGSWLSGSCSTGHNRKPPISKAA.IIGAVGVLV.LLMI.LVAVCPHR.PPAKD 556
Qy 613 GSDLDKPYTSTP.LVLHNMMALHYEDIMRTEBNLSKY.IIGHGASSTYKCVLKNCKP 672
Db 559 VYTSKRYRPA.RPCLV.LHNMMALHYDDIMKTEBNLSKY.IIGGASSTYKCVLKNCKP 618
Qy 673 VAIKRLYSHNPSOMKOFETELEMSSIKHRNLVSLQAVSLSHLSGL.FYDYLENGSLMDL 732
Db 619 VAIKRLYAHYPOSLKFEFETELETVSGIKHRNLVSLQGVSLSPVGNLL.FYDMEGCSLMDV 678
Qy 733 LH.GPRLKKT.LDWOTRLK.IAYGAAGLALY.LHDCSPRI.IIHDOVSSNN.LDPKLEARLTD 791
Db 679 LHGSSKKKKL.METELRL.IALGAAGLALY.LHDCSPRI.IIHDOVSSKN.LLDPKDEAHLTD 738
Qy 792 FGIAXSLCYSKASHTSYVMGTGYIDPEYARSLRTEKSDVY-----SYGVILLELLTRR 846
Db 739 FGIAXSLCYSKASHTSYVMGTGYIDPEYARSLRTEKSDVYRLMHCSAG----- 788
Qy 847 KAYDSSNN.LH.LIMS.KTGNNEVMEADPDITSTCDLGVNKKV.FQLALLCTKROPNDPRT 906
Db 789 -AADNDEBAGGRLS.ITASINEYMDVDPDIDIGTCDKDLGSVKLLQLALLCTKROPSPRPT 847
Qy 907 MHQVTRVLG.SFMLSQPP---AATDTSATLAGSCYDEYANL.KTPHVSNC--SSNSADAQ 962
Db 848 MHEVVRVLDOLVNPDP.PPKSAHQ.PQPSPAVPSYINEYVSLRGALSCANSTSTDAE 907
Qy 963 LFLRFGQVISONSE 976
Db 908 LFLKFGSAISONME 921

```

RESULT 7	ADJ49448
ID	ADJ49448 standard; protein; 921 AA.
XX	
AC	ADJ49448;
DT	06-MAY-2004 (first entry)
XX	
DE	Oil-associated gene related protein #948.
XX	
KW	oil-associated gene; transgenic; enhanced seed oil; vegetable oil
XX	
OS	Unidentified.
XX	
PN	US2004025202-A1.
XX	
PD	05-FEB-2004.
XX	
PF	14-MAR-2003; 2003US-00389566.
XX	
PR	15-MAR-2002; 2002US-0365301P.
PR	26-JUN-2002; 2002US-0391786P.
PR	26-JUN-2002; 2002US-0392018P.
XX	
PA	(LAUR/) LAURIE C C.
PA	(RAYA/) RAVANELLO M.
PA	(SAVA/) SAVAGE T.
PA	(LEDE/) LEDEAUX J R.
PA	(ROGE/) ROGERS J A.
XX	
PI	Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;
XX	
DR	WPI; 2004-142683/14.



QY 1 MALFRDVLGFLFCLSLVATVTSSEBGTLLLEIKKSKFDVANNVLYDWTSSPSDYCWMRG 60  
DB 1 MALFRDVLGFLFCLSLVATVTSSEBGTLLLEIKKSKFDVANNVLYDWTSSPSDYCWMRG 60  
QY 61 VSCENVTNNVVALNSDLNDGEISPAIGULKSLLSIDLRGNRLSGQIPPEIGDCSLON 120  
DB 61 VSCENVTNNVVALNSDLNDGEISPAIGULKSLLSIDLRGNRLSGQIPPEIGDCSLON 120  
QY 121 LDLSFNLGSDIPFSLSKQLBOLILKNNQLGPISTTSQIPNLKILDLAQKLSGEI 180  
DB 121 LDLSFNLGSDIPFSLSKQLBOLILKNNQLGPISTTSQIPNLKILDLAQKLSGEI 180  
QY 181 PRLIYNNVQVQYGLRGNNLVGNISPDLCQTLGMYFDVANNSTGSIPEITIGCTAFQV 240  
DB 181 PRLIYNNVQVQYGLRGNNLVGNISPDLCQTLGMYFDVANNSTGSIPEITIGCTAFQV 240  
QY 241 LDLSYNQLTGEIPFDIGFLOVATLSLOGNOLSGKIPSVIGLMQALAVLDLSGNLSSGIP 300  
DB 241 LDLSYNQLTGEIPFDIGFLOVATLSLOGNOLSGKIPSVIGLMQALAVLDLSGNLSSGIP 300  
QY 301 PILGNLTFTFKLYHNSKLTGSIPEELGNMSKLYLELNNHLTGHTPEELGKLTDLFDL 360  
DB 301 PILGNLTFTFKLYHNSKLTGSIPEELGNMSKLYLELNNHLTGHTPEELGKLTDLFDL 360  
QY 361 NVANNDEGPIPDHLSSTNLNSLVNHNKPSGTIPPAFQKLESMYLNLSNNIKGPI 420  
DB 361 NVANNDEGPIPDHLSSTNLNSLVNHNKPSGTIPPAFQKLESMYLNLSNNIKGPI 420  
QY 421 VELSRIGNLDTLDSNNKINGIIPSSIGDLLEHLKNNLSRNHITGVVPGFGNLRSMET 480  
DB 421 VELSRIGNLDTLDSNNKINGIIPSSIGDLLEHLKNNLSRNHITGVVPGFGNLRSMET 480  
QY 481 DLSNNDISGPIPEELNOLQNIILRLENNLTGVNGLANCLSTVYLVNHNHNVGDIPK 540  
DB 481 DLSNNDISGPIPEELNOLQNIILRLENNLTGVNGLANCLSTVYLVNHNHNVGDIPK 540  
QY 541 NNNFSRSPDSFICGNPGLCGSWLNSPCHDSRRIVRSISRPAIIGIIVILMLVLA 600  
DB 541 NNNFSRSPDSFICGNPGLCGSWLNSPCHDSRRIVRSISRPAIIGIIVILMLVLA 600  
QY 601 ACRPHNPFPFLDGS 614  
DB 601 ACRPHNPFPFLDGS 614

RESULT 9  
AD132616  
ID AD132616 standard; protein; 999 AA.  
AC AD132616;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Rice transpiration efficiency-related ERECTA protein.  
XX  
KW plant; transpiration efficiency; ERECTA; breeding; genetic engineering;  
XX rice; chromosome 6.  
XX  
OS *Oryza sativa*.  
XX  
PN WO2004005555-A1.  
PD 15-JAN-2004.  
PF 02-JUL-2003; 2003MO-AU000854.  
PR 02-JUL-2002; 2002AU-00003339.  
PA (AUSU) UNIV AUSTRALIAN NAT.  
PI Maule J, Farguham GD, Gilmore SR;  
XX  
XX

DR WPI; 2004-091390/09.  
DR N-PSDB; AD132615.  
XX  
PT Selecting plant having enhanced transpiration efficiency, useful for  
PT producing plant with enhanced transpiration efficiency comprising  
PT selecting plant expressing a genetic marker linked to the ERECTA locus in  
PT the genome of the plant.  
XX  
PS Claim 4; SEQ ID NO 4; 2099p; English.  
XX  
CC The invention relates to a novel method for selecting a plant having  
CC enhanced transpiration efficiency comprising detecting a genetic marker  
CC for transpiration efficiency, where the marker comprises a nucleotide  
CC sequence linked genetically to an ERECTA locus in the genome of the plant  
CC and selecting a plant that comprises or expresses the genetic marker. The  
CC method of the invention may be useful for selecting a plant having  
CC enhanced transpiration efficiency. The isolated ERECTA gene or allelic  
CC variant or protein-encoding region may be useful in the preparation of a  
CC genetic construct for modulating the transpiration efficiency of a plant.  
CC Furthermore, the ERECTA genes may be useful for producing plants having  
CC enhanced transpiration efficiency by both traditional plant breeding and  
CC genetic engineering approaches. The current sequence is that of the rice  
CC ERECTA protein of the invention which is encoded by DNA located on  
CC chromosome 6.  
XX  
SQ Sequence 999 AA;  
XX  
Query Match 61.7%; Score 3113; DB 8; Length 999;  
Best Local Similarity 63.1%; Pred. No. 9, 9e-234;  
Matches 618; Conservative 135; Mismatches 182; Indels 44; Gaps 9;  
QY 26 EGATLLEIKKSKFDVANNVLYDWTSSPSDYCWMRGVSCENVTNNVVALNSDLNDGEIS 85  
DB 35 EGKALMGVXKAGFMANALVDW--DGAADHACARGVTCDNASPAVALNLSNLTGSEIS 92  
QY 86 PAIGDLKSLSIDLRGNRLSGQIPPEIGDCSLONLDSFNLGSDIPFSLSKQLBOL 145  
DB 93 PAIGELKNLQFVLDKNNKLTGQIPDEIGDCISKLYVLDLGNLTYGQIPFSLSKQLBOL 152  
QY 146 ILKNNOLGPIPELSTQIPNLKILDLAQKLSGEIPRLIYNNVQVQYGLRGNNLVGNIS 205  
DB 153 ILKNNOLGPIPELSTQIPNLKILDLAQKLTGTDIRLRYNNVQVQYGLRGNSLTGTL 212  
QY 206 PDLCOPLGMYFDVNNNSLTGSIPEITIGCTAFQVLDLSYNQLTGEIPFDIGFLOVATLS 265  
DB 213 PDMCQLTGLMYFDVRGNLITGTIPESIGNCTSFPEIDISYNOISGPIVNIIGFLOVATLS 272  
QY 266 LOGNOLSGKIPSVIGLMQALAVLDLSGNLSSGIPILGNLTFTFKLYHNSKLTGSI 325  
DB 273 LOGNRLTGKIPDIVIGLMQALAVLDLSENELVGPPIPEILGNLSTYGLYHNSKLTGVI 332  
QY 326 ELGNMSKLYLELNDHNLTGHTPEELGKLTDLFDLVANNDEGPIPDHLSSTNLNSLN 385  
DB 333 ELGNMSKLYLQNDHNLVGTIPAEGLKLELELMLANNLOGPIPAISCTALNKN 392  
QY 386 VHGNNKPSGTIPPAFQKLESMYLNLSNNIKGPIPVELSRIGNLDTLDSNNKINGIIPS 445  
DB 393 VYGNKLNLSGIPAGFQKLESITLYLNLSNNFKGPIPEELGHIINLDTLDSYNEFGVPA 452  
QY 446 SLGDLLEHLKNNLSRNHITGVNGLANCLSTVYLVNHNHNVGDIPK 540  
DB 453 TIGDLLEHLKNNLSRNHITGVNGLANCLSTVYLVNHNHNVGDIPK 540  
QY 506 LNNNNLTGVN--GSLANCLSTVYLVNHNHNVGDIPK 550  
DB 513 LNNNNLTGVN--GSLANCLSTVYLVNHNHNVGDIPK 550  
QY 551 -----SFIGNPGLCGSMWNSPCHDSRRIVRSISRPAIIGIIVILMLV 598  
DB 566 ISDCNQYINHKCSFLNPNLHVYCDSSCGSHSQ--RVNISKTAIACIIIGFIILCVLL 624  
QY 599 IACRPHNPFPFLDGSIDKRVYVSTPKLYVILHNNMALHYVEDIMRTENISEKYYIIGGHA 658  
DB 599 IACRPHNPFPFLDGSIDKRVYVSTPKLYVILHNNMALHYVEDIMRTENISEKYYIIGGHA 658

Db 625 LAIYKTNQPOPLVKG-S-DKEPV-QGPPKLVVLQMDMAIHTYEDIMRLTENTLSEKTIIGYGA 682  
QY 659 SSTVYKCVLKNCKRVAIKRLYSHNPQSMKQFETELMSSIKRNLVSLQAYSLSHLSGL 718  
Db 683 SSTVYKCVLKNCKRVAIKRLYSHNPQSMKQFETELMSSIKRNLVSLQAYSLSHLSGL 742  
QY 719 LFPDYVLENGSLMDLHPTKKKTLDMPTRLKIAVGAQGLAYLHDCSPRIIHRDVYSSN 778  
Db 743 LFPDYVLENGSLMDLHPTKKKTLDMPTRLKIAVGAQGLAYLHDCSPRIIHRDVYSSN 802  
QY 779 ILDDKDLAARLTFGIAKSLCVSKSHSTYVMGTIGYIDEPARTSRLTEKSDVYSYGIY 838  
Db 803 ILDDENFEALSDPFGIAKCVPSAKSHASTYVLGTIGYIDEPARTSRLTEKSDVYSYGIY 862  
QY 839 LLELLRRKAVDDESNLHHLIMSKTGNNEVEMADPITSTCKDLGVYKVPFQALALCTK 898  
Db 863 LLELLRRKAVDDESNLHHLIMSKTGNNEVEMADPITSTCKDLGVYKVPFQALALCTK 922  
QY 899 ROPNDRPTMHQVTRVLSFPMLE--QPPATDTSATLAGSCYVDEVANLKTPHSVNCSM 956  
Db 923 RHPSDRPTMHQVTRVLSFPMLE--QPPATDTSATLAGSCYVDEVANLKTPHSVNCSM 979  
QY 957 SASDAQLFARFGVYISONS 975  
Db 980 SSDEQMFVRFGEVYSKHT 998  
RESULT 10  
ABB93915  
ID ABB93915 standard; protein; 966 AA.  
AC ABB93915;  
DT 31-MAY-2002 (first entry)  
DE Herbicidally active polypeptide SEQ ID NO 3126.  
XX Herbicidally active polypeptide SEQ ID NO 3126.  
XX Arabidopsis thaliana.  
XX WO200210210-A2.  
XX PD 07-FEB-2002.  
XX PF 28-AUG-2001; 2001WO-EP009892.  
XX PR 28-AUG-2001; 2001WO-EP009892.  
XX PA (FARB ) BAYER AG.  
XX PI Tietjen K, Weidler M;  
XX MPI; 2002-269010/31.  
XX PT Identifying plant target proteins for herbicidally active compounds,  
XX comprising aligning and comparing nucleic acid or amino acid sequences  
XX from plant with nucleic acid or amino acid sequences from non-plant  
XX organisms.  
PS Claim 5; SEQ ID NO 3126; 261pp + Sequence Listing; English.  
CC The invention relates to identifying target proteins (ABB90790-ABB94016)  
CC for herbicidally active compounds, comprising aligning and comparing  
CC nucleic acid or amino acid sequences from plant with nucleic acid or  
CC amino acid sequences from non-plant organisms using suitable search  
CC parameters, where plant sequences having an E-value greater by a factor  
CC of 3 than the E-value of most similar non-plant sequences are selected.  
CC The polypeptides or nucleic acids encoding them are useful for  
CC identifying modulators. The identified modulators are useful as  
CC herbicides  
XX  
SQ Sequence 966 AA;

Query Match 61.3%; Score 3091.5; DB 5; Length 966;  
Best Local Similarity 62.9%; Pred. No. 4.5e-232;  
Matches 610; Conservative 139; Mismatches 204; Indels 17; Gaps 6;  
QY 7 IVLGFELCLSLVATVSEBQATLLEIKKSPKVVNNVLYDMWTSPPSSDVCWVRGSCENV 66  
Db 12 LAMVGFN-VFGVASMNNNGKALMAIKSFSNLVNLMDMDVHNSDLCSWGVFCENV 69  
QY 67 TENVVALNSLDNLUDGEISPAIGDKSLSIDRGNRLSGQIPDEIGDCSSLQNLDSFN 126  
Db 70 SYGVSTINLSLNLGGEISPAIGDLRLNQSIDIQGNKLAQIPDEIGNCASLYVLDSEN 129  
QY 127 ELSGDIPFSISKLEQLIKNNOLIGPSTLSQIPNKIKIDLAKNKSIGEIPRIY 166  
Db 130 LLYGDIIPFSISKLEQLIKNNOLIGPSTLSQIPNKIKIDLAKNKSIGEIPRIY 189  
QY 187 NEVLYQVGLRGNLIVAGNISPDLCOLGLWYFDVRRNNSLTGSIPEITGNCTAFVLDLSYN 246  
Db 190 NEVLYQVGLRGNLIVAGNISPDLCOLGLWYFDVRRNNSLTGSIPEITGNCTAFVLDLSYN 249  
QY 247 QLTGEIPFDIGFQVATLSIQGNQSGKIPSVGLQALAVLDSGNLSGSIPIPIGLN 306  
Db 250 QLTGEIPYNIQVATLSIQGNRLTGRIPVIGLQALAVLDSGNLSGSIPIPIGLN 309  
QY 307 TFEKLYLHKNKLTGSIPELGNMSKLYLELDNHLTGHIPPELGLTDLFDLVANND 366  
Db 310 SFTGKLYLHGNMLTGPISPELGNMSKLYLELDNHLTGHIPPELGLTDLFDLVANND 369  
QY 367 LGGPIPDHLSCTNLNSLVNHNKFGSGTIPRAFOKESMTYLNLSNNIKGPIPEVLSRI 426  
Db 370 LVGPISGNISSCAALQFNHVGNLGSGTIPALFNLGSLTYLNLSNNFPGKIPEVLSRI 429  
QY 427 GNLDPLDLSNNKNGIIPSSLDGLEHLKNNLSRNHITGVVPGDFGRLBIMEIDLSND 486  
Db 430 INLDKLDLSGNNSGSIPLTGLDLEHLILNLSRNHISGOLPAFPGRLRSIQMIDVSNL 489  
QY 487 ISGPIPELNLQNLILRLNENNLGNV-GSLANCLSLVLNVSHNLTGVDPKXNNFS 545  
Db 490 LSGVITPELQOLNLSLILNKNKLGKIPDQNLNCTLVNLSVFNNSGCIYPMKNFS 549  
QY 546 RFPSPDSFTGNPGCGSLWNSPCHDSRTVAVSISRALIGLIGVILMLVLAACRPH 605  
Db 550 RFAPASFTVGNPIYCGWWSICGPIPKS-RV-FSRGALIGVIGVITLMLFVAYKSM 607  
QY 606 NPPFLDGLDKPVTYSTPKLVILHNNMALHYEDIMRMTENTSEKTIIGHGASSTYK 665  
Db 608 QOKKILOGSSKQ--AEGLTGLVILHMDMAIHTDDIMRVTEINENKEPIIGYGASSTYK 665  
QY 666 VLKNCKRVAIKRLYSHNPQSMKQFETELMSSIKRNLVSLQAYSLSHLSGLLFYYLE 725  
Db 666 ALKSSRPAIKRLYNOYPHNLREFETELTGISIRHNNVSLGVALSPGNNLFFDYME 725  
QY 726 NSGLMDLHPTKKKTLDMPTRLKIAVGAQGLAYLHDCSPRIIHRDVYSSNILLDKDL 785  
Db 726 NSGLMDLHPTKKKTLDMPTRLKIAVGAQGLAYLHDCSPRIIHRDVYSSNILLDKDL 785  
QY 786 EARLTPDGIKSLCVSKSHSTYVMGTIGYIDEPARTSRLTEKSDVYSYGIYVLELLTR 845  
Db 786 EARLTPDGIKSLCVSKSHSTYVMGTIGYIDEPARTSRLTEKSDVYSYGIYVLELLTR 845  
QY 846 RKAVDDESNLHHLIMSKTGNNEVEMADPITSTCKDLGVYKVPFQALALCTKROPDRP 905  
Db 846 RKAVDDESNLHHLIMSKTGNNEVEMADPITSTCKDLGVYKVPFQALALCTKROPDRP 905  
QY 906 TMHQVTRVLSFPMLEQPPATDTSATLAGSCYVDEVANLKTPHSVNCSMSASDAQFL 965  
Db 906 TMHQVTRVLSFPMLEQPPATDTSATLAGSCYVDEVANLKTPHSVNCSMSASDAQFL 965  
QY 966 RFGQVYISONS 975  
Db 966 RFGQVYISONS 975  
QY 956 QFREVISKSS 965  
Db 956 QFREVISKSS 965

```
RESULT 11
AD132622
ID AD132622 standard; protein: 966 AA.
AC
XX AD132622;
XX
DT 22-APR-2004 (first entry)
XX
DE Thale cress ERECTA homologue protein - SEQ ID 10.
XX
KW plant; transpiration efficiency; ERECTA; breeding; genetic engineering;
XX thale cress.
XX
OS Arabidopsis thaliana.
XX
PN W02004005555-A1.
XX
PD 15-JAN-2004.
XX
PF 02-JUL-2003; 2003MO-AU000854.
XX
PR 02-JUL-2002; 2002AU-00003339.
XX
PA (AUSU ) UNIV AUSTRALIAN NAT.
XX
PI Masle J, Farquhar GD, Gilmore SR;
XX
XX WPI, 2004-091390/09.
XX
DR N-PSDB; AD132621.
XX
PT Selecting plant having enhanced transpiration efficiency, useful for
XX producing plants with enhanced transcription efficiency comprising
XX PT selecting plants expressing a genetic marker linked to the ERECTA locus in
XX the genome of the plant.
XX
PS Claim 4; SEQ ID NO 10; 209pp; English.
XX
CC The invention relates to a novel method for selecting a plant having
XX enhanced transpiration efficiency comprising detecting a genetic marker
XX for transpiration efficiency, where the marker comprises a nucleotide
XX sequence linked genetically to an ERECTA locus in the genome of the plant
XX and selecting a plant that comprises or expresses the genetic marker. The
XX method of the invention may be useful for selecting a plant having
XX enhanced transpiration efficiency. The isolated ERECTA gene or allelic
XX variant or protein-encoding region may be useful in the preparation of a
XX genetic construct for modulating the transpiration efficiency of a plant.
XX Furthermore, the ERECTA genes may be useful for producing plants having
XX enhanced transcription efficiency by both traditional plant breeding and
XX genetic engineering approaches. The current sequence is that of the thale
XX cress ERECTA homologue protein of the invention.
XX
SQ Sequence 966 AA.
Query Match 61.3%; Score 3091.5; DB 8; Length 966;
Best Local Similarity 62.9%; Pred. No. 4.5e-232;
Matches 610; Conservative 139; Mismatches 204; Indels 17; Gaps 6;
QY 7 IVLLGFLFCISLVATYTSSEGATLLEIKSKFQVNNVLYWMTSPSSDVCVMRGVSCENV 66
DB 12 LAWVGFEM-VFGVASAMNNEGKALMAIKGSFSLVNNLMDWDVHNSDLCSMKGVCFCNV 69
QY 67 TFWVVALNLSLDNLNDEISPAIGDKLSLIDLRGNLSSGOIPDEIGDCSSLQNLDSFN 126
DB 70 SYVSVLSNLSSLDNGEISPAIGDKLRNLOSLDQSKLAQOIPDEISNCASLYLIDSEN 129
QY 127 ELSGDIPIFSISKUKQLEQLILKNNQLTGPIPTLSQIPNPKLIDLQNKLSGEIPLIYW 186
DB 130 LLYGDIPIFSISKUKQLEQLILKNNQLTGPIPTLSQIPNPKLIDLQNKLSGEIPLIYW 189
QY 187 NEVLOYLGLRGNNLVGNISPDLCQLTGLMYFDVRKNNLSLTSIPTENTCAFOYLDLSYN 246
DB 190 NEVLOYLGLRGNNLVGNISPDLCQLTGLMYFDVRKNNLSLTSIPTENTCAFOYLDLSYN 249
```

```
QY 247 QLTGEIPFDIGFQVAVTTLSSQGNQLSGKIPSVIGLQALAVLDLSGNLSSGIPILGNL 306
DB 250 QITGEIPYNGIFQVATLSSQGNRLTGRIPYVIGLQALAVLDLSGNLSSGIPILGNL 309
QY 307 TPTTEKLYLHNSKLTGSIPEELGMSKLYLLENDNLTGHIPEELGLTDLPLVANND 366
DB 310 SFTGKLYLHGNMLTGPISPELGNNRSYQLQNDNKLVTGIPPELGLTDLPLVANND 369
QY 367 LEEPIPDHLSGCCNLSLVNHNKPSGTIPAROKESMYLNLSSNNTGPIPEVLSRI 426
DB 370 LVGPISNLISSCALQFNVHNLSSGSIPLAFRLNLSGLTYLNLSSNFKGKIPVEIGHI 429
QY 427 GNLDTLDSNNKINGIIPSSIGDLEHLKKNLSRNHITGVVPGDFGLRISIMEIDLSND 486
DB 430 INLDKLDLSGNNFSGSIPLTGLDEHLILNLSRNHLSGLPAPAFGLRISIQMIDVSFNL 489
QY 487 ISGPPEELNQLNIIILRLNNTLGNV-GSLANCLSTVLNVSHNNLVGDIPIKNNFS 545
DB 490 LSGVIPLELQQLNLSLILNNKLGKIPDQLTNCFTLVNLVSNFNNLSGIVPPMKNFS 549
QY 546 RPSPDFIGNPGICGSMNSPCHDSRTVVSISRRAIIGIAGLVILLMVLIACRPH 605
DB 550 RFAPASVGNPVYLCGMVSGICGPLPKS-RV-FRGLALITVIGVITLTCMIFLAVYKSM 607
QY 606 NPPFLDGLSDKPEVTYTPKLVILHNMALHYEDIMRMTENLSEKXIIGHGASSTVYKC 665
DB 608 QOKKILQSSKQ--AGLTPLVLHMDMAHTFDIDIRVTENLNEKFIIOYGASSTVYKC 665
QY 666 VLKCKPVAIKRLYSHNPOSKOFTELEMLSSIKRNLVLSOAYSLSHLGSLFPDYLE 725
DB 666 ALKSSPIAIKRLYNOYPNHLREFELETERIGIRHRNIVLSLGYALSPTGNLLFYDME 725
QY 726 NSGLMPLLHGPTKKTLMDOTRLKIVGAAGLAVLHDCSPRIHRDVSSNILLDKOL 785
DB 726 NSGLMPLLHGSLKVKVLDWETRLKIVGAAGLAVLHDCSTPRIHRDSSNILLDENF 785
QY 786 EARLTDFIGIAKSLCVSKSHTSYVMGTIGYIDPEVARTSRLETKSDVSYGIVLELTR 845
DB 786 EHLSPGIAKSLPAKTHASTYVLGTIGYIDPEVARTSRINXKSDISYGVILLELTG 845
QY 846 RKAVDESNLHILIMSKTGNNEWEMADPITSTCDLGVYKVFQALALCTKROPNDP 905
DB 846 KKAVIDEAMHQLILSKADNTEAVEVDPEVTYCMDLGHIRTFQALALCTKRNPLEP 905
QY 906 TMOQTVRLGSFMLSOPPAATOTSATLAGSCVDEAVANKTSHSVSCSMASDAQFL 965
DB 906 TMEVSRVLSLVPISLQ-----VAKLPSLDHSTKLOENBEVNRNPDABAGWVF 955
QY 966 RFQOVISONS 975
DB 956 QFREVISKSS 965
RESULT 12
AED28155
ID AED28155 standard; protein: 967 AA.
XX
XX AED28155;
AC
XX 01-DEC-2005 (first entry)
XX
DE Arabidopsis thaliana ERECTA paralog, ERL2 protein.
XX
KW plant growth regulation; transgenic plant; crop improvement; ERL2.
XX
OS Arabidopsis thaliana.
XX
PN US2005223428-A1.
XX
PD 06-OCT-2005.
XX
PF 30-DEC-2004; 2004US-00027304.
```

XX 01-APR-2004; 2004US-0558529P.  
XX (TORI/) TORII K U.  
XX (SHPA/) SHPAK E D.  
XX Torii KU, Shpak ED;  
XX MPI: 2005-675788/69.  
XX N-PSDB; AED28154.  
PT Modulating plant height and organ shape comprises expressing, in plants,  
PT a transgene encoding an ERECTA-like protein lacking an active kinase  
PT domain.  
XX  
XX Claim 7; SEQ ID NO 8; 72pp; English.  
XX  
XX The present invention relates to a method for modulating plant height and  
XX organ shape. The method involves expressing a transgene in a plant, where  
XX the transgene encodes an ERECTA-like protein lacking an active kinase  
XX domain and where expression of the transgene modulates plant height or  
XX organ shape. ERECTA protein contains leucine-rich repeat receptor-like  
XX kinase (LRR-RLK) with 20 consecutive leucine-rich repeats (LRR) and  
XX functional Ser/Thr kinase activity. The invention is useful for producing  
XX transgenic plant and for enhancing the yield of a crop plant. The present  
XX sequence is the Arabidopsis thaliana ERECTA paralog, ERL2 protein.  
XX  
XX Sequence 967 AA;

Query Match 61.3%; Score 3089.5; DB 9; Length 967;  
Best Local Similarity 62.2%; Pred. No. 6.4e-232;  
Matches 605; Conservative 134; Mismatches 211; Indels 23; Gaps 6;

QY 11 GFLFCLSLV-----ATVSEBGLTLEIKSFKQVNNVLDVWTSPPSSDYCVARGVSC 63  
DB 9 GLFFCLGMVVFMLDGSVSPNNEGKALMAIKASFVAVNMMLDMVDVHNHDFCSMGVFC 68  
QY 64 ENVTFFVAVNLSDNLGDEISPAIGDLKSLISIDLRGNRLSGIDPDEIGDGLSGLNDL 123  
DB 69 DNVSLNVLNLSNLNLGDEISALDGLNMLSDIDQNGSLGQIDPDEIGNCVSLVYVD 128  
QY 124 SFNELSGDIPFSISKLEQLILKNNOLIGPISLTPSLQIPNLKIIDLAQNKLSGEIPRL 183  
DB 129 STNLFFGDIPIFSISKLEQLILKNNOLIGPISLTPSLQIPNLKIIDLAQNKLSGEIPRL 188  
QY 184 IYWNELVQLGLRGNLVGNISPDLCQLTGLWTFDVRNNSLTGSIPTGCTAFOYVLD 243  
DB 189 LYWNELVQLGLRGNLVGNISPDLCQLTGLWTFDVRNNSLTGSIPTGCTAFOYVLD 248  
QY 244 SYNOLGELIPDGLFOVATLSLQNGOLSGKISVIGLWQALVLDLGNLISGSPILL 303  
DB 249 STNQTIGVAPYNGIPIQVATLSLQNGOLSGKISVIGLWQALVLDLGNLISGSPILL 308  
QY 304 GNLTFTKELYSNKLKLGSIPELGNMSKLYLELDNHLTGAIPEELGTLTDLFOLANVA 363  
DB 309 GNLSFTGKLYHGNKLTGQIPPELGNMSRLSYQLNDNELVGTIPPELGLTDLFELINLA 368  
QY 364 NNDLBSGPIPDHLSCTNLNSLVNHNKFSCTIPRAFQKLESMTYLNLSNNIKGPIPEL 423  
DB 369 NNNLVGLIPSNISSCAALNQFNHGNFLSGAVLEFRNLGSLTYLNLSNSFGKIPAEEL 428  
QY 424 SRIGNLDTLDLNNKINGIIPSSLDGLEHLKNNLSRNHTGTVGVPDGFGLRIMEIDS 483  
DB 429 GHINIDTLDLGNNSGSPILTGLDLEHLILNLRNHLNGTLPAEFGNLSRIQIITIVS 488  
QY 484 NNDISGPIPEELNOLNIILRLNENNLGCV-GLSANCSTLVLVNVSNNLVDGPIPN 542  
DB 489 ENFLAIVITELQGLQNLINSLINNKKIKHCKIPDLQNGCSLANLINSFNNLSGIIIPMK 548  
QY 543 NTSRSPDSFTGNPGLCGSWLNSPCHDSRTTVSISRRAIIGLIGVILMLVLAAC 602  
DB 549 NTRRSPASFFGPNPFLCGWVNSICGSPSPKSGV-FTRVAVVICMVIGFILLICMIFIAV 607

QY 603 RPHNPPFDGSLDKPEVTSTPLVILHNMMLHVEDIMRMTENISEKYLIGHGASSTV 662  
DB 608 KSKQCKPVLKSGSKQP--EGSTKLVLHMDMAHTDIDIMRVTEINDEKYLIGHGASSTV 665  
QY 663 YKCVLKNCKPVALIKRLYSHNPQSMKQFETELMLSIKRNVLVSLOAYSLSHLGLLFPY 722  
DB 666 YKCTSKSRPIAIKRIYNOYPSNFRFETELLETIGSIRRNIVSLHGYALSPGNLLFPY 725  
QY 723 YLENGSLMDLHPPTKKTLMDPTRLKIAVGAQGLAYLHHDCPRTIHRDVSSNILLD 782  
DB 726 YLENGSLMDLHPGKKVLDWETRLKIAVGAQGLAYLHHDCPRTIHRDISSNILLD 785  
QY 783 KDLERLTDFGLAKSLCVSKSHTSTVMGTIGYIDEPYARTSLTKSPVSYGIVLLEL 842  
DB 786 GNFEARLSDFGIAKSLPATKTVASTVLTGIGYIDEPYARTSLTKSDDISYFGIVLLEL 845  
QY 843 LTRKAVDDESNLHLLIMSKTGNNEVMADPDITSTCKDLGVKKVFOALICTYRQPN 902  
DB 846 LTGKKAVDNEANLHQMLISKADNTVMEAVDAEVSVTGCMDSGHIKKTFQALALCTYRNP 905  
QY 903 DRPTMIOVTRVGLSFMLSQPPAATDTSATLASCYVDEYANLKTSHSVNCSMSASDAQ 962  
DB 906 ERPTMQEVSRRVLLSLVSPPPP-----KKLPSPARVOGEERRESHSDTTT-----PQ 953  
QY 963 LFLRFGOVISONS 975  
DB 954 WFOQFREDISKSS 966

RESULT 13  
AED28153  
ID AED28153 standard; protein; 966 AA.

XX AED28153;  
XX 01-DEC-2005 (first entry)  
XX  
XX Arabidopsis thaliana ERECTA paralog, ERL1 protein.  
XX  
XX Plant growth regulation; transgenic plant; crop improvement; ERL1.  
XX  
XX Arabidopsis thaliana.  
XX  
XX US2005223428-A1.  
XX  
XX 06-OCT-2005.  
XX  
XX 30-DEC-2004; 2004US-00027304.  
XX  
XX 01-APR-2004; 2004US-0558529P.  
XX  
XX (TORI/) TORII K U.  
XX (SHPA/) SHPAK E D.  
XX Torii KU, Shpak ED;  
XX MPI: 2005-675788/69.  
XX N-PSDB; AED28152.  
PT Modulating plant height and organ shape comprises expressing, in plants,  
PT a transgene encoding an ERECTA-like protein lacking an active kinase  
PT domain.  
XX  
XX Claim 5; SEQ ID NO 6; 72pp; English.  
XX  
XX The present invention relates to a method for modulating plant height and  
XX organ shape. The method involves expressing a transgene in a plant, where  
XX the transgene encodes an ERECTA-like protein lacking an active kinase  
XX domain and where expression of the transgene modulates plant height or  
XX organ shape. ERECTA protein contains leucine-rich repeat receptor-like  
XX kinase (LRR-RLK) with 20 consecutive leucine-rich repeats (LRR) and  
XX functional Ser/Thr kinase activity. The invention is useful for producing  
XX transgenic plant and for enhancing the yield of a crop plant. The present





Db 241 LTGRIPVEIGLMOALAVLDLSDNELTGPPIPIIGNLSTFGTKLYHGKMLTGQIPPELGNM 300  
Qy 331 SKLHYLELNDNHLTGHIPELGLKTLDFDLVANNDEGPDPHLSSTCTNLNSLNVGNK 390  
Db 301 SRLSYLQNDNELVGIPELGLKEQLFELTANNLVLGIPNSISSCALQPNVHGNF 360  
Qy 391 FSGTIPRAFOKLSMTYLNLSNNIKGPIPELSEIGNLDTLDSNNKINGIIPSSIGDL 450  
Db 361 LSGAVPLEFRNLGSLTYLNLSNFKGKIPALGHIINLDTLDSGNFSGSIPLTIGDL 420  
Qy 451 EHLKNNLSRNHTGVVPGDGFNLRSIMEIDLSNDSGPIPELNLQNLITLLRLENN 510  
Db 421 EHLILNLSRNHLNGTLPAEFGLRSIQIIDVSFNLGAVIPTELGLQNLINSLNNK 480  
Qy 511 LTGNV-GSLANCLSLTYLVNSHNNLVGDIKNNNSFRSPDSFGNGLGSMWNSPCHD 569  
Db 481 IHKIDQDLNCTSLANLNISFNLSGIIIPMKNTFRFSASFNGFLCGMWVGSICGP 540  
Qy 570 SRRTVVSISSRAIILGIAIGLVILMLVLIACRPHNPPELDGSLDKPYTSTPKLVIL 629  
Db 541 SLPKSQV-FTRVAVICMVLGFTILCMIFIAVYKSKQKQKVLKSSKQF--EGSTKLVL 597  
Qy 630 HNMALHYEDIMRMENLSSEKTIIGHGASTYKCYLKKCKVAIKRLYSHNPQSKQF 669  
Db 598 HMDMALHTDDIMRVENLDEKYLIGVASTYKCTSKTSRBIKRIYNOYPSNFRF 657  
Qy 690 ETELEMLSSIKHRLNLSLQAYSLSHGSLLFYDLENGSLMDLHGPTKKTLDMDTRLK 749  
Db 658 ETELELTGIRRHNIYSLHGYSALSPGNLLFYDMENGSLMDLHGPKKVKLDMETRLK 717  
Qy 750 IAYGAAQGLAYLHHDSPRIHRDVKSNILDLKDLKDLTDEGLAKSLCVSKSHSTYV 809  
Db 718 IAVGAQGLAYLHHDCTPRIHRDKSNILDLGNFEARLSDGLAKSIPATKYASTYV 777  
Qy 810 MGTIGYIDEVARTSLTERKSDYVSGIYVLELTLTKKAVDDSNLHMLMSTGNNEVA 869  
Db 778 LGTIGYIDEVARTSLTERKSDYVSGIYVLELTLTKKAVDDSNLHMLMSTGNNEVA 837  
Qy 870 ENADPITSTCKDLGVVKKVFOALCTCRQPNDRPTMHQVTRVLGSPMLSEOPPAATPT 929  
Db 838 EAVDAEVSTCTMDSGHIKKTFOALCTCRNPJERTMOEVSRLVLSLVSPPP----- 891  
Qy 930 SATLAGSCYVDEVANLCTPHSVNCSMSASDAQLFARFGQVISQNS 975  
Db 892 -KTLSPAKVQGEERRESHSDTT-----PQWVQFREDISKSS 931

RESULT 15  
AD132620  
ID AD132620 standard; protein, 932 AA.  
XX  
AC AD132620;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Thale cress ERECTA homologue protein - SEQ ID 8.  
XX  
KM plant; transpiration efficiency; ERECTA; breeding; genetic engineering;  
XX  
KM thale cress.  
XX  
OS Arabidopsis thaliana.  
XX  
OS  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 112..129  
FT /note= "Encoded by CTGACC"  
XX  
PN WO2004005555-A1.  
XX  
PD 15-JAN-2004.  
XX  
PF 02-JUL-2003; 2003WO-AU000854.  
XX  
PR 02-JUL-2002; 2002AU-00003339.

XX (AUSU ) UNIV AUSTRALIAN NAT.  
PA Masle J, Farguher GD, Gilmore SR;  
XX WPI; 2004-091390/09.  
DR N-PSDB; AD132619.  
DR  
XX  
PT Selecting plant having enhanced transpiration efficiency, useful for  
PT producing plants with enhanced transcription efficiency comprising  
PT selecting plant expressing a genetic marker linked to the ERECTA locus in  
PT the genome of the plant.  
XX  
PS Claim 4; SEQ ID NO 8; 209pp; English.  
XX  
XX The invention relates to a novel method for selecting a plant having  
CC enhanced transpiration efficiency comprising detecting a genetic marker  
CC for transpiration efficiency, where the marker comprises a nucleotide  
CC sequence linked genetically to an ERECTA locus in the genome of the plant  
CC and selecting a plant that comprises or expresses the genetic marker. The  
CC method of the invention may be useful for selecting a plant having  
CC enhanced transpiration efficiency. The isolated ERECTA gene or allelic  
CC variant or protein-encoding region may be useful in the preparation of a  
CC genetic construct for modulating the transpiration efficiency of a plant.  
CC Furthermore, the ERECTA genes may be useful for producing plants having  
CC enhanced transcription efficiency by both traditional plant breeding and  
CC genetic engineering approaches. The current sequence is that of the thale  
CC cress ERECTA homologue protein of the invention.  
XX  
SQ Sequence 932 AA;  
XX  
Query Match 60.7%; Score 3059; DB 8; Length 932;  
Best Local Similarity 63.1%; Pred No 1.5e-229;  
Matches 597; Conservative 131; Mismatches 202; Indels 16; Gaps 5;  
Qy 31 LBKKSFKDNNVLYDMWTPSSDYCVWRGVCENTFNVVALNLSDLMDGERISPAIGD 90  
Db 1 MAIKASFNVAMLLDMWDVHHDFCSMRGVFCNDVSLNVLSNLNLGESSALGD 60  
Qy 91 LKSLSLIDRGNRLSQIIDEIGDSSLONLDSFNELSGDIPEFSISKOLFOULKON 150  
Db 61 LNNLSIDIDQGNKLGQIDPEIGENCVSILAVDFSTLLRGDIPFISIKLQLEFLMKON 120  
Qy 151 QIIGPIPTLSQIIPNLIKIDLAONKLSGEIPRLIWNELVQYLGKGNLJGNSIDLCQ 210  
Db 121 QLTGPIPATLTQIPNLIKIDLAONKLSGEIPRLIWNELVQYLGKGNLJGNSIDLCQ 180  
Qy 211 LTGLWYFDVRNNSLNGSIPETIGNCTAFQVLDLSYNQLTGEIIPDIFGFOVATLSIQNQ 270  
Db 181 LTGLWYFDVRGNNLTGTIPESIGNCTSFELDVSYNQITGVIPYNGFQVATLSIQNQ 240  
Qy 271 LSGKIPSVIGLMOALAVLDLSDNLSSGSIPIPLGNLTFTKLYLHNSKLTGSIPELGNM 330  
Db 241 LTGRIPVEIGLMOALAVLDLSDNELTGPPIPIGNLSFGKLYLHGKMLTGQIPPELGNM 300  
Qy 331 SKLHYLELNDNHLTGHIPELGLKTLDFDLVANNDEGPDPHLSSTCTNLNSLNVGNK 390  
Db 301 SRLSYLQNDNELVGIPELGLKEQLFELTANNLVLGIPNSISSCALQPNVHGNF 360  
Qy 391 FSGTIPRAFOKLSMTYLNLSNNIKGPIPELSEIGNLDTLDSNNKINGIIPSSIGDL 450  
Db 361 LSGAVPLEFRNLGSLTYLNLSNFKGKIPALGHIINLDTLDSGNFSGSIPLTIGDL 420  
Qy 451 EHLKNNLSRNHTGVVPGDGFNLRSIMEIDLSNDSGPIPELNLQNLITLLRLENN 510  
Db 421 EHLILNLSRNHLNGTLPAEFGLRSIQIIDVSFNLGAVIPTELGLQNLINSLNNK 480  
Qy 511 LTGNV-GSLANCLSLTYLVNSHNNLVGDIKNNNSFRSPDSFGNGLGSMWNSPCHD 569  
Db 481 IHKIDQDLNCTSLANLNISFNLSGIIIPMKNTFRFSASFNGFLCGMWVGSICGP 540  
Qy 570 SRRTVVSISSRAIILGIAIGLVILMLVLIACRPHNPPELDGSLDKPYTSTPKLVIL 629

```
Db 541 SLPKSQV-FTRVAVICMVLGFTILICMIFIAVVKSKQKPEVLKSSKQP--EGSTKLVL 597
QY 630 HMMALHYVEDIMRMENISEKYIIGHGASSTVYKCVLKNCKRPATKRLYSHNPQSMKOF 689
Db 598 HMDMAIHTFDIDMRVTENLDEKYYIGGASSTVYKCTSKTSRPIAKRIYNQYPSNREF 657
QY 690 ETELEMSSIKHNLVSLQAVSLSHLSLLFYDYLENGSLMDLLHGPTKKKTLMDWTRLK 749
Db 658 ETELETIGSIRHRNIVSLHGVALSPFGNLLFYDYMENGLMDLLHGPGKKVXKLDWETRLK 717
QY 750 IAVGAAQGLAYLHHDSPRIIHRDVKSSNILLDKLEARLTDPGIAKSLCVSKSHSTYV 809
Db 718 IAVGAAQGLAYLHHDCTPRIIHRDIKSSNILLDGNFEARLSDFGIAKSIPIATKYASTYV 777
QY 810 MGTIGYIDPEYARTSRTEKSDVYSGIVLLELTRKAVDDESNLHLLMSKTGNNEVM 869
Db 778 LGTIGYIDPEYARTSRLENKSDIYSFGIVLELLTGKAVDNEANLHOMILSKADDNTVM 837
QY 870 EMADPDITSTCKDLGVVKVFOALALCTKRQPNDRPTMHQVTRVLGSFMLSEOPPATDT 929
Db 838 EAVDAEVSVCMDSGHIKKTFOALALCTKGNPLERPTMQEVSRLVLSLVPSPPP----- 891
QY 930 SATLAGSCYVDEVYANLKTPHSVNCSSMSASDAQLEFRFGVISON 975
Db 892 -KKLPSPAKVQEGEERRESHSDTT-----PQWFVQFREDISKSS 931
```

Search completed: September 2, 2006, 06:50:45  
Job time : 205 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OW protein - protein search, using sw model

Run on: September 2, 2006, 06:58:10 ; Search time 37 Seconds  
(without alignments)  
1816.756 Million cell updates/sec

Title: US-10-519-135-2  
Perfect score: 5043  
Sequence: 1 MALFRDIVLGFCLSLVA.....SASDAQLFRRGQVIGSONSE 976

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 250042 seqs, 68872936 residues

Total number of hits satisfying chosen parameters: 250042

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_New:\*

- 1: /EMC\_Celerra\_SIDS3/prodata/1/pubppaa/US09\_NEW\_PUB pep.\*
- 2: /EMC\_Celerra\_SIDS3/prodata/1/pubppaa/US06\_NEW\_PUB pep.\*
- 3: /EMC\_Celerra\_SIDS3/prodata/1/pubppaa/US07\_NEW\_PUB pep.\*
- 4: /EMC\_Celerra\_SIDS3/prodata/1/pubppaa/US08\_NEW\_PUB pep.\*
- 5: /EMC\_Celerra\_SIDS3/prodata/1/pubppaa/PCT\_NEW\_PUB pep.\*
- 6: /EMC\_Celerra\_SIDS3/prodata/1/pubppaa/US10\_NEW\_PUB pep.\*
- 7: /EMC\_Celerra\_SIDS3/prodata/1/pubppaa/US11\_NEW\_PUB pep.\*
- 8: /EMC\_Celerra\_SIDS3/prodata/1/pubppaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5043	100.0	976	6 US-10-519-135-2	Sequence 2, Appl1
2	5043	100.0	976	7 US-11-056-355B-46416	Sequence 46416, A
3	5043	100.0	976	7 US-11-056-355B-48175	Sequence 48175, A
4	3606	71.5	695	7 US-11-056-355B-46417	Sequence 46417, A
5	3606	71.5	695	7 US-11-056-355B-48176	Sequence 48176, A
6	3372.5	66.9	921	6 US-10-519-135-6	Sequence 6, Appl1
7	3364	66.7	647	7 US-11-056-355B-46418	Sequence 46418, A
8	3364	66.7	647	7 US-11-056-355B-48177	Sequence 48177, A
9	3113	61.7	999	6 US-10-519-135-4	Sequence 4, Appl1
10	3091.5	61.3	966	6 US-10-519-135-10	Sequence 10, Appl1
11	3059	60.7	932	6 US-10-519-135-8	Sequence 8, Appl1
12	2505.5	49.7	671	6 US-10-449-902-52071	Sequence 52071, A
13	2482	49.2	671	6 US-10-519-135-45	Sequence 45, Appl1
14	2247.5	44.6	550	6 US-10-953-349-22717	Sequence 22717, A
15	2055.5	40.8	504	6 US-10-953-349-22718	Sequence 22718, A
16	1966.5	39.0	481	6 US-10-953-349-22719	Sequence 22719, A
17	1446	28.7	1109	7 US-11-330-403-3817	Sequence 3817, Ap
18	1445	28.7	1210	7 US-11-056-355B-88228	Sequence 88228, A
19	1445	28.7	1210	7 US-11-056-355B-91984	Sequence 91984, A
20	1445	28.7	1252	7 US-11-056-355B-44895	Sequence 44895, A
21	1441	28.6	1109	7 US-11-330-403-9397	Sequence 9397, Ap
22	1421.5	28.2	985	7 US-11-056-355B-86230	Sequence 86230, A
23	1421.5	28.2	985	7 US-11-056-355B-91986	Sequence 91986, A
24	1421.5	28.2	1040	7 US-11-056-355B-88229	Sequence 88229, A
25	1421.5	28.2	1040	7 US-11-056-355B-91985	Sequence 91985, A

26	1417.5	28.1	448	6 US-10-519-135-20	Sequence 20, Appl1
27	1416.5	28.1	1046	7 US-11-056-355B-79289	Sequence 79289, A
28	1413	28.0	1081	7 US-11-056-355B-44896	Sequence 44896, A
29	1410.5	28.0	1003	7 US-11-056-355B-50497	Sequence 50497, A
30	1409	27.9	1072	6 US-10-449-902-53937	Sequence 53937, A
31	1405.5	27.9	1003	7 US-11-056-355B-48695	Sequence 48695, A
32	1401	27.8	1012	6 US-10-953-349-13624	Sequence 13624, A
33	1401	27.8	1025	6 US-10-953-349-13623	Sequence 13623, A
34	1397.5	27.7	1123	6 US-10-449-902-30892	Sequence 30892, A
35	1397	27.7	1123	6 US-10-953-349-4749	Sequence 4749, Ap
36	1380	27.4	942	7 US-11-056-355B-44897	Sequence 44897, A
37	1368.5	27.1	1002	7 US-11-056-355B-50734	Sequence 50734, A
38	1365.5	27.1	1192	7 US-11-056-355B-46297	Sequence 46297, A
39	1363.5	27.0	1040	6 US-10-449-902-41369	Sequence 41369, A
40	1354	26.8	386	7 US-11-056-355B-4049	Sequence 4049, Ap
41	1352.5	26.8	1041	7 US-11-056-355B-96010	Sequence 96010, A
42	1351.5	26.8	910	7 US-11-056-355B-79291	Sequence 79291, A
43	1351.5	26.8	970	7 US-11-056-355B-79290	Sequence 79290, A
44	1343	26.6	987	6 US-10-953-349-12072	Sequence 12072, A
45	1338.5	26.5	1000	7 US-11-056-355B-46298	Sequence 46298, A

ALIGNMENTS

RESULT 1  
US-10-519-135-2  
Sequence 2, Application US/10519135  
Publication No. US20060137041A1  
GENERAL INFORMATION:  
APPLICANT: The Australian National University  
TITLE OF INVENTION: METHOD OF PRODUCING PLANTS HAVING ENHANCED TRANSPIRATION EFFICIENT  
FILE REFERENCE: 94948/MRO  
CURRENT APPLICATION NUMBER: US/10/519,135  
CURRENT FILING DATE: 2004-12-22  
PRIOR APPLICATION NUMBER: AU P53339  
PRIOR FILING DATE: 2002-07-02  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 976  
TYPE: PRT  
ORGANISM: Arabidopsis thaliana ERECTA allele  
US-10-519-135-2

Query Match 100.0%; Score 5043; DB 6; Length 976;  
Best Local Similarity 100.0%; Pred. No. 1.4e-218;  
Matches 976; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MALFRDIVLGFCLSLVATVTSSEGAATLLETKSKFKVNNVLYMTTSPSSDYCYWRG	60
DB	1	MALFRDIVLGFCLSLVATVTSSEGAATLLETKSKFKVNNVLYMTTSPSSDYCYWRG	60
QY	61	VSCENYTFNVVALNLSDLNMDGEISPAIGDKLSLSDIRGNRLSGOIPPEIGDCSSLO	120
DB	61	VSCENYTFNVVALNLSDLNMDGEISPAIGDKLSLSDIRGNRLSGOIPPEIGDCSSLO	120
QY	121	LDLSFNEISGDIIPFSISKUOLEQLILKNNOIGIPSTLSQIPNLKIIDLAONKLSGEI	180
DB	121	LDLSFNEISGDIIPFSISKUOLEQLILKNNOIGIPSTLSQIPNLKIIDLAONKLSGEI	180
QY	181	PRLIYNEVLQYIGLGNLNVGNISDLQOLGLMFWFDRNNSLTGSIPTTGNCTAFQV	240
DB	181	PRLIYNEVLQYIGLGNLNVGNISDLQOLGLMFWFDRNNSLTGSIPTTGNCTAFQV	240
QY	241	LDLSYNQOLGGEIPFDIGFLOVATLSLQGNOLSGKISVGLMOALAVLDSGLNLSGISP	300
DB	241	LDLSYNQOLGGEIPFDIGFLOVATLSLQGNOLSGKISVGLMOALAVLDSGLNLSGISP	300
QY	301	PLTGNLTTEKLYLHNSKNLTGSIPELGNMSKLYHLELNDNHLTGHIPELGLKLTDLFDL	360
DB	301	PLTGNLTTEKLYLHNSKNLTGSIPELGNMSKLYHLELNDNHLTGHIPELGLKLTDLFDL	360

QY	361	AVANNDLGCPIDHLSCTNLNSLVNHGKPKFGSTIPRAFOKLESMYYLNLSSNNIKGP	420
Db	361	NVANNDLGCPIDHLSCTNLNSLVNHGKPKFGSTIPRAFOKLESMYYLNLSSNNIKGP	420
QY	421	VELSRTGNLDITDLSNNKNGIIIPSLGDL EHLKKNLNRNHTTGVVPGDFGNLSIMEI	480
Db	421	VELSRTGNLDITDLSNNKNGIIIPSLGDL EHLKKNLNRNHTTGVVPGDFGNLSIMEI	480
QY	481	DLSSNDISGPIPEELNQLNIILLRLENNLTGVNSSLANGSLCTVYLVNSHNLVGDIPK	540
Db	481	DLSSNDISGPIPEELNQLNIILLRLENNLTGVNSSLANGSLCTVYLVNSHNLVGDIPK	540
QY	541	NNNFRSPDSTIGNPGLCGSMWNSPCCHDSRRTVRVSISPAALIGLIGLVILLAVLIA	600
Db	541	NNNFRSPDSTIGNPGLCGSMWNSPCCHDSRRTVRVSISPAALIGLIGLVILLAVLIA	600
QY	601	ACRPHNPPEFLDGLDKPVYTSPTPKVLILHMNALHYEDIMMTENLSEKYLIIHGASS	660
Db	601	ACRPHNPPEFLDGLDKPVYTSPTPKVLILHMNALHYEDIMMTENLSEKYLIIHGASS	660
QY	661	TVYKCVLKNCKRVAIKRLYSANHPQSKQFETELMLSTIKHNLVSLQAYSLSHLGSLF	720
Db	661	TVYKCVLKNCKRVAIKRLYSANHPQSKQFETELMLSTIKHNLVSLQAYSLSHLGSLF	720
QY	721	YDLENGSLMDDLHGFTKKKTLDMDRLKLIAYGAAGOLVLIHHDSPRIIHRDVKSSNL	780
Db	721	YDLENGSLMDDLHGFTKKKTLDMDRLKLIAYGAAGOLVLIHHDSPRIIHRDVKSSNL	780
QY	781	LDKDLEARLTDFGIAGKSLCIVSKSHSTYYMGITGYIDPEVARTSRLTESKDVSYGIVLL	840
Db	781	LDKDLEARLTDFGIAGKSLCIVSKSHSTYYMGITGYIDPEVARTSRLTESKDVSYGIVLL	840
QY	841	ELTERRKAVDDSSNLHLLIMSKTGNNWEMADPDITSTCKDGVVKKVQQLALLCTKRQ	900
Db	841	ELTERRKAVDDSSNLHLLIMSKTGNNWEMADPDITSTCKDGVVKKVQQLALLCTKRQ	900
QY	901	PMDRPTMHQVTVLGSFMLSQEPAPATDTSATLAGSCYUDEYANLKTPHSVNCSMSASD	960
Db	901	PMDRPTMHQVTVLGSFMLSQEPAPATDTSATLAGSCYUDEYANLKTPHSVNCSMSASD	960
QY	961	AQLFLRFGQVISONSE 976	
Db	961	AQLFLRFGQVISONSE 976	
RESULT 2			
US-11-056-355B-46416			
; Sequence 46416, Application US/11056355B			
; Publication No. US20060150283A1			
; GENERAL INFORMATION:			
; APPLICANT: Brover, Vyacheslav			
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding			
; FILE REFERENCE: 2750-1590P02			
; CURRENT APPLICATION NUMBER: US/11/056,355B			
; CURRENT FILING DATE: 2005-02-14			
; PRIOR APPLICATION NUMBER: 60/544,190			
; PRIOR FILING DATE: 2004-02-13			
; NUMBER OF SEQ ID NOS: 119966			
; SEQ ID NO 46416			
; LENGTH: 976			
; TYPE: pct			
; ORGANISM: Arabidopsis thaliana			
; FEATURE:			
; NAME/KEY: peptide			
; LOCATION: (1)..(976)			
; OTHER INFORMATION: Ceres Seq. ID no. 13578686			
US-11-056-355B-46416			

Query Match	100.0%;	Score 5043;	DB 7;	Length 976;
Best Local Similarity	100.0%;	Pred. No. 1.4e-218;		

Matches 976; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MALPFDVILGFLCFLSLVATVTSSEKATLEIKKSPCDVANNVYDMMTPSSSDYCWRG	60
Db	1	MALPFDVILGFLCFLSLVATVTSSEKATLEIKKSPCDVANNVYDMMTPSSSDYCWRG	60
QY	61	VSCENVTENNVALNLSIDLNDGEISPAIGDLKSLSLDLGRNLSGQIPDEIGDCSSLON	120
Db	61	VSCENVTENNVALNLSIDLNDGEISPAIGDLKSLSLDLGRNLSGQIPDEIGDCSSLON	120
QY	121	LDLSFNEISGQIPPSISKLOEOLILKNNOLIGIPSTLSQIPPLKTLDLAONKLSGEI	180
Db	121	LDLSFNEISGQIPPSISKLOEOLILKNNOLIGIPSTLSQIPPLKTLDLAONKLSGEI	180
QY	181	PRLIYMWNEVLQYLGKGNLVGNISPDLCQITGLMYFDVRNNSLTGSIPETIGNCTAFQV	240
Db	181	PRLIYMWNEVLQYLGKGNLVGNISPDLCQITGLMYFDVRNNSLTGSIPETIGNCTAFQV	240
QY	241	LDLSVNOULTGPIPPGIFLOVATLISLONOISGKPSYIGMOALAVLDSLGNLISGSIIP	300
Db	241	LDLSVNOULTGPIPPGIFLOVATLISLONOISGKPSYIGMOALAVLDSLGNLISGSIIP	300
QY	301	PILGNLTETKELYLHNSNLTGSIIPPELGNMKSCLHYLELNDMLTGHIPPELGKLTDLFDL	360
Db	301	PILGNLTETKELYLHNSNLTGSIIPPELGNMKSCLHYLELNDMLTGHIPPELGKLTDLFDL	360
QY	361	NVANNDEGSIIPDLHSSCTNLSNLNVHKNKSGTIPRAFOKLESMTYLNLSNNIKGPIIP	420
Db	361	NVANNDEGSIIPDLHSSCTNLSNLNVHKNKSGTIPRAFOKLESMTYLNLSNNIKGPIIP	420
QY	421	VELSRIGNLDITLDSNNKINGIIPESLGDLEHLKMNLSRNHITGVVPGDFGNLSIMEI	480
Db	421	VELSRIGNLDITLDSNNKINGIIPESLGDLEHLKMNLSRNHITGVVPGDFGNLSIMEI	480
QY	481	DLSSNDISGPIPEELNLOQNTILRLKENNNLTGVNCSLANCLSLVLNVSHNNLVGDIIPK	540
Db	481	DLSSNDISGPIPEELNLOQNTILRLKENNNLTGVNCSLANCLSLVLNVSHNNLVGDIIPK	540
QY	541	NNNFSRSPDSFTIGNPGLCGSWLNSPCHDSRRTVVSISRAALIGIALIGVILMLVILIA	600
Db	541	NNNFSRSPDSFTIGNPGLCGSWLNSPCHDSRRTVVSISRAALIGIALIGVILMLVILIA	600
QY	601	ACRPNNPPFLDGSIDKPYTYSTPCLVILHNMMLAHVEDIIRMTENISEKTIIGHGASS	660
Db	601	ACRPNNPPFLDGSIDKPYTYSTPCLVILHNMMLAHVEDIIRMTENISEKTIIGHGASS	660
QY	661	TYVKKVCLNCKNPVAKRLYSHNPQSMKQFTELEWLTSSIKRNLVSLQAYSLSHLGSILF	720
Db	661	TYVKKVCLNCKNPVAKRLYSHNPQSMKQFTELEWLTSSIKRNLVSLQAYSLSHLGSILF	720
QY	721	YDYLENGSLMDLHGPIPKKTLIDMDTRLKIAYGAAGLAIYLHDDCSPRIIHDVYSSNLT	780
Db	721	YDYLENGSLMDLHGPIPKKTLIDMDTRLKIAYGAAGLAIYLHDDCSPRIIHDVYSSNLT	780
QY	781	LDKDLKALTFBGIAKSLCVSKSHSTYVMGTYIGYIDEPYARTSLTEKSDVYSYGVILL	840
Db	781	LDKDLKALTFBGIAKSLCVSKSHSTYVMGTYIGYIDEPYARTSLTEKSDVYSYGVILL	840
QY	841	ELLTRRKAVDDESNIHLHLSKTNNEVEMADPDITSTCKDLGVKKYFQALALICTKQ	900
Db	841	ELLTRRKAVDDESNIHLHLSKTNNEVEMADPDITSTCKDLGVKKYFQALALICTKQ	900
QY	901	PNDRTMHOVTRVGSFMLSSEOPPAATDTSATLASSCVDEYANLKTPHSVNCSMSASD	960
Db	901	PNDRTMHOVTRVGSFMLSSEOPPAATDTSATLASSCVDEYANLKTPHSVNCSMSASD	960
QY	961	AOLFLRFQOVISONSE 976	
Db	961	AOLFLRFQOVISONSE 976	

RESULT 3  
US-11-056-355B-48175

; Sequence 48175, Application US/11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nikolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; FILE OF INVENTION: Polyptides Encoded Thereby  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 48175  
; LENGTH: 976  
; TYPE: prt  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(976)  
; OTHER INFORMATION: Ceres Seq. ID no. 13578686  
US-11-056-355B-48175

Query Match 100.0%; Score 5043; DB 7; Length 976;  
Best Local Similarity 100.0%; Pred. No. 1.4e-218;  
Matches 976; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALFRIVLGFICLSLVATVYTSSECATLLETKSKSKDVNNVLYDMTTPSSDYCYWRG 60  
DB 1 MALFRIVLGFICLSLVATVYTSSECATLLETKSKSKDVNNVLYDMTTPSSDYCYWRG 60  
QY 61 VSCENTFNVVALNLSDLNDEGISPAIGDKSLSLDLKGNRLSGOIPPEIGDCSLON 120  
DB 61 VSCENTFNVVALNLSDLNDEGISPAIGDKSLSLDLKGNRLSGOIPPEIGDCSLON 120  
QY 121 LDISFNEISGDIPIFSISKLEQLEQILKNNQLIGIPSTLSQIPNLKIIDLAKNLSGET 180  
DB 121 LDISFNEISGDIPIFSISKLEQLEQILKNNQLIGIPSTLSQIPNLKIIDLAKNLSGET 180  
QY 181 PRLIYNEVLYQVGLGNNLVGNISPDLCQTLGWYDVNNLSLTSIPTTGNCTAFQV 240  
DB 181 PRLIYNEVLYQVGLGNNLVGNISPDLCQTLGWYDVNNLSLTSIPTTGNCTAFQV 240  
QY 241 LDISYNQLTGEIPFDIGFLOVATLSLOGNLSGKIPSVIGLMOALAVLDSGNLSSGIP 300  
DB 241 LDISYNQLTGEIPFDIGFLOVATLSLOGNLSGKIPSVIGLMOALAVLDSGNLSSGIP 300  
QY 301 PILGNLTFEKLYLHNSKLTGSIPELGNMSKLYLELNDNHLTGHIPELGLKLTDLFDL 360  
DB 301 PILGNLTFEKLYLHNSKLTGSIPELGNMSKLYLELNDNHLTGHIPELGLKLTDLFDL 360  
QY 361 NVANNLEGP1PHLSSCTNLNSLVNHNKFSGTTIPPAFOKLESMTYLANSSNNIKGP1P 420  
DB 361 NVANNLEGP1PHLSSCTNLNSLVNHNKFSGTTIPPAFOKLESMTYLANSSNNIKGP1P 420  
QY 421 VELSRIGNLDTLDSNNKINGIIPSSIGDLEHLKXNLSRNHITGVVPGDFGNLSIMEI 480  
DB 421 VELSRIGNLDTLDSNNKINGIIPSSIGDLEHLKXNLSRNHITGVVPGDFGNLSIMEI 480  
QY 481 DLSNNDISGPIPELNLQNIILRLLENNNLTVGNVSLANCLSLTVLVNSHNNLVGDIPK 540  
DB 481 DLSNNDISGPIPELNLQNIILRLLENNNLTVGNVSLANCLSLTVLVNSHNNLVGDIPK 540  
QY 541 NNNFSFSPDSFGNGGLCSMWLNSPCHDSRRVTVRSISRAALIGLAVILMLVLA 600  
DB 541 NNNFSFSPDSFGNGGLCSMWLNSPCHDSRRVTVRSISRAALIGLAVILMLVLA 600  
QY 601 ACRPHNPPELDSLPKPVYVSTPKVYLHNNMALHYEDIMMNTENLSKYYIIGHGASS 660  
DB 601 ACRPHNPPELDSLPKPVYVSTPKVYLHNNMALHYEDIMMNTENLSKYYIIGHGASS 660  
QY 661 TVYKCVLKNCKPAVAKRLYSHNPQSMKQFTELEMLSSIKGRNLVSLQAVSLSLGSLIF 720  
DB 661 TVYKCVLKNCKPAVAKRLYSHNPQSMKQFTELEMLSSIKGRNLVSLQAVSLSLGSLIF 720

DB 661 TVYKCVLKNCKPAVAKRLYSHNPQSMKQFTELEMLSSIKGRNLVSLQAVSLSLGSLIF 720  
QY 721 YDYLENGSLMDLHGPDKKTLMDRILKAYAGAOLAVLHDCSPRIIHRDVKSNIL 780  
DB 721 YDYLENGSLMDLHGPDKKTLMDRILKAYAGAOLAVLHDCSPRIIHRDVKSNIL 780  
QY 781 LDDLEARLDPFGLIAKSLCVSKSHTSTYWGCTIGYIDPEYARTSRUTEKSDVYSYGLVL 840  
DB 781 LDDLEARLDPFGLIAKSLCVSKSHTSTYWGCTIGYIDPEYARTSRUTEKSDVYSYGLVL 840  
QY 841 ELITRRKAVDSESNLHLNLSKTGNNEWMADPDITSTCKDGVYKVFQALLCTKQ 900  
DB 841 ELITRRKAVDSESNLHLNLSKTGNNEWMADPDITSTCKDGVYKVFQALLCTKQ 900  
QY 901 PNDPPTHQVTRVLSFMSSEPPAATDTSATLASCYDEVANIKTPHSCVNCSSMSASD 960  
DB 901 PNDPPTHQVTRVLSFMSSEPPAATDTSATLASCYDEVANIKTPHSCVNCSSMSASD 960  
QY 961 AOLFLRFQVYISQNSE 976  
DB 961 AOLFLRFQVYISQNSE 976

## RESULT 4

US-11-056-355B-46417  
; Sequence 46417, Application US/11056355B  
; Publication No. US20060150283A1

; GENERAL INFORMATION:  
; APPLICANT: Brover, Vyacheslav  
; APPLICANT: Alexandrov, Nikolai  
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
; FILE OF INVENTION: Polyptides Encoded Thereby  
; FILE REFERENCE: 2750-1590PUS2  
; CURRENT APPLICATION NUMBER: US/11/056,355B  
; CURRENT FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: 60/544,190  
; PRIOR FILING DATE: 2004-02-13  
; NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 46417  
; LENGTH: 695  
; TYPE: prt  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
; NAME/KEY: peptide  
; LOCATION: (1)..(695)  
; OTHER INFORMATION: Ceres Seq. ID no. 13578687  
US-11-056-355B-46417

Query Match 71.5%; Score 3606; DB 7; Length 695;  
Best Local Similarity 100.0%; Pred. No. 1.8e-154;  
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 282 MQALAVLDSGNLSSGSIPIILGNLTFEKLYLHNSKLTGSIPELGNMSKLYLELNDN 341  
DB 1 MQALAVLDSGNLSSGSIPIILGNLTFEKLYLHNSKLTGSIPELGNMSKLYLELNDN 341  
QY 342 HLTGHIPELGLKLTDLFDLVANNLEGP1PHLSSCTNLNSLVNHNKFSGTTIPPAFOK 401  
DB 342 HLTGHIPELGLKLTDLFDLVANNLEGP1PHLSSCTNLNSLVNHNKFSGTTIPPAFOK 401  
QY 402 LBSMTYLANSSNNIKGP1PELNLQNIILRLLENNNLTVGNVSLANCLSLTVLVNSHNNLVGDIPK 461  
DB 402 LBSMTYLANSSNNIKGP1PELNLQNIILRLLENNNLTVGNVSLANCLSLTVLVNSHNNLVGDIPK 461  
QY 462 HITGVVPGDFGNLSIMEIDLSNNDISGPIPELNLQNIILRLLENNNLTVGNVSLANCL 521  
DB 462 HITGVVPGDFGNLSIMEIDLSNNDISGPIPELNLQNIILRLLENNNLTVGNVSLANCL 521  
QY 522 LSLTVLVNSHNNLVGDI PKNNNFSRPSDFGNPGLCSMWLNSPCHDSRRVTVRSISRA 581  
DB 522 LSLTVLVNSHNNLVGDI PKNNNFSRPSDFGNPGLCSMWLNSPCHDSRRVTVRSISRA 581  
QY 582 ALIGLIGLAVILMLVLAACRPHNPPELDSLPKPVYVSTPKVYLHNNMALHYEDI 641  
DB 582 ALIGLIGLAVILMLVLAACRPHNPPELDSLPKPVYVSTPKVYLHNNMALHYEDI 641

```
|||||
Db 301 AIIIGIAIGVILMLVIAACRPHNPPLDGLSDKDPVTSTPKLVILHNMALHYVEDI 360
QY MRMTENSEKXIIIGHGASSTVYKCVLKNCKPVAIKRLYSHNPOSMKOFETELEMSSIKH 701
Db 642 MRMTENSEKXIIIGHGASSTVYKCVLKNCKPVAIKRLYSHNPOSMKOFETELEMSSIKH 420
QY 361 MRMTENSEKXIIIGHGASSTVYKCVLKNCKPVAIKRLYSHNPOSMKOFETELEMSSIKH 420
QY 702 RNVLSDAYSLSHLSGLLFPDYLENGSLMDLHGPTKKKTLDMWTRKIAVGAAGLAVL 761
Db 421 RNVLSDAYSLSHLSGLLFPDYLENGSLMDLHGPTKKKTLDMWTRKIAVGAAGLAVL 480
QY 762 HHDCSPRIHRDVKSSNILLDKDLKDLFDPGIAKSLCVSKSHTSTYVMGTIGYIDPEYA 821
Db 481 HHDCSPRIHRDVKSSNILLDKDLKDLFDPGIAKSLCVSKSHTSTYVMGTIGYIDPEYA 540
QY 822 RTSRLTEKSDVYSYGIVLELLELTRRKAVDDESNLHHLIMSKTGNNEMEMADPDITSTCK 881
Db 541 RTSRLTEKSDVYSYGIVLELLELTRRKAVDDESNLHHLIMSKTGNNEMEMADPDITSTCK 600
QY 882 DLGVVKKVFPQALLCTKRQPNDRPTMHQVTRVLGSPMLSEQPPAATDTSATLAGSCYVDE 941
Db 601 DLGVVKKVFPQALLCTKRQPNDRPTMHQVTRVLGSPMLSEQPPAATDTSATLAGSCYVDE 660
QY 942 YANLKTPHSVNCSMSASDAQFLRFQOVISONSE 976
Db 661 YANLKTPHSVNCSMSASDAQFLRFQOVISONSE 695
```

```
RESULT 5
US-11-056-355B-48176
; Sequence 48176, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056, 355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544, 190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 48176
; LENGTH: 695
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(695)
; OTHER INFORMATION: Ceres Seq. ID no. 13578687
US-11-056-355B-48176
```

```
Query Match 71.5%; Score 3606; DB 7; Length 695;
Best Local Similarity 100.0%; Pred. No. 1,8e-154;
Matches 695; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 282 MOALAVADLSGNLSGSIPIPLIGNLFTTEKLYLHNSNKLTSIGPELGNSMKLHYLENDN 341
Db 1 MOALAVADLSGNLSGSIPIPLIGNLFTTEKLYLHNSNKLTSIGPELGNSMKLHYLENDN 60
QY 342 HLTGHIPELQKLTDLFDLVANNNDLGPIDHLSCTNLNSLVNHNKFSGTIPRAFOK 401
Db 61 HLTGHIPELQKLTDLFDLVANNNDLGPIDHLSCTNLNSLVNHNKFSGTIPRAFOK 120
QY 402 LBSMTYLNSSNNIKGPIPELSLIGNLDLTLDSNNKINGIIPBSLGDLEHLKMNLSRN 461
Db 121 LBSMTYLNSSNNIKGPIPELSLIGNLDLTLDSNNKINGIIPBSLGDLEHLKMNLSRN 180
QY 462 HITGVVGDGPNRSIMEIDLSSNDISGPIPEELNOKNTIILLELNNNLTGAVSLANC 521
Db 181 HITGVVGDGPNRSIMEIDLSSNDISGPIPEELNOKNTIILLELNNNLTGAVSLANC 240
```

```
QY 522 LSLTVLNVSNNVLVDI PKXNNFSRFPDSFGICNPGLCGSMWNSPCHDSRRTVRSISRA 561
Db 241 LSLTVLNVSNNVLVDI PKXNNFSRFPDSFGICNPGLCGSMWNSPCHDSRRTVRSISRA 300
QY 582 AIIIGIAIGVILMLVIAACRPHNPPLDGLSDKDPVTSTPKLVILHNMALHYVEDI 641
Db 301 AIIIGIAIGVILMLVIAACRPHNPPLDGLSDKDPVTSTPKLVILHNMALHYVEDI 360
QY 642 MRMTENSEKXIIIGHGASSTVYKCVLKNCKPVAIKRLYSHNPOSMKOFETELEMSSIKH 701
Db 361 MRMTENSEKXIIIGHGASSTVYKCVLKNCKPVAIKRLYSHNPOSMKOFETELEMSSIKH 420
QY 702 RNVLSDAYSLSHLSGLLFPDYLENGSLMDLHGPTKKKTLDMWTRKIAVGAAGLAVL 761
Db 421 RNVLSDAYSLSHLSGLLFPDYLENGSLMDLHGPTKKKTLDMWTRKIAVGAAGLAVL 480
QY 762 HHDCSPRIHRDVKSSNILLDKDLKDLFDPGIAKSLCVSKSHTSTYVMGTIGYIDPEYA 821
Db 481 HHDCSPRIHRDVKSSNILLDKDLKDLFDPGIAKSLCVSKSHTSTYVMGTIGYIDPEYA 540
QY 822 RTSRLTEKSDVYSYGIVLELLELTRRKAVDDESNLHHLIMSKTGNNEMEMADPDITSTCK 881
Db 541 RTSRLTEKSDVYSYGIVLELLELTRRKAVDDESNLHHLIMSKTGNNEMEMADPDITSTCK 600
QY 882 DLGVVKKVFPQALLCTKRQPNDRPTMHQVTRVLGSPMLSEQPPAATDTSATLAGSCYVDE 941
Db 601 DLGVVKKVFPQALLCTKRQPNDRPTMHQVTRVLGSPMLSEQPPAATDTSATLAGSCYVDE 660
QY 942 YANLKTPHSVNCSMSASDAQFLRFQOVISONSE 976
Db 661 YANLKTPHSVNCSMSASDAQFLRFQOVISONSE 695
```

```
RESULT 6
US-10-519-135-6
; Sequence 6, Application US/10519135
; Publication No. US20060137041A1
; GENERAL INFORMATION:
; APPLICANT: The Australian National University
; TITLE OF INVENTION: METHOD OF PRODUCING PLANTS HAVING ENHANCED TRANSPIRATION EFFICIENT
; FILE OF INVENTION: PLANTS PRODUCED THEREFROM
; FILE REFERENCE: 94948/MRO
; CURRENT APPLICATION NUMBER: US/10/519, 135
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: AU PS3339
; PRIOR FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 921
; TYPE: PRT
; ORGANISM: Sorghum ERECTA
US-10-519-135-6
```

```
Query Match 66.3%; Score 3372.5; DB 6; Length 921;
Best Local Similarity 68.4%; Pred. No. 6,7e-144;
Matches 666; Conservative 96; Mismatches 141; Indels 71; Gaps 8;
QY 13 LFLCLSVATVTSREGATLEIKKSPKDVNNVLDWMTTSPSSDYCWVRGVCENVTENVVA 72
Db 9 LVALDLVAVAADGATLVEIKKSFRRVGVLDVMA--GDDVCSMRGVLCNVTRAVAA 65
QY 73 LNLSDNLDELSPALGDLKSLSIDLRGNRLSGQIPDEIGDCSSLOMLDLSFNELSGDI 132
Db 66 LNLSDNLDELSPALGDLKSLSIDLRGNRLSGQIPDEIGDCSSLOMLDLSFNELSGDI 125
QY 133 PFSISKUKOLELILKNNOLGPIPESTLSQIPVUKLIDLAKNTLSEIPIPLIYWNVLOY 192
Db 126 PFSISKUKOLELILKNNOLGPIPESTLSQIPVUKLIDLAKNTLSEIPIPLIYWNVLOY 185
QY 193 LGRGNLVENISPDLCQGLGLWYFPVRNNSLGSIPETIGNCTAROVLDLSNOLTGEI 252
Db 186 L-----DVKNNSLTGVLPDITIGNCTSFQVLDLSNRRFTGPI 221
```



```

QY 253 PDIIGFQVATLISQGNOLSGKIPSVIGLMOALAVLDLSGNLSSGSPILIGLNTFTTEKL 312
DB 222 PFNIGFQVATLISQGNKFGPIPSVIGLMOALAVLDLSTNOLSGSPILISGLNTYTEKL 281
QY 313 YLHSHNKLTSIPPELGNMSKLHYLELNDNLGCHIPELGLKTDLPDLVANNDDLEGP 372
DB 282 YIQGNKLTGSIPELGNMSTLHYELNDNOLTSIPPELGRITGLPDLNANHLBEP 341
QY 373 DHSSCTNLNSLVNHNKFSGTTIPRAFQKESMTYMLSSNNIKGPIPVLSRIGNLDTL 432
DB 342 DNLSSCVNLNSFVAVGKMLNGTTIPRSRLKESMTYMLSSNIFSGSIPIEISRINNDDL 401
QY 433 DLSNNKNGIIPSSIGLLEHLKMLSRNHITGVVPPDPCGLRSIMEIDLSSNDISGP 492
DB 402 DLSNNMTGPIPSISGLLEHLRLNSKNGLVGFIIPAFGLNLSVMEIDLNYHGLG 461
QY 493 BEINLOQNIILLRLNENNLGNVGLANCLSLTVLVNHNHNLVGDIPKNNNFSRFPDSF 552
DB 462 QLEMLQNLML-----LVNYSNNLAGVVPADNNFTFPDSF 498
QY 553 IGNPGLCGSLNLPFGCHDSRTVVISIRPAIIGLIGLVILMLVLAACRPHNPPFLD 612
DB 499 LGNPGLCGYMLGSSCRSTGHHEKPEISKAAIIGVAVGLVILMLVLAACRPHRPAFKD 558
QY 613 GSLDKPVTSTPKLVILHMMALHVEDIRMTENLSEKTIIGHGASTYKCVLKNCKP 672
DB 559 VTVSKPRNAPPKLVILHMMALHVEDIRMTENLSEKTIIGHGASTYKCVLKNCKP 618
QY 673 VAIKRLVSHNPQSKQFETELMLSLIKHNLVSLQVSLSHLSGLLFYDLNGSLMDL 732
DB 619 VAIKRLVSHNPQSKQFETELMLSLIKHNLVSLQVSLSHLSGLLFYDLNGSLMDL 678
QY 733 LH-GPTKKTLDMDTLKIAYGAAQGLAYLHHDSPRIIHRDVKSNIILDKLEARTD 791
DB 679 LHSKSSKXKLDWETRLRIALGAAQGLAYLHHDSPRIIHRDVKSNIILDKLEARTD 738
QY 792 FGIAXSLCVSKSHSTVVMGTIGYIDPEYARTSLRTEKSDVY-----SYGVILLELTR 846
DB 739 FGIAXSLCVSKSHSTVVMGTIGYIDPEYARTSLRTEKSDVY-----SYGVILLELTR 788
QY 847 KAVDDESNLHLHLSKTNNEVEMADPITSTCKDLGVVKKVFOALLCTKRQPNDRPT 906
DB 789 -AADWQASQORILSKTASNEVMDTVDPDIDGIDCKDLGEVKKLFQALLCTKRQPNDRPT 847
QY 907 MHOVTRVLSFMLSSEOP---AATDTSATLAGSCYDEVYANLKTTPHSVNC-SSMSASDAQ 962
DB 848 MHEVVRVLDCLVNPDPKPPSAHQLPQSPVAPVPSYINEVYSLRGTCALSCANSTSTDAE 907
QY 963 LFLRFGQVISONSE 976
DB 908 LFLRFGQVISONSE 921

```

RESULT 7  
US-11-056-355B-46418

```

; Sequence 46418, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 46418
; LENGTH: 647
; TYPE: prt
; ORGANISM: Arabidopsis thaliana

```

```

; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(647)
; OTHER INFORMATION: Ceres Seq. ID no. 13578688
US-11-056-355B-46418

```

```

Query Match 66.7%; Score 3364; DB 7; Length 647;
Best Local Similarity 100.0%; Pred. No. 1,le-143;
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 330 MSKLYHLELNDNLGHIPELGLKTDLPDLVANNDDLEGPDPHSSCTNLNSLVNHN 389
DB 1 MSKLYHLELNDNLGHIPELGLKTDLPDLVANNDDLEGPDPHSSCTNLNSLVNHN 60
QY 390 KFSGTTIPRAFQKESMTYMLSSNNIKGPIPVLSRIGNLDTLDSNNKNGIIPSSIGD 449
DB 61 KFSGTTIPRAFQKESMTYMLSSNNIKGPIPVLSRIGNLDTLDSNNKNGIIPSSIGD 120
QY 450 LEHLKMLNSRNHITGVVPPDPCGLRSIMEIDLSSNDISGPPELNOQNIILLRLENN 509
DB 121 LEHLKMLNSRNHITGVVPPDPCGLRSIMEIDLSSNDISGPPELNOQNIILLRLENN 180
QY 510 NLGNVGLANCLSLTVLVNHNHNLVGDIPKNNNFSRFPDSFTGNPGLCGSLNLPFGCHD 569
DB 181 NLGNVGLANCLSLTVLVNHNHNLVGDIPKNNNFSRFPDSFTGNPGLCGSLNLPFGCHD 240
QY 570 SRRTVVISIRPAIIGLIGLVILMLVLAACRPHNPPFLDGLDKPVTSTPKLVIL 629
DB 241 SRRTVVISIRPAIIGLIGLVILMLVLAACRPHNPPFLDGLDKPVTSTPKLVIL 300
QY 630 HMMALHVEDIRMTENLSEKTIIGHGASTYKCVLKNCKPVAIKRLVSHNPQSKQF 689
DB 301 HMMALHVEDIRMTENLSEKTIIGHGASTYKCVLKNCKPVAIKRLVSHNPQSKQF 360
QY 690 ETELEMLSLIKHNLVSLQVSLSHLSGLLFYDLNGSLMDLHGPTRKKTLDMDTRLK 749
DB 361 ETELEMLSLIKHNLVSLQVSLSHLSGLLFYDLNGSLMDLHGPTRKKTLDMDTRLK 420
QY 750 IAYGAAQGLAYLHHDSPRIIHRDVKSNIILDKLEARTDGIAXSLCVSKSHSTVY 809
DB 421 IAYGAAQGLAYLHHDSPRIIHRDVKSNIILDKLEARTDGIAXSLCVSKSHSTVY 480
QY 810 MGTIGYIDPEYARTSLRTEKSDVSYGIVLLELTRKKAVDDESNLHLHLSKTNNEV 869
DB 481 MGTIGYIDPEYARTSLRTEKSDVSYGIVLLELTRKKAVDDESNLHLHLSKTNNEV 540
QY 870 EMADPITSTCKDLGVVKKVFOALLCTKRQPNDRPTMHOVTRVLSFMLSSEOPPAATDT 929
DB 541 EMADPITSTCKDLGVVKKVFOALLCTKRQPNDRPTMHOVTRVLSFMLSSEOPPAATDT 600
QY 930 SATLAGSCYDEVYANLKTTPHSVNCSSMSASDAQLFLRFGQVISONSE 976
DB 601 SATLAGSCYDEVYANLKTTPHSVNCSSMSASDAQLFLRFGQVISONSE 647

```

RESULT 8

```

US-11-056-355B-48177
; Sequence 48177, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 48177
; LENGTH: 647
; TYPE: prt

```

ORGANISM: Arabidopsis thaliana  
FEATURE:  
NAME/KEY: peptide  
LOCATION: (1)-(647)  
OTHER INFORMATION: Cerec Seq. ID no. 13578688  
US-11-056-355B-48177

Query Match 66.7%; Score 3364; DB 7; Length 647;  
Best Local Similarity 100.0%; Pred. No. 1,1e-143; Indels 0; Gaps 0;  
Matches 647; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 330 MSKIHVELENDNHLTGHIPEPELGLTDLFDLVANNDIEGPIPDHLSCTNLNLVHGN 389  
DB 1 MSKIHVELENDNHLTGHIPEPELGLTDLFDLVANNDIEGPIPDHLSCTNLNLVHGN 60  
QY 390 KFSGTIPRAPOKESMYNLNLSNNIKGPIPELISRIQNLDTLDLSNNKINGIIPSSIGD 449  
DB 61 KFSGTIPRAPOKESMYNLNLSNNIKGPIPELISRIQNLDTLDLSNNKINGIIPSSIGD 120  
QY 450 LEHLKKNLSRNHITGVPGDFGNLRIMEIDLSNNDISGPIPEELNQLONIILRLENN 509  
DB 121 LEHLKKNLSRNHITGVPGDFGNLRIMEIDLSNNDISGPIPEELNQLONIILRLENN 180  
QY 510 NLGNVGSLANCLSTVLVNSHNNLVGDIPEKNNFSRPSDFTGNPGLCGSWLNSPCHD 569  
DB 181 NLGNVGSLANCLSTVLVNSHNNLVGDIPEKNNFSRPSDFTGNPGLCGSWLNSPCHD 240  
QY 570 SRRVRSISRAALIGLIGLVLMLVLAACRPHNPPELDGSLDKPVYSTRPKLVIL 629  
DB 241 SRRVRSISRAALIGLIGLVLMLVLAACRPHNPPELDGSLDKPVYSTRPKLVIL 300  
QY 630 HNNMALHVEYEDIMMTEENLSEKYLIGHGASSTVYKCVLKNCKPAIKRLVSHNPSKQF 689  
DB 301 HNNMALHVEYEDIMMTEENLSEKYLIGHGASSTVYKCVLKNCKPAIKRLVSHNPSKQF 360  
QY 690 ETELEMLSSIKRNLVSLQVYSLHLSGLFYDYLENGSLMDLHGTKKKTLDMWTRLK 749  
DB 361 ETELEMLSSIKRNLVSLQVYSLHLSGLFYDYLENGSLMDLHGTKKKTLDMWTRLK 420  
QY 750 IAYGAAGGLAYLHHDGSPRIIHRDVKSNTLDDKEARLTDPGIASLCSKSHSTYV 809  
DB 421 IAYGAAGGLAYLHHDGSPRIIHRDVKSNTLDDKEARLTDPGIASLCSKSHSTYV 480  
QY 810 MGTIGYIDPEYARTSRLEKSDVYSYGIVLLELLTRRKAVDDESNTLHLSMKTGNNEV 869  
DB 481 MGTIGYIDPEYARTSRLEKSDVYSYGIVLLELLTRRKAVDDESNTLHLSMKTGNNEV 540  
QY 870 EMADPDITSTCKDGVVKKVFOALLCTKROPNRPPTHQVTRVLGSPMLSEOPPAATDT 929  
DB 541 EMADPDITSTCKDGVVKKVFOALLCTKROPNRPPTHQVTRVLGSPMLSEOPPAATDT 600  
QY 930 SATLAGSCYDEVYANLKTPHSVNCSMSASDAQFLRFQGVISONSE 976  
DB 601 SATLAGSCYDEVYANLKTPHSVNCSMSASDAQFLRFQGVISONSE 647

RESULT 9  
US-10-519-135-4  
Sequence 4, Application US/10519135  
Publication NO. US20060137041A1  
GENERAL INFORMATION:  
APPLICANT: The Australian National University  
TITLE OF INVENTION: METHOD OF PRODUCING PLANTS HAVING ENHANCED TRANSPIRATION EFFICIENCY  
FILE REFERENCE: 94948/MRO  
CURRENT APPLICATION NUMBER: US/10/519,135  
CURRENT FILING DATE: 2004-12-22  
PRIOR APPLICATION NUMBER: AU P53339  
NUMBER OF SEQ ID NOS: 45  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4  
LENGTH: 999

TYPE: PRT  
ORGANISM: rice ERECTA  
US-10-519-135-4

Query Match 61.7%; Score 3113; DB 6; Length 999;  
Best Local Similarity 63.1%; Pred. No. 2.9e-132;  
Matches 618; Conservative 135; Mismatches 182; Indels 44; Gaps 9;

QY 26 EGATLEIKKSPFDVNNVLYDWTTPSPSDYRCVARGVSCVTFNNVALNLSNDLDEIS 85  
DB 35 EGKALMGVAKGFGANANALVDM--DGAADHCANRGVTCDNASFAVLALNLSNLTGGEIS 92  
QY 86 PAIGDKSLSLIDLRGNRLSGQIPDEIGDSSIQNLIDLSFNEISGDIPEGISKQLQLEQL 145  
DB 93 PAIGELKNLQFVLDLKGKMLTGQIPDEIGDCISLKYLDLSGNLLYGDIPFISXKLQLEEL 152  
QY 146 ILKKNQLGPIPESTLSQIPMLKTLDLAONKLSGEIPELTYWNEVLOYLGLRGNNLVGNIS 205  
DB 153 ILKKNQLGPIPESTLSQIPMLKTLDLAONKLTGDIPELTYWNEVLOYLGLRGNSLTGTLIS 212  
QY 206 PDLCOLTGLMYFVRRNNSLTGSIPEITGNCTAFQVLDLSYNQLTGEIPDIFGLQVATLS 265  
DB 213 PDMCOLTGLMYFVRRNNSLTGSIPEITGNCTAFQVLDLSYNQLTGEIPDIFGLQVATLS 272  
QY 266 LQGNQLSGKIPEYIGLMQALAVLDLSGNLISGSIPEILGNLTETKLYLHNSKLTGSIIP 325  
DB 273 LQGNRLTGKIPDYIAGMQALAVLDLSENELVGPISITLGNLSYTGKLYLHGNKLTGVIP 332  
QY 326 ELGNMSKTLHLELNDNHLTGHIPEPELGLTDLFDLVANNDIEGPIPDHLSCTNLNLVHGN 385  
DB 333 ELGNMSKTLHLELNDNHLTGHIPEPELGLTDLFDLVANNDIEGPIPDHLSCTNLNLVHGN 392  
QY 386 VHGKFSGTIPRAPOKESMYNLNLSNNIKGPIPELISRIQNLDTLDLSNNKINGIIP 445  
DB 393 VGNKKNLSGIPAGFQKLESLTYLNLSSNNKNGIPELGHIIILDTLDLSYNFSEGVPA 452  
QY 446 SLQDLLEHLKKNLSRNHITGVPGDFGNLRIMEIDLSNNDISGPIPEELNQLONIILRLENN 505  
DB 453 TIGLEHLLELNLKHLDPVPAEFENLRSVQVIMSSNNLSGSIPEELGQLQNLNLSLI 512  
QY 506 LENNNLITGVN--GSLANCLSTVLVNSHNNLVGDIPEKNNFSRPSDFTGNPGLCGSWLNSPCHD 550  
DB 513 LENNNLITGVN--GSLANCLSTVLVNSHNNLVGDIPEKNNFSRPSDFTGNPGLCGSWLNSPCHD 555  
QY 551 -----SFIGPGLCGSWLNSPCHDSRRVRSISRAALIGLIGLVLMLV 598  
DB 566 ISDCNQYIHNKCSFGLGPNLHAYCQDSSCGHSGQ--RVNISKRAICIIIGFIILLCVLL 624  
QY 599 IAACRPHNPPELDGSLDKVYVSTRKLVLIHNNMALHVEYEDIMMTEENLSEKYLIGHG 658  
DB 625 LAIYKTNQPOPLVKGSDKEV--CGPPKLVVLQMDMAIHTEYEDIMRLEENLSEKYLIGHG 682  
QY 659 SSTYVYKCVLKNCKPAIKRLVSHNPSKQFETELEMLSSIKRNLVSLQVYSLHLSGL 718  
DB 683 SSTYVYKCVLKNCKPAIKRLVSHNPSKQFETELEMLSSIKRNLVSLQVYSLHLSGL 742  
QY 719 LFYDYLENGSLMDLHGTKKKTLDMWTRLKLIAYGAAGGLAYLHHDGSPRIIHRDVKSSN 778  
DB 743 LFYDYMEGSLMDLHGTKKKTLDMWTRLKLIAYGAAGGLAYLHHDGSPRIIHRDVKSSN 802  
QY 779 ILDDKDLAARLTGPGIAKSLCSKSHSTYVMGTIGYIDPEYARTSRLEKSDVYSYGI 838  
DB 803 ILDDENFEAHLSPFGIAKCPVSAKSHASTYVLTGIGYIDPEYARTSRLEKSDVYSYGI 862  
QY 839 LLELLTRRKAVDDESNTLHLSMKTGNNEVEMADPDITSTCKDGVVKKVFOALLCTK 898  
DB 863 LLELLTRRKAVDDESNTLHLSMKTGNNEVEMADPDITSTCKDGVVKKVFOALLCTK 922  
QY 899 ROPNDRPTHQVTRVLGSPMLSE--OPPAATDSATLAGSCYDEVYANLKTPHSVNCSMS 956  
DB 923 RHPSDRPTHQVTRVLGSPMLSE--OPPAATDSATLAGSCYDEVYANLKTPHSVNCSMS 979  
QY 957 SASDAQFLRFQGVISONSE 975



```

Oy      391 FSGTIRAPQKLESMFTYMLSSNNIKGPIPVBLSTIGLDTLDLSNKNINIISSIGDL    450
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      361 LSAVPLPEFFNGSLTYLNLSSSSEFGAKI PAELGHI INLDITDLSGNNSFSISLTGLDL    420
Oy      451 EHLLKNLSSNHITGVVPDPFGNLSIMEIDLSNNDISGPIPEELNQLONIILRENNN    510
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      421 EHLIILNSSNHLNGTLPAEPGNLSIQIIDVSFPFLAGVIPTELGGQLQNIINSILANNK    480
Oy      511 LTGNV-GSLANCLSTVLIVNSHNNLVGDI PKANNFSRPSPDOSFIGNPGLGSMLNSPCHD    569
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      481 IHKIPDOLNCFCSLANLINISFNNSLGII PPKMKNTRFPSASFPGNPFLCGNWGISICGP    540
Oy      570 SRTTVASISRALLDIAIGLVILLMVLIACRNHPNPPFLDSJDXKPVTYSIPKXIVIL    629
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      541 SLRKSV-ETFRVAVICMWLGFTLLICMTFIAYVKSQOKVPALGSSKQP--EGSTKLIVIL    597
Oy      630 HNMALHVEDIMRMTEENSEKYIIGHGASTVYCALKNCCKPVAIKRLYSHNPOSKOF    689
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      598 HMOMALHTPDIMRYENDELDEKIICYGASSIVYCTSKTSRPALIKRIYINQYSNREF    657
Oy      690 ETELEMLSIKARNVLSDAYSLSHGSLFPDYLENGLMDLLHGPTKKKTLDWDTRLK    749
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      658 ETELETIGSI RHRNIVSLHGVALSPFGNLLFPDYMNESNLWDLLHGPKVKVGLDMETRLLK    717
Oy      750 IAVGAAGLAUYLHHDCSPRIHRDVSSNILDLDKLEARLTDPFAGSLCXSKESTSYV    809
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      718 IAVGAAGLAVYLHHDCTPRRIHRDISNVILLDGNFERLSDFGLAISIPATKYASTVV    777
Oy      810 MGTIGYIDPEYARTSRLTRKSDVYSYGIVLLELTRRAVDDESNTLHLIMSKTGNEVM    869
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      778 LGTIGYIDPEYARTSNLRKSDIYSYGIVLEELLKGKAVIDEAMNLHQMLISKADMTVM    837
Oy      870 EMADPDITSTCKDLGVYKKVFOALILCTKROPNDRPPTHQOTRVLYUGSMLSQOPAAITDT    929
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      838 EAVDAEVSVCWMSDGHIKKTFOLFALCTGRNFLERPTQOEVSRYLSSLVPSPP-----    893
Oy      930 SATLAGSCYDEVANYLKTPHSVNCSSMASDAQLFLAFGOYISONS    975
Db      892 -KLLPSPAKVOGEGERRESHSDTT----PQVFQRFREDISKSS    931

RESULT 12
US-10-449-902-52071
; Sequence 52071, Application US/104499902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: JP/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52071
; LENGTH: 671
; TYPE: PRN
; ORGANISM: Oryza sativa
; OS-10-449-902-52071
```

```

Query Match      49.7%;   Score 2505.5;  DB 6;  Length 671;
Best Local Similarity 73.7%;   Pred. No.2.9e-105;
Matches 479;  Conservative 68;  Mismatches 100;  Indels 3;  Gaps 1.

OY      13  LFCLSVATVTSSEGATLLEIKKSKVDNNVNYLDWTTSPSSDPCWARGVSCENTVFNNVA 72
      |  |||  ::::|:|||||:|||||  |||  ||||  |:||||  |

```

```

Db      13  LALLLVAVAANDCGSTLEIKKSPFRNDVNLVYDMA---GGDYCSMRGVLCNDVNTFAVAA  69
Qy      73  LNLSDLANLDEGISPAIGDKSLSLSDLRGNRLSGQIPDEIGDCSSLONLDSFNELSGDI  132
Db      70  LNLGSLNNGEISPAVGRKGIIVSIDLKSNGLSGQIPDEIGDCSSLTLLDSFNSLGDGI  129
Qy     133  PFSISKLEBOLILKNNOLIGIPETLSQIPVLKTLIDLAONKLSGEBIPRLIYNEVLQY  192
Db     130  PFSYSKLEHIBELILKNNOLIGVITPSQLPMLKTLIDLAONKLSGEBIPRLIYNEVLQY  189
Qy     193  LGLRGNLNLVGNISPDLCQLTGLMYPDVRRNSLTGSIIPETIGNTAFQVLDLSTYNLTGEI  252
Db     190  LGLRGNNLNLEGISPDICQLTGLMYPDVKNNSLTGSIIPETIGNTCSFQVLDLSTYKLSGSI  249
Qy     253  PPDIGFLOVATISLGNQOLSGKIPSYTIGLMQALVLDLSNLLSGSIPPLIGNTTFPEKL  312
Db     250  PFNIGFLOVATISLGNMFTGPIPSYTIGLMQALVLDLSYNQLSGPIPSITIGNTTFPEKL  309
Qy     313  YLHSHKLTGSIIPPELGNNSKLHYLELNDNHLTGHIPEELGKLTDLFDLNTVAANDLEEGIP  372
Db     310  YMOGKLTGSIIPPELGNNSTLHYLELNDNQLSGFIPEPEKLTGLFDLNLANNFEGIP  369
Qy     373  DHLSSCTNLNSLNVHGNKFSGTIIPRAFQKLESMTYLNLSNNIKGPIPELSRIGNLDTL  432
Db     370  DNISSCVNLNSPNAVGNRLNGTIIPELHKLESMTYLNLSNFIPLSGSIPETLSRINNLDTL  429
Qy     433  DLSNNKINGIIPSSLGDELEHLKNNLSRNHITGVGDPGNLRSIMEIDLSNDISGPI  492
Db     430  DLSNMITGPIPTTSGLEHLRLNLSNNGLVGFIPEAEIGNLKSIMEIDMSNNHLLGGIIP  489
Qy     493  EELNOLQNIILRLNENNLVTGNVGSPLANCLSTLVLVVSHNNLKGDIPEKNNNSFRSPDSF  552
Db     490  OELGTLQMLMLNLTNNNTITGVDVSSLSLMCFSLNLTIVNSYNNLKGAVPTDNNFSFSDSF  549
Qy     553  IGNPGLCGSWLNSPCHDSRRTVVSISRPAALIGIALIGVLVILMLVLIACRPHNPPLD  612
Db     550  LGNPGLCGYWLNSCRSSGHOQKPLISKAAALIGIAGVLVILMLIIVAVCRPHSPVFKD  609
Qy     613  GSLDKPYRYTTPKVIILHNNMALHYEDIMRMTENISEKTIIGHGASSTV  662
Db     610  VVSXKPYVSNVPPKVIILHNNLSLVLVEDIMTMTENISEKTIIGHGASSTV  659

```

```

RESULT 13
US-10-519-135-45
Sequence 45, Application US/10519135
Publication No. US20060137041A1
GENERAL INFORMATION:
APPLICANT: The Australian National University
TITLE OF INVENTION: METHOD OF PRODUCING PLANTS HAVING ENHANCED TRANSPIRATION EFFICIENCY
FILE REFERENCE: 94948/MRO
CURRENT APPLICATION NUMBER: US/10/519,135
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: AU PS3339
PRIOR FILING DATE: 2002-07-02
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin version 3.1
SEQ ID NO 45
LENGTH: 675
TYPE: PRT
ORGANISM: maize ERECTA
US-10-519-135-45

```

	Query Match	49.2%;	Score 2482;	DB 6;	Length 675;
	Best Local Similarity	70.7%;	Pred. No. 3-104;		
	Matches	474;	Conservative 79;	Mismatches 105;	Indels 12; Gaps 3.
Qy	317	NKLTGSIPEPELGNSSKHYLELNHNLGTHPEPELGTITDLPDNLVANNDEIGRPIDHS			376
Db	4	NRLTGSIPPELGNSSSTHYLELNNDLQGSIPPELGRITGTFDNLVANNHLEGPIDHS			63
Qy	377	SCTNLNSLVNAGNFKSGTIPRAFOKLESMTYLNLSNNIKGPIPEVLSRIGLNDTLIDSN			436

```
Db 64 SCVNLSFNAVGKLNKNTIPRSRLKLESMTYVLYLSSPFGSIPBELSRINNIDTDLSC 123
QY 437 NKINGIIPSSLGDLLEHLKKNLSRNHITGVVPODFGLASIMEIDUSNNDISGPPELN 496
Db 124 NMATGPIPSISGNLEHLRLNLKNDLVGFI PAEFGRLRSVMEIDLSYNHGGIIPOLG 183
QY 497 QLONIILRLENNNTGNVSLANCLSLTVLANSYSHNNLVGDIPIKNNNSFSPDSFGNP 556
Db 184 MLONLMLKLKNNNTVGDVSLMNCSTLNILNVSYNLAGAVPDDNFTFSHDSFGNP 243
QY 557 GLCGSWLNSPCHDSRRTVRVSIISRAAIIIGIAGLVILLMVLIAACRPHNPPELDSGL 616
Db 244 GLCGWLGSSCRGTGRDRKPKISKAALIGAVGLVILLMILVAVCRPHNPFAKATVS 303
QY 617 KPVYTSPTKLVIIHMNNALHYVEDIMRTENLSBKTIIGHGASSTVYKCVLKNCKPVAIK 676
Db 304 KPVSNGPPEKLVIIHMNNALHYVEDIMRTENLSBKTIIGHGASSTVYKCVLKNCKPVAIK 363
QY 677 RLVSHPQSKOPETELEMSSIKHRVLVSLQAVSLSHLGLFPDYLENGSLMDLIH-G 735
Db 364 KLVAAHYQSKEFELETELVGSIKRNVLVSLQGISLVGNLLFYAVMESGLMDVLHGG 423
QY 736 PTKKKTLDMDTRKIAVGAAGLAVLHDCSPRIIHRDVKSSNILLDKDLKLEARLTDFGIA 795
Db 424 SSKKNLDWTRIRIALGAAGLAVLHDCSPRIIHRDVKSKNILLDKDLKLEARLTDFGIA 483
QY 796 KSLCVSKSHTSTYVMTGTYIDPEYARTSLTEKSDVSYGIVLELTLTRKAVDESNL 855
Db 484 KSLCVSKSHTSTYVMTGTYIDPEYARTSLTEKSDVSYGIVLELTLTRKAVDESNL 543
QY 856 HHLIMSKTGNNEVEMADPDITSTCKDLGVKKVYFQALICTKROPDRPTMHQVRVLG 915
Db 544 HHLILKTAENEMETVDPVGDTCCKDLGEVKKLFQALICTKROPDRPTMHQVRVLG 603
QY 916 SFMLSEQPP-----AATDTSATLAGSCYVDEYANIKTPHSVNC-SMSASDAQLF 964
Db 604 CLVNPPEPPOQOQKAAHHHQLPPSPRPAYDEVLSLRTGALSCANSSSTSDALEF 663
QY 965 LRFQVISON 974
Db 664 LKRGVAISON 673

RESULT 14
US-10-953-349-22717
; Sequence 22717, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22717
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-22717

Query Match 44.6%; Score 2247.5; DB 6; length 550;
Best Local Similarity 77.7%; Pred. No. 8.3e-94;
Matches 429; Conservative 51; Mismatches 63; Indels 9; Gaps 2;
```

```
QY 432 LDISNNKINGIIPSSLGDLLEHLKKNLSRNHITGVVPODFGLASIMEIDUSNNDISGP 491
Db 1 LDISNNKLVGSIIPSSLDLLEHLKKNLSRNHITGVVPAEFGNLSVMEIDLSNQLSGFI 60
QY 492 PEELNQLQNMISRLLENNKLTGCVASLSSCLSLSLNVSYNKLVGFIPTSNFTREPPDS 551
```

```
Db 61 PEELNQLQNMISRLLENNKLTGCVASLSSCLSLSLNVSYNKLVGFIPTSNFTREPPDS 120
QY 552 FIGNPGLCGSWLNSPCHDSRRTVRVSIISRAAIIIGIAGLVILLMVLIAACRPHNPPEL 611
Db 121 FIGNPGLCGSWLNPCHGARPSERVTLSRAAIIIGIAGLVILLMVLIAACRPHNSPFP 180
QY 612 DGLDKPVTSTPTKLVIIHMNNALHYVEDIMRTENLSBKTIIGHGASSTVYKCVLKNCK 671
Db 181 DGSFDPKFINSPPKLVIIHMNNALHYVEDIMRTENLSBKTIIGHGASSTVYKCVLKNCK 240
QY 672 PVAIKRLYSHPQSKOPETELEMSSIKHRVLVSLQAVSLSHLGLFPDYLENGSLMD 731
Db 241 PVAIKRLYSHPQSKOPETELEVTSIKHRNVSLSQGISLSPYGHILFPDYMENGLMD 300
QY 732 LHPPTKKTLDMDTRKIAVGAAGLAVLHDCSPRIIHRDVKSSNILLDKDLKLEARLT 791
Db 301 LHPPTKKTLDMDLELKLALGAAGLAVLHDCSPRIIHRDVKSSNILLDKDLKLEARLT 360
QY 792 FGIASLCSKSTSTYVMTGTYIDPEYARTSLTEKSDVSYGIVLELTLTRRAVD 851
Db 361 FGIASLCSKSTSTYVMTGTYIDPEYARTSLTEKSDVSYGIVLELTLTRRAVD 420
QY 852 ESNLHRLINSGTGNNEVEMADPDITSTCKDLGVKKVYFQALICTKROPDRPTMHQVT 911
Db 421 ESNLHRLINSGTGNNEVEMADPDITATCKDLGAVKVYFQALICTKROPDRPTMHQVT 480
QY 912 RVLSGFMLEQPP-----PAATDTSATLAGSCYVDEYANIKTPHSVNC-SMSASDAQLF 964
Db 481 RVLSGVLVPSIIPKQLADLPAPNSPAKV--PQVDEYANIKTPHVNCSNSTSDAQLF 538
QY 965 LRFQVISON 976
Db 539 LKRGVAISON 550

RESULT 15
US-10-953-349-22718
; Sequence 22718, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22718
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-22718

Query Match 40.8%; Score 2055.5; DB 6; length 504;
Best Local Similarity 77.9%; Pred. No. 2.9e-85;
Matches 394; Conservative 43; Mismatches 60; Indels 9; Gaps 2;
```

```
QY 478 MEIDLSNNDISGPPELNQLQNMISRLLENNKLTGCVASLSSCLSLSLNVSYNKLVG 537
Db 1 MEIDLSNQLSGFIPEELNQLQNMISRLLENNKLTGCVASLSSCLSLSLNVSYNKLVG 60
QY 538 IPIKNNFSPSPSFGNPGCLCGSWLNSPCHDSRRTVRVSIISRAAIIIGIAGLVILLMV 597
Db 61 IPIKNNFTRPPPSFGNPGCLCGSWLNPCHGARPSERVTLSRAAIIIGIAGLVILLMV 120
QY 598 LIAACRPHNPPELDSLDKPVTSPTKLVIIHMNNALHYVEDIMRTENLSBKTIIGHG 657
Db 121 LVAACRPHNSPFPDSFDKPIFSPKLVIIHMNNALHYVEDIMRTENLSBKTIIGHG 180
QY 658 ASSTVYKCVLKNCKPVAIKRLYSHPQSKOPETELEMSSIKHRVLVSLQAVSLSHLS 717
Db 181 ASSTVYKCVLKNCKPVAIKRLYSHPQSKOPETELEVTSIKHRNVSLSQGISLSPYGH 240
```



GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: September 2, 2006, 06:57:15 ; Search time 186 Seconds  
(without alignments)  
2430.633 Million cell updates/sec

Title: US-10-519-135-2

Perfect score: 5043

Sequence: 1 MALFRIVLGFCLSLVA.....SASDAQFLRFQGVQVQNSSE 976

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

2097797

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Maximum Match 100%

Database : Published Applications AA Main:

- 1: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US07\_PUBCOMB.pep.\*
- 2: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US08\_PUBCOMB.pep.\*
- 3: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US09\_PUBCOMB.pep.\*
- 4: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US10\_PUBCOMB.pep.\*
- 5: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US108\_PUBCOMB.pep.\*
- 6: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5043	100.0	976	US-11-027-304-2	Sequence 2, Appl1
2	3602.5	71.4	838	US-10-425-114-58433	Sequence 58433, A
3	3592.5	71.2	985	US-10-424-599-171008	Sequence 171008, A
4	3372.5	66.9	921	US-10-389-566-1452	Sequence 1452, Ap
5	3167	62.8	614	US-11-027-304-4	Sequence 4, Appl1
6	3141.5	62.3	907	US-10-437-963-123824	Sequence 123824, A
7	3089.5	61.3	967	US-11-027-304-8	Sequence 8, Appl1
8	3079.5	61.1	966	US-11-027-304-6	Sequence 6, Appl1
9	2931	58.1	909	US-10-425-115-367213	Sequence 367213, A
10	2921.5	57.9	885	US-10-437-963-169553	Sequence 169553, A
11	2791	55.3	764	US-10-425-114-58448	Sequence 58448, A
12	2712	53.8	764	US-10-425-115-262277	Sequence 262277, A
13	2484.5	49.3	962	US-10-437-963-121441	Sequence 121441, A
14	2384.5	47.3	578	US-10-425-114-45783	Sequence 45783, A
15	2322.5	46.1	611	US-11-027-304-12	Sequence 12, Appl1
16	2259.5	44.8	613	US-10-427-304-86	Sequence 86, Appl1
17	2236.5	44.3	541	US-10-425-114-43982	Sequence 43982, A
18	2215	43.9	713	US-10-425-114-58001	Sequence 58001, A
19	2010	39.9	621	US-11-027-304-88	Sequence 88, Appl1
20	1968.5	39.0	619	US-11-027-304-12	Sequence 12, Appl1
21	1956.5	38.8	458	US-11-027-304-10	Sequence 10, Appl1
22	1596	31.6	458	US-10-425-114-53788	Sequence 53788, A
23	1568	31.1	502	US-10-101-464A-945	Sequence 945, App
24	1568	30.6	502	US-10-864-252-945	Sequence 945, App
25	1543	30.1	426	US-10-425-114-59439	Sequence 59439, A
26	1529.5	30.3	464	US-10-424-599-268366	Sequence 268366, A
27	1489	29.5	1102	US-11-096-568A-27957	Sequence 27957, A

28	1484	29.4	1097	6	US-11-096-568A-27959	Sequence 27959, A
29	1484	29.4	1098	6	US-11-096-568A-27958	Sequence 27958, A
30	1474.5	29.2	402	4	US-10-425-115-242582	Sequence 242582, A
31	1446	28.7	1109	4	US-10-389-566-2378	Sequence 2378, Ap
32	1441	28.6	1109	4	US-10-389-566-1136	Sequence 1136, Ap
33	1432.5	28.4	998	4	US-10-101-464A-931	Sequence 931, App
34	1432.5	28.4	998	5	US-10-864-252-931	Sequence 931, App
35	1424.5	28.2	1029	4	US-10-437-963-164029	Sequence 164029, A
36	1421.5	28.2	1057	4	US-10-437-963-191288	Sequence 191288, A
37	1404.5	27.9	998	4	US-10-101-464A-895	Sequence 895, App
38	1404.5	27.9	998	5	US-10-864-252-895	Sequence 895, App
39	1401.5	27.8	1010	4	US-10-424-599-195812	Sequence 195812, A
40	1399.5	27.8	1030	4	US-10-437-963-158754	Sequence 158754, A
41	1393.5	27.6	370	4	US-10-101-464A-944	Sequence 944, App
42	1393.5	27.6	370	5	US-10-864-252-944	Sequence 944, App
43	1386	27.5	452	4	US-10-425-115-229873	Sequence 229873, A
44	1384.5	27.5	1021	4	US-10-101-464A-954	Sequence 954, App
45	1384.5	27.5	1021	5	US-10-864-252-954	Sequence 954, App

ALIGNMENTS

RESULT 1									
US-11-027-304-2									
; Sequence 2, Application US/11027304									
; Publication NO. US20050223428A1									
; GENERAL INFORMATION:									
; APPLICANT: Torii, Keiko U.									
; APPLICANT: Shpak, Elena D.									
; TITLE OF INVENTION: METHODS FOR MODULATING PLANT GROWTH									
; FILE REFERENCE: UMOT122663									
; CURRENT APPLICATION NUMBER: US/11/027,304									
; PRIOR FILING DATE: 2004-12-30									
; PRIOR APPLICATION NUMBER: US 60/558,529									
; NUMBER OF SEQ ID NOS: 88									
; SOFTWARE: PatentIn version 3.2									
; SEQ ID NO 2									
; LENGTH: 976									
; TYPE: PRT									
; ORGANISM: Arabidopsis Thaliana									
US-11-027-304-2									
Query Match									
Best Local Similarity 100.0%; Score 5043; DB 6; Length 976;									
Matches 976; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	MALFRIVLGFCLSLVATVTSSEGA	TLLEIKSFKDVNNVLYWMTTSPSSDYC	WVRG	60				
Db	1	MALFRIVLGFCLSLVATVTSSEGA	TLLEIKSFKDVNNVLYWMTTSPSSDYC	WVRG	60				
Qy	61	VSCENYFNVALNLSDLNLDGEIS	PAIDLKSLSIDLGNRLSGQIPDEIGD	CSLQ	120				
Db	61	VSCENYFNVALNLSDLNLDGEIS	PAIDLKSLSIDLGNRLSGQIPDEIGD	CSLQ	120				
Qy	121	LDLSFNEISDIPFSISKQLEQL	LILKNQNLIGPISLSQIPNKILDLA	NKLSGEI	180				
Db	121	LDLSFNEISDIPFSISKQLEQL	LILKNQNLIGPISLSQIPNKILDLA	NKLSGEI	180				
Qy	181	PRLIYNEVLYQYGLGNLNVGNI	SPDLCOLTGLWFDVRRNLSLTGSI	PETIGNCTA	FQV	240			
Db	181	PRLIYNEVLYQYGLGNLNVGNI	SPDLCOLTGLWFDVRRNLSLTGSI	PETIGNCTA	FQV	240			
Qy	241	LDLSYNQLTGEIPFDIGLOVAT	LSIQNQLSGKIPSVIGLMQALAV	LDLSGNLSGS	300				
Db	241	LDLSYNQLTGEIPFDIGLOVAT	LSIQNQLSGKIPSVIGLMQALAV	LDLSGNLSGS	300				
Qy	301	PIIIGNLTPEKLYLHNNKLTGS	IPPELGNNSKLAHYELNDNHLTGH	IPPELGLTDL	FDL	360			
Db	301	PIIIGNLTPEKLYLHNNKLTGS	IPPELGNNSKLAHYELNDNHLTGH	IPPELGLTDL	FDL	360			
Qy	361	NVANNDLEGPDPHLSSCTNLN	SLNHNKFSCTIPRAFOKLESMTY	LNLSNNIKGPI	420				
Db	361	NVANNDLEGPDPHLSSCTNLN	SLNHNKFSCTIPRAFOKLESMTY	LNLSNNIKGPI	420				



```
Db 361 NVANNDEGPDPHLSSTCTNLNSLVNHGKFKSGTTPPAFOGLESMYTLNLSNNIKGP 420
Qy 421 VELSRIGLDTLDSNNKINGIIPSSIGDLEHLLKMLSRNHTGVYPGDFGNLRSTMEI 480
Db 421 VELSRIGLDTLDSNNKINGIIPSSIGDLEHLLKMLSRNHTGVYPGDFGNLRSTMEI 480
Qy 481 DLSNNDISGPIPELNLONIIILRLENNLTGVVSGLANCLSTVLNVSNLWGIIPK 540
Db 481 DLSNNDISGPIPELNLONIIILRLENNLTGVVSGLANCLSTVLNVSNLWGIIPK 540
Qy 541 NNNFSRSPDSFIGNPGLCGSMWNSPCHDSRTYVSI SRAIIGIAGVILMLVLA 600
Db 541 NNNFSRSPDSFIGNPGLCGSMWNSPCHDSRTYVSI SRAIIGIAGVILMLVLA 600
Qy 601 ACRPHNPPFLDGLDKRPVYTPKVLILHNNALHYEDIMRTENLSEKXIIGHGASS 660
Db 601 ACRPHNPPFLDGLDKRPVYTPKVLILHNNALHYEDIMRTENLSEKXIIGHGASS 660
Qy 661 TVYKCVLKNCPVAIKRLYSHNPQSMKOFETELEMSSIKHRNLVSLQAYSLHSLFLF 720
Db 661 TVYKCVLKNCPVAIKRLYSHNPQSMKOFETELEMSSIKHRNLVSLQAYSLHSLFLF 720
Qy 721 YDYLENGSLMDLHGPTKKKTLMDTRKLA YGAAGLAVLHHDSPRIIHRDVXSNIL 780
Db 721 YDYLENGSLMDLHGPTKKKTLMDTRKLA YGAAGLAVLHHDSPRIIHRDVXSNIL 780
Qy 781 LDKDLERLTDGFAKSLCVSKSHSTYVWGTTIGYIDPEYARTSLTEKSDVSYGVLL 840
Db 781 LDKDLERLTDGFAKSLCVSKSHSTYVWGTTIGYIDPEYARTSLTEKSDVSYGVLL 840
Qy 841 ELTTRRAVDDESLHLLMSKTGNNEVEMADPDITSTCDLG VVKVFOALLCRKQ 900
Db 841 ELTTRRAVDDESLHLLMSKTGNNEVEMADPDITSTCDLG VVKVFOALLCRKQ 900
Qy 901 PNDPRTMHOVTRVLSFMLS EOPPAATDTSAITLASCYVDEVANLKT PHSVNCSMSASD 960
Db 901 PNDPRTMHOVTRVLSFMLS EOPPAATDTSAITLASCYVDEVANLKT PHSVNCSMSASD 960
Qy 961 AOLFLRFGVISONSE 976
Db 961 AOLFLRFGVISONSE 976
```

```
RESULT 2
US-10-425-114-58433
; Sequence 58433, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 58433
; LENGTH: 838
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: JC-GMFL02220115B11_Flt.pep
US-10-425-114-58433
```

```
Query Match 71.4%; Score 3602.5; DB 4; Length 838;
Best Local Similarity 82.0%; Pred. No. 9e-241;
Matches 688; Conservative 66; Mismatches 76; Indels 9; Gaps 2;
```

```
Qy 145 LILKNNQLIGPIPSLTSQLPNLKILDLAONKLSGEIPRLIYNNVLYQLRGNNLVGNI 204
Db 2 LILKNNQLIGPIPSLTSQLPDLKILDLAONNLSGEIPRLIYNNVLYQLRGNNLVGSL 61
Qy 205 SPDLCOQLTGLMYDVRNNSITGSI PETIGNCTAPQVLDLSYNOLTGEIIPDIDGLOYATL 264
Db 62 SPMCCQLTGLMYDVRNNSITGSI PENIGNCTAFQVLDLSYNOLTGEIPENIGLOYATL 121
Qy 265 SLOGNOLSGKIPVYIGQMOLAVLVLDSGNLSGSIPPIIGNLTFOTKLYHSNKLTSIP 324
Db 122 SLOGNKLSGHI PVYIGQMOLAVLVLDSGNLSGSIPPIIGNLTYTEKLYHGNKLTFIP 181
Qy 325 PELGNNSKLAHYLELNDNHLTGHIIPPELGKLTDLFDLVANNNDGEPDPHLSSTCTNLNSL 384
Db 182 PELGNNSKLAHYLELNDNHLSGHIIPPELGKLTDLFDLVANNNDGEPDPHLSSTCTNLNSL 241
Qy 385 NVHGNKFSGTTPPAFOGLESMYTLNLSNNIKGP IPELSRIGLDTLDSNNKINGIIP 444
Db 242 NVHGNKLNLSIPSLQGLESMYTLNLSNNIQAIPPELSRIGLDTLDSNNNLVGSIP 301
Qy 445 SSIQDLEHLLKMLSRNHTGVVPGDFGNLRSTMEITDLSNNDISGPIPELNLONIIIL 504
Db 302 SSIQDLEHLLKMLSRNHTGIIIPAEFGNLSVMEIDLSNNQSLGIPDELSQLQNNISL 361
Qy 505 RLENNNLTVGNVSGLANCLSTVLNVSNLWGIIPKNNFSRSPDSFIGNPGLCGSMWLN 564
Db 362 RLENNNLTVGNVSLNSICISLFLNVSNLKFVYIPNSNNTFRPPDSFIGNPGLCGSMWLN 421
Qy 565 SPCHDSRTYVSI SRAIIGIAGVILMLVLAACRPHNPPFLDGLDKRPVYTP 624
Db 422 LPCHGARPSERVLSKAAIIGITLGVILMLVLAACRPHSPSPFPDGSFDPKRVNFSPP 481
Qy 625 KLVILHNNMALHYEDIMRTENLSEKXIIGHGASSTVYKCVLKNCPVAIKRLYSHNPQ 684
Db 482 KLVILHNNMALHYEDIMRTENLSEKXIIGHGASSTVYKCVLKNCPVAIKRLYSHNPQ 541
Qy 685 SMKOFETELEMSSIKHRNLVSLQAYSLHSLFLFYDYLENGSLMDLHGPTKKKTLMD 744
Db 542 CIKEFETELETGVS IKHRNLVSLQGYSLSPYGHLLFDYVYENGSLMDLHGPTKKKTLMD 601
Qy 745 DTRKLA YGAAGLAVLHHDSPRIIHRDVXSNILDKDLERLTDGFAKSLCVSKSH 804
Db 602 ELRLKIALGAAGLAVLHHDCCPRIIHRDVXSNILDDAFEEHLLTDGFAKSLCPKSH 661
Qy 805 TSYVWGTTIGYIDPEYARTSLTEKSDVSYGVLELITRRRAVDDESLHLLMSKTG 864
Db 662 TSYVWGTTIGYIDPEYARTSLTEKSDVSYGVLELITGRRAVDDESLHLLMSKAA 721
Qy 865 NNEVEMADPDITSTCDLG VVKVFOALLCRKQPNDRPTMHOVTRVLSFMLS EOP- 923
Db 722 TNVMEVDPDITATCTCDLGAVKVVQALLCRKQPADRPTHNHTVTRVLSFVLSVTPP 781
Qy 924 -----PAATDTSAITLASCYVDEVANLKT PHSVNCSMSASDAQFLRFGVISONSE 976
Db 782 KQLAALPPASNPASKV--PCYVDEVANLKT PHLVNCPMSMSTSDAOLFLRGEVISONSE 838
```

```
RESULT 3
US-10-424-599-171008
; Sequence 171008, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 171008
```

```
; LENGTH: 985
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(985)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT847_125435C.1.pep
US-10-424-599-171008
```

```
Query Match          71.2%; Score 3592.5; DB 4; Length 985;
Best Local Similarity 72.3%; Pred. No. 5.5e-240;
Matches 715; Conservative 94; Mismatches 163; Indels 17; Gaps 6;
```

```
QY 1 MALPRLVILGFLFCLSLVATVTSSECATLLETKSKFDVNNVLYDMTTPSSDYCYWRG 60
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 1 MAERFGLIATLALICLS-VNSVESDDGATLLEIKKSFSDVDNVLVDMTSPSSDYCAMRG 59
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 61 VSCENVTENVVALNLSDLNLDGEISPAIGDKSL---SIDLRGNRLSGOIPDEIGDCSS 117
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 60 IACDNVTENVVALNLSGLNLDGEISPAIGDKSLAGRAVDNESN-LHHLIWSKAATNAV 118
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 118 LQNLDSFNEISGDIPEPS---ISKLKQLEQLIKNNQLIGRIPSTLSQIPNLKILDLAQN 174
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 119 METVDPDITATGKDLXSKLIISLYYAQKGIILGQLIGQVTVVLSQIPDKILDLAQN 178
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 175 KLSGEIPRLIYNNVLYQLGRGNLVGNISPDLCQLTGLMYPDVNNLSLTSIPETIGN 234
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 179 NLGGEIPSLISKDEVLQYLYNNLTTLHLVTSPLXCLQGTGSSSCLEKQSKTYVERILN 238
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 235 CTAFOVLDLSYNQLTGEPIDIGFOVATLSLQCNLSGKIPSYIGLMQALVLDLSGNL 294
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 239 XKSFSIIDSYNKLTETIIPNIGLQVATTSLOQNKLSGHI PPYIGLMQALVLDLSGNM 298
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 295 LSGSIPILGNLTFTTEKLYLHNSKLTGSIPELGNMSKLYLELNDHNLTGHIPELGLK 354
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 299 LSGSIPILGNLTFTTEKLYLHNSKLTGSIPELGNMSKLYLELNDHNLTGHIPELGLK 358
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 355 TDLPDLVANNDLBGPIDPHLSCTNLNSLVHGNKFSGTPPRAFOKLESMYTYLNSNN 414
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 359 TDLFDLVANNNLKGPISPLSSCKNLNSLVHGNKLTGSIPELQLESMYTYLNSNN 418
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 415 IKGPVPELSRIGNLDTLDSNNKINGITPSISGDLHLLKMLSRHITGVPGDGNL 474
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 419 LQGAIPLELSRIGLDTLDSNNNLVGSIPSSJADEHLKLTNLSRNKLGIIPAEIGNL 478
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 475 RSIMEIDLSNNDISGPIPEELNQLNIILRLNNNLTVGNVSLANCLSLTVLVNSHNL 534
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 479 RSIMEIDLSNNOGLIPDELSQONNMISLRLENKLTGPAVASLNCISLTLNVSYNK 538
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 535 VGGIPKNNNSRSPSPSFTGNPGICGSLWNSPCHDSRTYRVVSIIRAIIIGIAGLYIL 594
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 539 FGVIPTSNNTFRPPSPSFTGNPGICGSLWNLPGHGAPSERVTLSSKAAIIGITGALVIL 598
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 595 LAMVLIACRHPNPPLDGLDKVYTSPTPKLYTLHNNMALHYVEDIMRMTNLSKXYII 654
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 599 LAMVLIARDDRGRSPFPDGSFDPKRVNFSPPKLYLHNNMALHYVEDIMRMTNLSKXYII 658
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 655 GHGASSIVYKCVLKNCKRPAVKRLYSNHPQSKOFETELMNLISIKRNLVSLQAVSLSH 714
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 659 GYGASSIVYKCVLKNCKRPAVKRIYSHYPOCIKEFELEFVTSIKRNLVSLQAVSLSP 718
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 715 LGSLLFPDYLENGSLMULLHGPTKKTLDMDTRLKIVGAAGQAGLYAHHCSPRIIRDV 774
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 719 YGHLLFPDYVENESLMDLHGPTKKKLDWELRLKILGAAQAGLYAHHCSPRIIRDV 778
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 775 KSSNIIILDKLEARLTDFGIAKSLCVSKSHSTYVMGTIGYIDEPVARTSRILEKSVYS 834
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 779 KSSNIIILADPBEPLDTDFGIAKSLCPKSKSHSTYIMGTIGYIDEPVARTSRILEKSVYS 838
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 835 YGIVLELLTRRAKAVDNESNLHLLMSKGTGNNVEMADPDITSTCKDLGVVKKVFOAL 894
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
```

```
Db 839 YGIVLELLTRRAKAVDNESNLHLLMSKATNAVMEVDPDITATCKDLGAVKKVFOAL 898
QY 895 LCTKROPDRPTMHQVTRVGSFMLSQEP-----PAADTSATLACGCVDEYANLKT 947
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 899 LCTKROPDRPTMHQVTRVGSFMLSNTPEKQALALPPASNPASKV--PCYDEYANLKT 956
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 948 PHNSVCSMSASDAQFLFARGOVISONSE 976
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 957 PHLVNCSMSSTDAQFLFKRGVEISONSE 985
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
```

## RESULT 4

```
US-10-389-566-1452
; Sequence 1452, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1452
; LENGTH: 921
; TYPE: PRT
; ORGANISM: Sorghum bicolor
US-10-389-566-1452
```

```
Query Match          66.9%; Score 3372.5; DB 4; Length 921;
Best Local Similarity 68.4%; Pred. No. 9.1e-225;
Matches 666; Conservative 96; Mismatches 141; Indels 71; Gaps 8;
```

```
QY 13 LFCLSIIVATVTSSECATLLEIKKSFQDVNNVLYDMTTPSSDYCYWRGVSCENVTNNVA 72
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 9 LVALLVAVAVADGATLVIRIKKSFNNVGVLYDMA---GDVCSWRGVLCDDVTFVAVAA 65
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 73 LINSDLNLDGEISPAIGDKLSLSIDLKGNRLSGOIPDEIGDCSSLQNLDSFNEISGDI 132
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 66 LINSGLNLDGEISPAVGSLSVLSIDLKSGLSGOIPDEIGDCSSLRTPDPSFNNLDGDI 125
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 133 PFSISKLKQLEQLIKNNQLIGPISPTLSQIPNLKILDLAQNRLSGEIPRLIYNNVLYQY 192
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 126 PFSISKLKHENLILKNNQLIGAIPTLSQIPNLKILDLAQNRLSGEIPRLIYNNVLYQY 185
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 193 LGRGNLVGNISPDLCQLTGLMYPDVNNLSLTSIPETIGNCTAFOVLDLSYNQLTGEI 252
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 186 L-----DVKNNSLTLGVIPDITIGNCTSFQVLDLSYNRFEGPI 221
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 253 PDIIGFOVATLSLQCNLSGKIPSYIGLMQALVLDLSGNLSGSIPTIGLTLTEKYL 312
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 222 PFNIGFOVATTSLOQNKFTGPISVIGLMQALVLDLSYNQSGSIPSTLGNLTYTEKL 281
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 313 YLHNSKLTGSIPELGNMSKLYLELNDHNLTGHIPELGLKTDLPDLVANNDLBGPIDP 372
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 282 YIGQNKLTGSIPELGNMSTLHYLELNDQNTGSIPELGRLTGLDMLANNHLSGPIP 341
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 373 DLSLSCNTNLNSLVHGNKFSGTPPRAFOKLESMYTYLNSNNIKGPIPVELSINGLDTL 432
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 342 DNLSSCVNLNSFVAYNKLNLTGTPISRLKLESMTYLNLSNFSIGSIPIELSRINNDTL 401
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 433 DLSNNKINGITPSISGLDHLKMLNSRNHITGVPGDGNLRSIMEIDLSNNDISGPIP 492
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 402 DLSNNMTGPIPSISGLHLLRLNLKNGLVGFIPAEFGNLSVMEIDLSYNHLLGGLIP 461
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 493 EELNQLQNIILRLNNNLTVGNVSLANCLSLTVLVNSHNNLVGDIIPKNNNFSRFPSPDR 552
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
```

```
Db 462 OELEMLQNLM-----LANSYNNLAGVVPADNNFRFPSPDSF 498
QY 553 IGRPGGLGSLNBPCHDSRRTVSVISRRAIILGAIIGVILMLVLAACRPNNPFLD 612
Db 499 LGNPGJCGVYLSSCRGTGHEKEPPISKAAIIGVAVGLVILMLIVAACRPNNPFAFKD 558
QY 613 GSIDKPVYTPKLVILHMMALHVEDIMRMTENISEKYIIGHGASSTYKCVLKCKKP 672
Db 559 VYVSKPVRNAPKLVILHMMALHVEDIMRMTENISEKYIIGHGASSTYKCVLKCKKP 618
QY 673 VAIKRLYSNHPQSMKQFETELMLSSIKHKNLVSLQVLSLHSGSLFYDYLENGSLWLD 732
Db 619 VAIKRLYAHYPOSLKEFETELETGSIKHKNLVSLQVLSLHSGSLFYDYLENGSLWLDV 678
QY 733 LH-GPTKKKTLDMDTLRLKIVGAAGLAVYHDCSPRIHRDVSKNILLDKOLEALTD 791
Db 679 LHGGSSKKKKLDMETRLRIALGAAQGLAVYHDCSPRIHRDVSKNILLDKOLEALTD 738
QY 792 FGIASLSLVSKSHSTYVMGTIGYIDPEYARTSRUTEKSDVY-----SYGIVLELTLTR 846
Db 739 FGIASLSLVSKSHSTYVMGTIGYIDPEYARTSRUTEKSDVYRLMHCSAG----- 788
QY 847 KAVDESNNLHLIMSKTGNNEVEMADPDITSTCKDGVVKKVQFALALCTKQPNDRPT 906
Db 789 -AADWQASGQRLISKTSASNEVMDTVPDIDTCKDGEVKKLFQALALCTKQPNDRPT 847
QY 907 MHQVTRLGSMLESEPP---AATDTSATLAGSCVDEYANLTKPHSVCN-SSMSASDAQ 962
Db 848 MHEVVRVLDCLVMPDPKPSAHQLPQSPVPSVINEYVSLKRTGALSCANSTSTSDAE 907
QY 963 LFLRFGQVISONSE 976
Db 908 LFLKFGAISQNM 921
```

```
RESULT 5
US-11-027-304-4
; Sequence 4, Application US/11027304
; Publication No. US20050223428A1
; GENERAL INFORMATION:
; APPLICANT: Torii, Keiko U.
; APPLICANT: Shpak, Elena D.
; TITLE OF INVENTION: METHODS FOR MODULATING PLANT GROWTH
; FILE REFERENCE: UMOTL22663
; CURRENT APPLICATION NUMBER: US/11/027,304
; PRIORITY FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: US 60/558,529
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
US-11-027-304-4
```

Query Match 62.8%; Score 3167; DB 6; Length 614;  
Best Local Similarity 100.0%; Pred. No. 9.3e-211; Indels 0; Gaps 0;

```
Matches 614; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MALFRDIVLLGFELCSLVATVTSSEGAATLEIKKSFQDVNNVLYDWTSPSSDYCVWRG 60
Db 1 MALFRDIVLLGFELCSLVATVTSSEGAATLEIKKSFQDVNNVLYDWTSPSSDYCVWRG 60
QY 61 VSCENVTNNVVALNLSLNDGEISPAIGDKSLSLDLAGNRISGQIPDEIGCCSLQNL 120
Db 61 VSCENVTNNVVALNLSLNDGEISPAIGDKSLSLDLAGNRISGQIPDEIGCCSLQNL 120
QY 121 LDISPNEISGDIPEISIKLQLEQLIKKNQLIGPITSTISQIPNLITLDAQKLSGEI 180
Db 121 LDISPNEISGDIPEISIKLQLEQLIKKNQLIGPITSTISQIPNLITLDAQKLSGEI 180
```

```
QY 181 PRLIYNEVQLYGLGRNNLVGNISPDLCQLTGLWYFDVRNNSLTGISPETIGNCTAFQV 240
Db 181 PRLIYNEVQLYGLGRNNLVGNISPDLCQLTGLWYFDVRNNSLTGISPETIGNCTAFQV 240
QY 241 LDISYNQLTGEIIPFDIGFLOVATLSIQGNQLSKISFVIGLMALAVLDLSGNLSGSIP 300
Db 241 LDISYNQLTGEIIPFDIGFLOVATLSIQGNQLSKISFVIGLMALAVLDLSGNLSGSIP 300
QY 301 PILGNLTFEKLYLHNSKLTGSIPELGNMSKLIYELNDNHLTGHIPELGLTDLFDL 360
Db 301 PILGNLTFEKLYLHNSKLTGSIPELGNMSKLIYELNDNHLTGHIPELGLTDLFDL 360
QY 361 NVANNDDLEGPIDPHLSSCTNLNSLVNHNKFSGTIPRAFOKLESMTYLLNSNNIKPIP 420
Db 361 NVANNDDLEGPIDPHLSSCTNLNSLVNHNKFSGTIPRAFOKLESMTYLLNSNNIKPIP 420
QY 421 VELSRIGNLDLTLSSNNKINGIIPSSIGLEHLKKNLSNNHTTGVPDPFGMLRSIMEI 480
Db 421 VELSRIGNLDLTLSSNNKINGIIPSSIGLEHLKKNLSNNHTTGVPDPFGMLRSIMEI 480
QY 481 DLSNNDISGPIPELNLQNLIIILRLNNNLTGNSGLANCLSTVLYNASHNNLVGDIPK 540
Db 481 DLSNNDISGPIPELNLQNLIIILRLNNNLTGNSGLANCLSTVLYNASHNNLVGDIPK 540
QY 541 NNNFSRSPDSFIGNFGLCGSWLNSPCHDSRRTVRVSISRRAIILGAIIGLVILLMVLIA 600
Db 541 NNNFSRSPDSFIGNFGLCGSWLNSPCHDSRRTVRVSISRRAIILGAIIGLVILLMVLIA 600
QY 601 ACRPHNPPPLDGS 614
Db 601 ACRPHNPPPLDGS 614
```

```
RESULT 6
US-10-437-963-123824
; Sequence 123824, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; PRIORITY FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 123824
; LENGTH: 907
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(907)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_26620C.1.pep
US-10-437-963-123824
```

Query Match 62.3%; Score 3141.5; DB 4; Length 907;  
Best Local Similarity 65.1%; Pred. No. 9.2e-209; Indels 81; Gaps 11;  
Matches 631; Conservative 94; Mismatches 164; Indels 81; Gaps 11;

```
QY 13 LFCISLVATVTSSEGAATLEIKKSFQDVNNVLYDWTSPSSDYCVWRGVSCENVTNNVVA 72
Db 13 LVALLVAVAVADGSLTLEIKKSFQDVNNVLYDWTSPSSDYCVWRGVSCENVTNNVVA 72
QY 73 LNSLDNLNDEISPAIGDKSLSLT-DLRGNRLSGQIPDEIGCCSLQNLDISPNEISGDI 131
```

```

Db 70 LNTSGNLGGEISPAVGRKGVSMYGRGGVL-----CCCEEMW-----LAGA 113
Qy 132 IPPSISKLKLEQLILKKNQILGIPBTSISQIPNLKILDLAONKLSSEIPRLIYMWVLO 191
Db 114 WTRS-----MLTKNNQILGIPBTSISQIPNLKILDLAONKLSSEIPRLIYMWVLO 165
Qy 192 YLGLRGNLVGNISPDLCQLTGLMYFDVRRNNSLGSIPETIGNTAQOVLDISNOLTGE 251
Db 166 YLGLRGNLVGNISPDLCQLTGLMYFDVRRNNSLGSIPETIGNTAQOVLDISNOLTGE 201
Qy 252 IPPDIGLOVATLSLQGNOLSGKIPSVIGMOALAVLDLSGNLSGSIPIPIGLNPTFEK 311
Db 202 IPIINIGLOVATLSLQGNOLSGKIPSVIGMOALAVLDLSGNLSGSIPIPIGLNPTFEK 261
Qy 312 LYHSNKLTSIPPELGNSKLHYLELNDNLGHIPEPELGLTDLFDLVANNDEGP 371
Db 262 LYMOGNKLTPPELGNSKLHYLELNDNLGHIPEPELGLTDLFDLVANNDEGP 321
Qy 372 PDHLSCTNLNSLVHGNKFSGITPRAFOKLESMTYLNLSNNIKGPIPELSRIGLDT 431
Db 322 PDHLSCTNLNSLVHGNKFSGITPRAFOKLESMTYLNLSNNIKGPIPELSRIGLDT 381
Qy 432 LDISNNKINGIIPSSIGDLEHLKKNLSRNHITGVVPGDFGNLSIMEIDLNNDISGPI 491
Db 382 ENLSN---NGLV-----GFIPELGNLSIMEIDLNNHGLGLI 417
Qy 492 PEELELQNLILRLLENNNLITGVNSLANCLSLTVLVNSHNNLVGDI PKNNNFSRSPDS 551
Db 418 POELGLONLMLNLKNNITGTVSILMNFSLINILVNSYNNLAGVPTDNNFSRSPDS 477
Qy 552 FIGNPGICGWSLSPCHDSRRTRVVISRAIIGIAGLVILMLVLAACRPNNPEPL 611
Db 478 FLBNPGICGWSLSPCHDSRRTRVVISRAIIGIAGLVILMLVLAACRPNNPEPL 537
Qy 612 DGLSDPVTSTPKLVLILHNNMALHYVEDIMRMTENLSEKXIIGHGASSTVYKCVLKNCK 671
Db 538 DVSVPKRVSVNPKVLVLILHNNMALHYVEDIMRMTENLSEKXIIGHGASSTVYKCVLKNCK 597
Qy 672 PVAIKLVSHPKQFETELMSSIKRNLVSLQVSLSHLSGLTFDYLENGSLMD 731
Db 598 PVAIKLVSHPKQFETELMSSIKRNLVSLQVSLSHLSGLTFDYLENGSLMD 657
Qy 732 LILH-GPKKKKTLMDPRKTLAYGAOGLAYLHDCSPRIIHRDVKSNLILDLDEARLT 790
Db 658 VLHEGPKKKKTLMDPRKTLAYGAOGLAYLHDCSPRIIHRDVKSNLILDLDEARLT 717
Qy 791 DFGIAKSLCVSKSHSTVYMGITIGYIDPEYARTSRLTEKSDVYSYGIVLELTLTRKAVD 850
Db 718 DFGIAKSLCVSKSHSTVYMGITIGYIDPEYARTSRLTEKSDVYSYGIVLELTLTRKAVD 777
Qy 851 DESNLHLIMSKTGNNEVEMADPDITSTCKDLGVKKVFOALALCTKROPNDRTMHQV 910
Db 778 QRVOSPSXILSKTGNNEVEMADPDITSTCKDLGVKKVFOALALCTKROPNDRTMHQV 837
Qy 911 TRVLGSFMLSQPPAATDTSA---TLAGSCYVDEYANLTKTPHVSNGSMS--ASDAQFLR 966
Db 838 VRVLDCVLRDPDPKSAQOLAMPORPAVPSPYINEYVSLRGTSVLSGANSSTSDAELFLK 897
Qy 967 FGVVISONSSE 976
Db 898 FGEVISQNTSE 907

```

```

RESULT 7
US-11-027-304-8
; Sequence 8, Application US/11027304
; Publication No. US20050223428A1
; GENERAL INFORMATION:
; APPLICANT: Torii, Keiko U.
; APPLICANT: Shpak, Elena D.
; TITLE OF INVENTION: METHODS FOR MODULATING PLANT GROWTH
; FILE REFERENCE: UMOT122663

```

```

; CURRENT APPLICATION NUMBER: US/11/027,304
; CURRENT FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: US 60/558,529
; PRIOR FILING DATE: 2004-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 967
; TYPE: PRN
; ORGANISM: Arabidopsis Thaliana
US-11-027-304-8

Query Match          61.3%; Score 3089.5; DB 6; Length 967;
Best Local Similarity 62.2%; Pred. No. 4e+205;
Matches 605; Conservative 134; Mismatches 211; Indels 23; Gaps 6;

Qy 11 GFLFCLSLV-----ATVSEBGAATLEIKSPKQVNNVLYDMTSPSSDYCVMRGVSC 63
Db 9 GLFFCLGMVFMVLGVSVMNNNEGKALMAIKAFSNVANNLDMDDVHNHDFCSMRGVFC 68
Qy 64 ENTVFNVALNSDLNLDGEISPAIGDLSLSIDLRGNRLSQIPDEIGDCSSLOMLD 123
Db 69 DNVSLNVVSLNSLNLMDGELSGLDLMNLQSIDLQGNKLGQOIPDEIGNCVSLAYVDF 128
Qy 124 SFNELSGDIPFISIKLKOLELILKNNQILGIPBTSISQIPNLKILDLAONKLSGEIPRL 183
Db 129 STNLEFGDIPFISIKLKOLELILKNNQILGIPBTSISQIPNLKILDLAONKLSGEIPRL 188
Qy 184 IYMWVLYQVYGLRGNLVGNISPDLCQLTGLMYFDVRRNNSLTSIPETIGNTAQOVLD 243
Db 189 LYMWVLYQVYGLRGNLVGNISPDLCQLTGLMYFDVRRNNSLTSIPETIGNTAQOVLD 248
Qy 244 SYNOILGELIPDGLQVATLSLQGNOLSGKIPSVIGMOALAVLDLSGNLSGSIPIPI 303
Db 249 SYNOILGELIPDGLQVATLSLQGNOLSGKIPSVIGMOALAVLDLSGNLSGSIPIPI 308
Qy 304 GNLTFTEKLYHSNKLTSIPPELGNSKLHYLELNDNLGHIPEPELGLTDLFDLVANVA 363
Db 309 GNLTFTEKLYHSNKLTSIPPELGNSKLHYLELNDNLGHIPEPELGLTDLFDLVANVA 368
Qy 364 NNDLEGPIDHLSCTNLNSLVHGNKFSGITPRAFOKLESMTYLNLSNNIKGPIPEVL 423
Db 369 NNDLEGPIDHLSCTNLNSLVHGNKFSGITPRAFOKLESMTYLNLSNNIKGPIPEVL 428
Qy 424 SRIGNDITDLSSNNKINGIIPSSIGDLEHLKKNLSRNHITGVVPGDFGNLSIMEIDL 483
Db 429 GHIIINDITDLSSNNKINGIIPSSIGDLEHLKKNLSRNHITGVVPGDFGNLSIMEIDL 488
Qy 484 NNDISGPIPELQNLILRLLENNNLGNV--GSLANCLSLTVLVNSHNNLVGDI PKN 542
Db 489 ENFLAGVIFELGQOLQNLILRLLENNNLGNV--GSLANCLSLTVLVNSHNNLVGDI PKN 548
Qy 543 NPSRFSPPDSEFIGNPGICGWSLSPCHDSRRTRVVISRAIIGIAGLVILMLVLAAC 602
Db 549 NPSRFSPPDSEFIGNPGICGWSLSPCHDSRRTRVVISRAIIGIAGLVILMLVLAAC 607
Qy 603 RPHNPPPELIDGSLDKVYVSTPKVLILHNNMALHYVEDIMRMTENLSEKXIIGHGASSTV 662
Db 608 RPHNPPPELIDGSLDKVYVSTPKVLILHNNMALHYVEDIMRMTENLSEKXIIGHGASSTV 665
Qy 663 YKCVLKNCKPVAIKRILYSHNPOSQFETELMSSIKRNLVSLQVSLSHLSGLTFDY 722
Db 666 YKCVLKNCKPVAIKRILYSHNPOSQFETELMSSIKRNLVSLQVSLSHLSGLTFDY 725
Qy 723 YLENGSLMDLHGPRTKKTLDMDTRKLIAYGAOGLAYLHDCSPRIIHRDVKSNLILDL 782
Db 726 YLENGSLMDLHGPRTKKTLDMDTRKLIAYGAOGLAYLHDCSPRIIHRDVKSNLILDL 785
Qy 783 KDLERALTDPGIAKSLCVSKSHSTVYMGITIGYIDPEYARTSRLTEKSDVYSYGIVLEL 842
Db 786 GNFPEARLSDFGIAKSLPARKTYASTVVLGTYIDPEYARTSRLTEKSDVYSYGIVLEL 845
Qy 843 LTRKRAVDESNLHLIMSKTGNNEVEMADPDITSTCKDLGVKKVFOALALCTKROPN 902

```

```

Db      846  LTGKAYDNEANLHOMLISKADDNVTMEAVDAEVSVTCMDSHIKKTQALCTKRNPL 905
Oy      903  DRPTMHQVTRVLGSEFMLEQPPAATDTSATLAGSCYDEYANLKTPHSYNCSMSASDAQ 962
Db      906  ERPTMOEVSRLVLLSLVPSPPP-----KKLPSPAKVQGEERRESHSDITTT-----FQ 953
Oy      963  LFLRFGQVISON5 975
Db      954  WFOGFRDLSK5S 966

RESULT 8
US-11-027-304-6
; Sequence 6, Application US/11027304
; Publication No. US2005023428A1
; GENERAL INFORMATION:
; APPLICANT: Torii, Keiko U.
; TITLE OF INVENTION: METHODS FOR MODULATING PLANT GROWTH
; FILE REFERENCE: UWOTL22663
; CURRENT APPLICATION NUMBER: US/11/027.304
; PRIOR FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: US 60/558,529
; PRIOR FILING DATE: 2004-04-01
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 966
; TYPE: FRT
; ORGANISM: Arabidopsis Thaliana
; US-11-027-304-6

```

Query Match	61.1%	Score 3079.5	DB 6	Length 966
Best Local Similarity	62.7%	Match No. 2e-204		
Matches 608	Conservative 140	Mismatches 205	Indels 17	Gaps 6
QY	7	IVLLGFLFCLSLVAVTVTSEEGATLLLEIKKSFEDVANNVYDWMTSPSSDYCVWRGVSCENV	66	
Db	12	LAMVGFV--VEGVASAMNNEKALMAIKGSPSNLVNMLDDVDVNSDLCMRGVFCENV	69	
QY	67	TENVVALNSDLNLDEGISPAIGDKSLSIDLRGNRLSGQIPDEIGDCCSLQNLDSFN	126	
Db	70	SYSVAVLSLSSLNIGGEISPAIGDRNQSIDLQGNKLAGQIPDEIGNCASLVYDLSFN	129	
QY	127	ELSGDIPRSIKLQLEBOLLKNNOLLIPISLTSLQINMLKIDLAOKLGSERRLVW	186	
Db	130	LLVYDIPRSIKLQLETLNKKNNOLLTPVPVPTLLQIENLRKLDLAGNHLTGELISRLVW	189	
QY	187	NEVVOYGLGRNNLVGNISPDLCOLGTGWYEDVRNNSTGSIPIETIGNCTAFVOLDISYN	246	
Db	190	NEVVOYGLGRNNLTGTLSSDMCQLTGLMYEDVRNNLTGTLPEISIGNCTSFQIOLDISYN	249	
QY	247	QLTGEIPPDIGFLOYAITSLOGNOLSGKIPSVIGLMOALAVLDSGNLLSGSIPPIIGNL	306	
Db	250	QITGEIPYNIQVATLSLOGNRLTGRIPEVIGLMOALAVLDSNDELVEPIPIILGNL	309	
QY	307	TTFETKLYHSKULGSPPELGNSKLAHYLELDNHLTGHIPEELGKLTDLFDLVANNDD	366	
Db	310	SFTKLYLHGMLTGPIPELGGNSRSLYLQINDKLVGTIPEELGKLEQFELMLANSR	369	
QY	367	LEGEPIPHLSSCTYMLNSLVGNKPSGRTIPRAFQKLESMETYLNLSNNIKGPIPELTSRI	426	
Db	370	LVGPIPSNISSCALNQFNHVGNNLLSGSILPLAFRLGSLTYLNLSNNFKGPIPELCHI	429	
QY	427	GNLDTLDSNNKINGIIPSSJGDLLEHLIKMLSRNHTGTVVPGDFGNLRSTWEIDLSSND	486	
Db	430	INDKPLDSGNPFSGSIPLTGLGDLLEHLITLNSRHLTSGQIPAEFGNLSRIQMDIVSFNL	489	
QY	487	ISGPIPEELNOLNITLLRLENNMLTGV--GSLANCLSTVLYNVSHNLTGDIPIKNNSS	545	
Db	490	LSGVIPEELGQLONSLILNNKKLHGKIIPDLTNCFTLVNLNVSFNNLSGIVPMKQPS	549	

```

QY 546 R$P$D$F$G$N$P$G$L$C$G$M$L$N$P$C$H$D$R$T$R$V$R$S$I$P$A$I$L$G$V$Y$M$L$M$V$L$A$C$R$P$H 605
Db 550 R$P$A$F$V$G$N$P$Y$L$C$G$W$G$S$I$G$P$L$P$K$S-RV-F$R$G$A$L$I$C$V$I$G$V$Y$M$L$C$M$I$F$L$A$Y$K$M 607
QY 606 N$P$P$F$D$G$S$I$D$P$V$T$S$T$R$P$K$V$I$L$M$M$N$A$L$H$Y$E$D$I$M$T$E$N$T$E$S$K$Y$I$G$H$A$S$T$Y$Y$K 665
Db 608 Q$K$K$U$L$Q$G$S$K$Q--A$E$G$L$K$V$Y$M$L$M$D$A$H$T$F$D$I$M$K$V$E$N$T$E$N$L$E$K$U$L$I$G$G$A$S$T$Y$Y$K 665
QY 666 V$L$K$C$K$P$V$A$I$K$U$L$Y$H$N$P$O$M$K$Q$F$E$T$E$M$L$S$I$K$R$N$V$S$L$O$A$Y$S$I$H$G$S$L$F$Y$Y$E 725
Db 666 A$L$K$S$P$P$I$A$I$K$U$L$Y$O$P$H$N$L$R$E$F$E$T$E$T$G$S$I$R$H$R$V$S$L$H$O$Y$A$S$P$G$N$L$F$Y$D$Y$M$E 725
QY 726 N$G$S$I$M$L$L$G$P$T$K$K$T$L$D$M$D$R$L$A$Y$A$O$G$L$A$Y$H$H$D$C$P$R$I$H$D$V$K$S$N$L$L$D$K$L 785
Db 726 N$G$S$I$M$L$L$H$G$L$K$K$Y$K$G$M$E$T$R$K$A$V$G$A$O$G$L$A$Y$H$H$D$C$P$R$I$H$D$V$K$S$N$L$L$D$E$N$F 785
QY 786 E$A$R$L$D$F$G$I$A$K$S$C$V$K$S$H$T$S$Y$V$G$T$G$Y$D$I$D$E$V$A$R$T$S$R$L$T$E$K$S$D$V$Y$G$V$Y$L$E$L$L$R 845
Db 786 E$A$H$I$S$F$G$I$A$K$S$I$P$A$S$K$T$A$S$T$Y$V$G$T$G$Y$D$I$D$E$V$A$R$T$S$R$I$N$E$K$S$D$Y$S$G$V$Y$L$E$L$L$T$G 845
QY 846 R$K$A$V$D$E$S$U$L$H$L$I$M$S$K$T$G$N$N$E$V$M$E$A$R$D$I$T$S$C$K$L$G$V$Y$K$Y$F$O$A$L$L$C$T$R$Q$P$D$R 905
Db 846 K$K$A$V$D$E$A$N$H$O$L$I$S$K$D$D$N$T$M$A$V$D$E$V$T$V$C$M$D$G$H$R$K$F$O$A$L$L$C$T$R$N$P$E$R$P 905
QY 906 T$M$Q$V$T$R$V$L$G$F$M$L$S$E$Q$P$A$T$D$T$S$A$T$A$G$S$C$Y$V$D$E$V$A$N$L$K$T$P$H$V$N$C$S$M$S$A$D$A$Q$L$P$L 965
Db 906 T$M$L$E$V$S$R$V$L$L$S$V$P$S$Q-----V$A$K$L$P$S$I$D$H$S$T$K$Y$L$Q$E$N$E$V$R$P$D$A$S$Q$W$F$V 955
QY 966 R$G$O$V$I$S$O$N$S 975
Db 956 Q$F$R$E$V$I$S$K$S 965

```

```

RESULT 9
US-10-425-115-367213
; Sequence 367213, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated w
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 367213
; LENGTH: 909
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(909)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MR14577_98067C.1.pep
US-10-425-115-367213

Query Match          58.1%; Score 2931; DB 4; Length 909;
Beat Local Similarity 64.5%; Pred. No. 3.6e-194;
Matches 590; Conservative 121; Mismatches 176; Indels 28; Gaps 10

Qy      77  DNLWDEISPAIGDKLSLIDLRGNRKSQGPPEIGDCSSLWLDSPFELSGLDIPFSI 136
Db      5  DNLWGEISPAIGDKLSQPFVDLKLKLNKLTGQIPPEIGDCVSLKYLDSGNLLVGDIPFSI 64

Qy      137 SKUKOLEQIILKNNOIGIPETTSQIPNLKIILDAQNKSGEIPRLIYNNEVLQYGLR 196
Db      65  SKUKOLEDILKNNOITGPPISTLSQIPNLKTLIDLAQNKLTGDPRLIYNNEVLQYGLR 124

Qy      197 GNNLVGNISPDLCOLTGILWYFDPVRNNSLTGSIPEITGNCTAFQVLIDLSYNQLTGEIIPDI 256

```

```
125 GNSLTGTLSPDMCQTLGLMYFDIRGNNTLTGTEGIGNCTSFELIDISYNQISGEIPYNI 184
257 GFLQVATLSIQNGQSGKIPSVIGLMOALVLDLISGULSGSPILIGNLTFFEKLYLHS 316
185 GYLQVATLSLHRRLKIGKIPVIGLMOALVLDLISENELVGPPIIGNLSYGLKVLHG 244
317 NKLTSIPPELGMSKLAHYLELNDNLTHGHPPELGKLTDLFDLNVANNDLEGPIDHLS 376
245 NKLTHGHPPELGMSKLSYQLNDNLVGTIPALGLTDLFELNANNNLEGHIPANIS 304
377 SCTNLSLVNHNKFSGTIPRAPOKESMTYLLSSNNIKGPIPELSRIGNDTDLNLSN 436
305 SCGALKKENYGNRLNGSIPAGFOKLESLEYLNLSSNSFKQGPSELGIVNLDITLDSY 364
437 NKLNGIIPSSLDLEHLKLNLSRNHTGVPGDGLRLSIMEIDLSNNISIGIPBELN 496
365 NEFSGPVPTIGLEHLELNLKNSLHLSVPAEFGMLRSVQVIMSSNNLSGLPELGL 424
497 QLQNIILRLNENNLGTGNV-GSLANCLSLVLANVSHNNL-----VGDIPKNNNFSRSPD 550
425 QLQNLDSLIANNNSLAGEIPRAQLNCFSLVTLVYIQQLMARPIEKLKVPN-----GX 479
551 SFTGNPGLCGSWINSPCHDSRRTRVVISISRAILGLAIGLVTLLMYLLAACRPHNPPF 610
480 SFMGNLMLAHYCODSSCGSHSGT-KVISRTAVACMLIGFVILLCTVLAIFYKT-NQPOL 537
611 LDGSLDKPVTYTPKLVILHMNALHYEDIMRTENLSKYTIIGHASSTYVCULKNC 670
538 PEKASDKPV-QGPPKIVLQMDMAVHTYEDIMRLTEMLSEKYYIIGYASSIVYRCDLKSG 596
671 KPAVKRLVSHNPOSMKOFETELMELSSIKHRNLVSLQAVSLSHLSGLLFPDYLENGSLW 730
597 KAIIVAKRLVSOYHNSLREFTELETIGSIHRNLVSLHGSLSLPHGULLYDIWENGSLW 656
731 DLLHGPTKKKTLDMDTRLKIAYGAAQGLAVLHDCSPRIIHRDVKSSNILLDXLEARLT 790
657 DLLHGFSKVKVTKLMDTRLRIAVGAQGLAVLHDCNPRIVHADVSSNILLDGSFEHLHS 716
791 DFGIASLVCYSKSHSTYVNGTIGYIDPEYARTSRLETEKSDVSYGVVLELTLRRAVD 850
717 DFGIACVPAKSHASTYVGTIGYIDPEYARTSRLEKSDVSYFGVVLLELTLRRAVD 776
851 DESNHLHLIMSKTGNNEVEMADPDITSTCKDGVVKKVQLALLCTKROPNDPRTMGV 910
777 NBSNHLQLISKADDDVTMAVDEVSVTCTDMVLKAKAFQALALCTKRHPADRPMAEV 836
911 TRVLGSFMLESEOPPA-TDTSATLAGSCYVDEYAN-LKTPHSV-----NCSMSASD 960
837 ARVL-----LSLPPAKKPPASKAAASAAAGDYTRFLATAADLRGGVADDDTGDNSSD 892
961 AQLFARFGOYISONS 975
893 EQWFEVFEVTSKHT 907
```

RESULT 10  
US-10-437-963-169553  
; Sequence 169553, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Roga, Thomas J.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Bing  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963

```
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 169553  
; LENGTH: 885  
; TYPE: PRN  
; ORGANISM: Oryza sativa  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(885)  
; OTHER INFORMATION: unsure at all xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT_MRT4530_67963C.1.pep  
US-10-437-963-169553  
  
Query Match 57.9%; Score 2921.5; DB 4; Length 885;  
Best Local Similarity 60.1%; Pred. No. 1.6e-193;  
Matches 599; Conservative 96; Mismatches 147; Indels 155; Gaps 13;  
  
13 LFCLSVATVTSSEGAATLEIKKSPFDVNNVLYDWT-TSPSSDYCVWRGVSCENVTFNV 71  
11 LAAIILAVAAADDDGQTLLEIKKSPFRVDNVLYDMAAGDAPRRCYCSRGVLCNVTFAVA 70  
72 ALNLSLNDLDETSIPAIGDKLSLIDLKGNRLSGQIPDEIGCCSLQNLDSLPELNSGD 131  
71 AL-----DLKSNELSGQIPDEIGCTSIKT----- 95  
132 IFFSISKLQLEQILLKNNQILGPIPTLSQIPNLKILDAONKLSGEIPRLIYNNELQ 191  
96 -----LILKNNQLVGMIPSTLSQLENLKILDAONKLSGEIPRLIYNNELQ 142  
192 YL-----GLRGNLVGNISPDLCQTLGLWYFVRNNSLTGSIPTETGNCFAQ 239  
143 YLNLKNCNVQIYRGLRSNNLBSLSPEMQQLGLWY----- 179  
240 VLDLSYNQLTGEIPEDIGVQVATLSIQNGQSGKIPSVIGLMOALVLDLISGULSGSI 239  
180 -LDLSYNRLTGEIPFNIGVQVATLSIQNGQSGKIPSVIGLMOALVLDLISGULSGPI 238  
300 PPIIGNLTFFEKLYLHNSNKLTSIPPELGMSKLAHYLELNDNLTHGHPPELGKLTDLFD 359  
239 PSILGNLTYTEKLYLQGNRLTGSIPPELGMSKLAHY----- 274  
360 IYVANNNDLEGPIDPHLSCTNLSLVNHNKFSGTIPRAPOKESMTYLLSSNNIKGPI 419  
275 IYVANNNDLEGPIDPHLSCTNLSLVNHNKFSGTIPRAPOKESMTYLLSSNNIKGPI 310  
420 PVELSRIGNLDTLDSNNKINGIIPSSLDLEHLKLNLSRNHTGVPGDGLRLSIME 479  
311 PIELAKKKNLDTLDSNNVAGIIPALISGLEHLRLNFSNNNLVGYIPAEFGNLSIME 370  
480 I-----DLSSNDISGPIPELNLQNLITLLENNNLGNVGLANCLSLVLANVSHN 532  
371 IFLFCFSDLSNHLGGLIPQEVGMQLNLILKLENNNTIGDVSSILNCSLVLANVSYN 430  
533 NLVGDIPKNNNFSRFPDSFTGNPGCGSWINSPCHDSRRTRVVISISRAIILGIAIGLV 592  
431 NLVGIPTDNNFSRFPDSFTGNPGCGSWINSPCHDSRRTRVVISISRAIILGIAIGLV 490  
593 ILLMVLIAACRPHNPPFLDGLSDKPVTS-----TPKLVILHMNALHYEDIMKMT 646  
491 ILLMVLIAACRPHNPPFLDGLSDKPVTS-----TPKLVILHMNALHYEDIMKMT 550  
647 NLSKYYIIGHASSTYVCULKCKCKVAIKRLYSHNPOSMKOFETELMELSSIKHNLVS 706  
551 NLSKYYIIGHASSTYVCULKCKCKVAIKRLYSHNPOSMKOFETELMELSSIKHNLVS 610  
707 LQAVSLSHLSGLLFPDYLENGSLMDLH-GPTKKKTLDMDTRLKIAYGAAQGLAVLHDC 765  
611 LQAVSLSPAGNLFPDYLENGSLMDVLAHSSSKQKLDHEARIRILGAAQGLAVLHDC 670  
766 SPRIIHRDVKSSNILLDKLEARLDFGIASLVCYSKSHSTYVNGTIGYIDPEYARTSR 825  
671 NPRIIHRDVKSSNILLDKLEARLDFGIASLVCYSKSHSTYVNGTIGYIDPEYARTSR 730
```



OY	826	LTEKSDVSYGIVLIELLTRRAVDDESNLHLLMSKTGNNEVMEMADPITSCKDGLCV	885
Dd	731	LNESKDYYXLMHCPCGATYTRQKAXNENCLMHLILSKADNTVMEMVPEDIDTCDLGE	790
OY	886	VKKYFQLALLCTKRPQNDPTMHQVTRYLVSGFMLEBP-----PATDTSATLAASCYVD	940
Dd	791	VKKYFQLALLCSKRQPSDRPTMEHVVRVLDCLYPDPPSKPALPALPOSTIVPS--YVN	848
OY	941	EYANLKTPHSVNC-SSMSASDAOLFRLFGOVISONSE 976	
Dd	849	EYSLRGSTLSCENSASSDAELFLKFGEVISONTMTE 885	
 RESULT 11 US-10-425-114-58448			
Sequence 58448, Application US/10425114			
Publication No. US2004003488A1			
GENERAL INFORMATION:			
APPLICANT: Liu, Jingdong			
APPLICANT: Zhou, Yihua			
APPLICANT: Kovalic, David K.			
APPLICANT: Screen, Steven E			
APPLICANT: Tabaska, Jack E			
APPLICANT: Cao, Yongwei			
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With			
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement			
FILE REFERENCE: 38-21(53313)B			
CURRENT APPLICATION NUMBER: US/10/425, 114			
CURRENT FILING DATE: 2003-04-28			
NUMBER OF SEQ ID NOS: 73128			
SEQ ID NO 58448			
LENGTH: 764			
TYPE: PRT			
ORGANISM: Zea mays			
FEATURE:			
OTHER INFORMATION: Clone ID: UC-ZMFLB73041E04_FLI.pep			
US-10-425-114-58448			
 Query Match            55.3%; Score 2791; DB 4; Length 764;			
Best Local Similarity   71.8%; Pred. No. 1,5e-184;			
Matches 535; Conservative 85; Mismatches 113; Indels 12; Gaps 3;			
OY	242	DLSYNQLTGEIPEFDIGLOVATTLSQGNLGSKIPSVIGLMOALAVLDLSGMLSGSIPP	301
Dd	18	DLSYNRFGPIRPFNGIFLOVALTLISLGKNKFTGPISPVIGLMOALAVLDLSTYNLGSPIRS	77
OY	302	ILGNLTTFEKLYLSHNKLTGSIPELIGNNSKLIHYELDNHULTGHIPELGIKLTDLFDLN	361
Dd	78	ILGNLTYTEKLYMQGNRLTGISIPELIGNNSTHYELDNNOGTGISIPELIGRLTGDFDN	137
OY	362	VANNLEGPIPHLSSCTNLNSLWNGNFSGCITPAFOKLESMTMYLANSNNIKPIPV	421
Dd	138	LANNLEGPIPNLSSCVNLNSFNNAAGNLANGTIPSRLKLSMTMYLANSNFISSGIPI	197
OY	422	ELSIRIGNDLTDLSNNKINGIIPSSIGDELHKMLSRNHITGVVPGDFGNLRIMEID	481
Dd	198	ELSRINNDLTDLDSNMWTMGPIPSISIGNLEHLRLNLSKNDLVGFPAFGMLRSMEID	257
OY	482	LSNNDISGPIPELNLONIIILRLERNNLTVGVSGLANCLSLTYLVNSHNNLVGDIPKN	541
Dd	258	LSYNNLGGIIPOLMLQWIMLTKLENNNI TGDVSSLNMCFSINTLVSYNNLAGAVPTD	317
OY	542	NNFSRFSPDSFIGNGLGSMWNSPCHDRRTYRVASISAAIILGAILGVLILMWLIA	601
Dd	318	NNFTFRSHDSFGNGLGCIYMWLGSSCRSTGHDKDPISRAAIIGAVAGVILLMTLVAV	377
OY	602	CRPHNPPEFLDGLDKPYVTYSTPKULVILMMNALHYVEDIMRETMENLSEKYIIIGHGASST	661
Dd	378	CRPHHPPAFKDATVKSPVNGBPRLVYLHMNALHFDDIMRETMENLSEKYIIIGVGASST	437
OY	662	VYKCYLKNCKPAIRKLYSHNQSKQFETELMSSITGRNLVSTQAISHLGSLLEY	721

Db	438	VYKCVLKNCKEVAALKLYAHNPQSLKEPTELETETGSIKRHLVLSIQGSLSBPVGUNLPF	497
Oy	722	DYLENGSILMDLH-GPTKKTKTLDWDTRLKIAYGAAGALYLHHDCSPRIIHRDVKSNTL	780
Db	498	DYMEGSILMDVLHEBSSSKKNKLDMVTLRIRIALGAAGALYLHDCSPRIIHRDVKSNTL	557
Oy	781	LKDLEAFLTPGLAKSLCVSKSHSTSYMGTIGYIDEPYATSRILETSDDVYSYGVLL	840
Db	558	LDKDYEAFHTDFGIKSLCVCSTKTHSTSYMGTIGYIDEPYATSRILETSDDVYSYGVLL	617
Oy	841	EELTRKRYVDDESNNLHLIMSKTGNNVEMNDPITSCDKLGAVKYFOALCTKREQ	900
Db	618	EELTRKRYVDDECNLHLILSTASNEVMETDPVGDICRDLGEVKLFOLALLCTKQQ	677
Oy	901	PNDREPMQYTRVLGSFMLSEQP-----AATDSATLAGCYVDENALNKPMS	950
Db	678	PSDRRTMEHVRRVLDCLVNPEPPQPQQOQKAHAHQLPQPSPAYDEVYSLRGTA	737
Oy	951	VNC-SSMSADPOLFRFGOVISON 974	
Db	738	LSCANSSSTSDAELFKFEAISQN 762	
 RESULT 12 US-10-425-115-262277			
; Sequence 262277, Application US/10425115			
; Publication No. US20040214272A1			
; GENERAL INFORMATION:			
; APPLICANT: La Rosa, Thomas J.			
; APPLICANT: Kovalic, David K.			
; APPLICANT: Zhou, Yihua			
; APPLICANT: Cao, Yongwei			
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With			
; TITLE OF INVENTION: Plants			
; FILE REFERENCE: 38-21(53222)B			
; CURRENT APPLICATION NUMBER: US/10/425,115			
; CURRENT FILING DATE: 2003-04-28			
; NUMBER OF SEQ ID NOS: 369326			
; SEQ ID NO 262277			
; LENGTH: 764			
; TYPE: PRT			
; ORGANISM: Zea mays			
; FEATURE:			
; NAME/KEY: unsure			
; LOCATION: (1)..(764)			
; OTHER INFORMATION: unsure at all Xaa locations			
; FEATURE:			
; OTHER INFORMATION: Clone ID: MRT4577_17080C.1.pep			
US-10-425-115-262277			
 Query Match                53.8%; Score 2712; DB 4; Length 764;			
Best Local Similarity 70.1%; Pred. No.4.e-179;			
Matches 522; Conservative 85; Mismatches 126; Indels 12; Gaps 3;			
Oy	242	DLSYNQLGELIPFDLGFLOVATLISLQGNLSKRSIVIGLMQALNLDSLNLSSGIPP	301
Db	18	DLSYNRFPGPIPFNIGFLOVATLISLQGNKFETPIBSVIGLMQALNLDSLNLSSGIPBS	77
Oy	302	ILGNLTPEKYLHNKTLGSIPELEGNNSKLHYELELNHNLTGHIPELEGKLTDFPDN	361
Db	78	ILGNLTPEKLYMGNRLLTGISPELEGNMSTHYLELNDNLGTSIPPELGRITGFLDN	137
Oy	362	VAANDLEGPIPDHLLSCCTNLNSLVNHGKFSGITPAFQKLESMTYLNLSNNIKGPPIP	421
Db	138	LANNHLEGPIDPLNSSCVNLNSFNAYGNKLTNGTIPRSLRKLESMTYLNLSNFISSGIP	197
Oy	422	EISRIGNDITDLSNNKINGITPSSLGDIHELKMLSNKHNTGGVPDGFNLRSMIED	481
Db	198	EISRINNDDITDLSNNMGTPIPSIGNIEHLRLNLSTNDLVGFTPAEFGNLRSMIED	257
Oy	482	LSNNDISGPPELNLQNIILRLENNULTGNVGSLACLSTVTVNVEHNNLVGDI PKN	541
Db	258	LSYNHGGLIPBELMLQNLMLKLENNNITGDVSSLMNCFSLINIINVSNNLAGAVPTD	317



QY 542 NNFSPFSDPFIQNGPGLGSGWLNPCCHDSRTYVSVISRAAIIIGIATIGLVIILMLVIAA 601  
 DB 318 NNTFRSHDFLQNGPGLGSGWLNPCCHDSRTYVSVISRAAIIIGIATIGLVIILMLVIAA 377  
 QY 602 CRPHNPPLDGLSDKPVYTPKLVILHNMALHYEDIMRMENTLSEKXIIIGHGASST 661  
 DB 378 CRPHNPPLDGLSDKPVYTPKLVILHNMALHYEDIMRMENTLSEKXIIIGHGASST 437  
 QY 662 VYKCVLKNCRPAVAKRLYSNHPQSMKOFETELMSSIKRNLVSLQAYSLSHLSGLTFY 721  
 DB 438 VYKCVLKNCRPAVAKRLYSNHPQSMKOFETELMSSIKRNLVSLQAYSLSHLSGLTFY 497  
 QY 722 DYENSGSLMVLH-GPTKKTLDMDTFLKTAAYGAAGLAVLHHDSPRIIHRDVKSNIL 780  
 DB 498 DYENSGSLMVLH-GPTKKTLDMDTFLKTAAYGAAGLAVLHHDSPRIIHRDVKSNIL 557  
 QY 781 LDKDLEARLTDGIAKSLCVSKSHSTYVWGTTGYIDPEYARTSRLTEKSDVYSYGIIVL 840  
 DB 558 LDKDLEARLTDGIAKSLCVSKSHSTYVWGTTGYIDPEYARTSRLTEKSDVYSYGIIVL 617  
 QY 841 ELITRRKAVDDESNLHILMSKTGNNEMEMADPDITSTCKDGVKKVQALALCTKRQ 900  
 DB 618 GAADROEASGQRKNLHILMSKTGNNEMEMADPDITSTCKDGVKKVQALALCTKRQ 677  
 QY 901 PNDPRTMHQVTRVYLGSPMLSEOP-----AATDSATLAGSCYDVEYANLKTPHS 950  
 DB 678 PNDPRTMHQVTRVYLGSPMLSEOP-----AATDSATLAGSCYDVEYANLKTPHS 737  
 QY 951 VNC-SSMSASDAQFLFRFGOVISON 974  
 DB 738 LSCANSSTSDAELFLKFGAISON 762

RESULT 13  
 US-10-437-963-121441  
 ; Sequence 121441, Application US/10437963  
 ; Publication No. US20040123343A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Wu, Wei  
 ; APPLICANT: Boukharov, Andrey A.  
 ; APPLICANT: Barabuk, Brad  
 ; APPLICANT: Li, Ping  
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53221)B  
 ; CURRENT APPLICATION NUMBER: US/10/437, 963  
 ; CURRENT FILING DATE: 2003-05-14  
 ; NUMBER OF SEQ ID NOS: 204966  
 ; SEQ ID NO 121441  
 ; LENGTH: 962  
 ; TYPE: PRT  
 ; ORGANISM: Oryza sativa  
 ; FEATURE:  
 ; NAME/KEY: unsure  
 ; LOCATION: (1)..(962)  
 ; OTHER INFORMATION: unsure at all Xaa locations  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_24466C.1.pep  
 US-10-437-963-121441

Query Match 49.3%; Score 2484.5; DB 4; Length 962;  
 Best Local Similarity 53.0%; Pred. No. 3.5e-163;  
 Matches 528; Conservative 140; Mismatches 196; Indels 133; Gaps 18;

QY 26 EGATLLEIKSFDVNNVLYDMTSSDYCWARGSCVENTFNVVAL----- 73  
 DB 35 EGKALMGVKGAFGNAAVALVDM--DGADHCAWGVTCDNASFAVALSLDISBALFVM 92

QY 74 -----NLSDNLNDEISPAIGDLKSLSLDLKGNRLSGOIPPEIGDCSS 117  
 DB 93 LKRIFWRVFPCYKNNLSNLNDEISPAIGDLKSLSLDLKGNRLSGOIPPEIGDCSS 138  
 QY 118 LQNLDSFNLSDIPPSISKQLQLEOLIKNNQLIGPIPSLSQIPNLKILDLQNKLS 177  
 DB 139 -----LYGDIDFSSISKQLQLEOLIKNNQLIGPIPSLSQIPNLKILDLQNKLT 188  
 QY 178 GEIPRLTYMNEVQYGLRGNNLVGNISPDLCQTLGMYDVANNLSLTSIPETIGCTA 237  
 DB 189 GDIPRLTYMNEVQYGLRGNNLVGNISPDLCQTLGMYDVANNLSLTSIPETIGCTA 248  
 QY 238 FOVLDSYNQLTGEIPEDIFLOVATLSQGNQSLGKIPSVIGLQALVLDLSGNLSS 297  
 DB 249 FEILDISYNOISGEIPENIGFOVATLSQGNQSLGKIPSVIGLQALVLDLSGNLSS 298  
 QY 298 SIPIILGNLTFTKLYLHNSKLTGSIPPEIGNSKLHYLELNDNLTHGIIPEELGKLTDL 357  
 DB 299 -----LYLHGNKLTGVIPPELGNNSIRSYGKMFNDELVGTIPAEIGKLEEL 344  
 QY 358 FDLNVANNDLEGP1PDHLSCTNLNSLVHGNK-----FSGTIPARQKL 402  
 DB 345 FELNLANNLQGP1PANISSCTAONTMSYGSKILDENFEAHLSDGIAKCVPSA--KS 402  
 QY 403 ESMTYLNSLNNTKGP1PELRSIGNLDTLSDNNKINGIIPESLGLDEHLKMA----- 456  
 DB 403 HASTY-----VLGHT-----INLDTLDSYNESGVPATIGV--LLQLLTNKKA 447  
 QY 457 --NLNRHITGVVPGDFGNLRSIMEIDLNSNDISGPIPEELNOLQNIILLENLNLGN 514  
 DB 448 VDNESNLHQLILSKAD--ANTVME--AXNNLSGSIPEELQOLNLDLSLITNNKFPSS 501  
 QY 515 VGLANCLSTVLVANSNNLVGDIPKNNNSRSPSPSFGNPGLCGSLNCPCHDSRTV 574  
 DB 502 DRPTMELQVLVLSLPASSIA--TPRTVDYSPVAXSTVGNPLHYVCOSSGSHSGQ-- 559  
 QY 575 RVASISRAAIIIGIATIGLVIILMLVIAACRPHNPPLDGLSDKPVYTPKLVILHNMMA 634  
 DB 560 RVASISRAAIIIGIATIGLVIILMLVIAACRPHNPPLDGLSDKPVYTPKLVILHNMMA 617  
 QY 635 LHVYEDIMRMENTLSEKXIIIGHGASSTVYKCVLKNCRPAVAKRLYSNHPQSMKOFETE 694  
 DB 618 LHVYEDIMRMENTLSEKXIIIGHGASSTVYKCVLKNCRPAVAKRLYSNHPQSMKOFETE 677  
 QY 695 MLSIKRNLVSVQAYSLSHLSGLTFDYDLENESLMDLHGPKKTTLDMDTFLKTAAYGA 754  
 DB 678 TISIRHRLVSVQAYSLSHLSGLTFDYDLENESLMDLHGPKKTTLDMDTFLKTAAYGA 737  
 QY 755 AGLAVLHHDSPRIIHRDVKSNILDLKDLKTLDFGIAKSLCVSKSHSTYVWGTTG 814  
 DB 738 AGLAVLHHDSPRIIHRDVKSNILDLKDLKTLDFGIAKSLCVSKSHSTYVWGTTG 797  
 QY 815 YIDPEYARTSRLTEKSDVYSYGIIVLELITRRRAVDDESNLHILMSKTGNNEMEMADP 874  
 DB 798 YIDPEYARTSRLTEKSDVYSYGIIVLELITRRRAVDDESNLHILMSKTGNNEMEMADP 857  
 QY 875 DITSTCKDGVKKVQALALCTKRQPNDRPTMHQVTRVYLGSMLE--QPPAATPSAT 932  
 DB 858 EVSVTCIDMGLVAKAQALALCTKRQPNDRPTMHQVTRVYLGSMLE--QPPAATPSAT 917  
 QY 933 LAGSCYDVEYANLKTPHSVNCSMSASDAQFLFRFGO 969  
 DB 918 LASTTTA--ADMRGHDVTDIGNSSSDEQWFRFGE 951

RESULT 14  
 US-10-425-114-45783  
 ; Sequence 45783, Application US/10425114  
 ; Publication No. US20040034888A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Liu, Jingdong  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Kovalic, David K.

```

: APPLICANT: Screen, Steven E
: APPLICANT: Tabaska, Jack E
: APPLICANT: Cao, Yongwei
: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
: TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
: FILE REFERENCE: 38-21(53313)B
: CURRENT APPLICATION NUMBER: US/10/425,114
: CURRENT FILING DATE: 2003-04-28
: NUMBER OF SEQ ID NOS: 73128
: SEQ ID NO 45783
: LENGTH: 578
: TYPE: PRT
: ORGANISM: Glycine max
: FEATURE:
: OTHER INFORMATION: Clone ID: 700954473_FLI.pep
: US-10-425-114-45783

```

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: September 2, 2006, 06:56:20 ; Search time 51 Seconds

(without alignments)  
1675.096 Million cell updates/sec

Title: US-10-519-135-2

Perfect score: 5043

Sequence: 1 MALFRIIVLLGFPLCLSLVA.....SASDAQFLRFQGVISQNSE 976

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /EMC Celerra AIDS/prodata/2/iaa/5 COMB pep:\*
- 2: /EMC Celerra AIDS/prodata/2/iaa/6 COMB pep:\*
- 3: /EMC Celerra AIDS/prodata/2/iaa/7 COMB pep:\*
- 4: /EMC Celerra AIDS/prodata/2/iaa/H COMB pep:\*
- 5: /EMC Celerra AIDS/prodata/2/iaa/PCTUS COMB pep:\*
- 6: /EMC Celerra AIDS/prodata/2/iaa/RE COMB pep:\*
- 7: /EMC Celerra AIDS/prodata/2/iaa/backfillseq pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1568	31.1	502	2	US-10-101-464A-945
2	1432.5	28.4	998	2	US-10-101-464A-931
3	1404.5	27.9	998	2	US-10-101-464A-895
4	1393.5	27.6	370	2	US-10-101-464A-944
5	1384.5	27.5	1021	2	US-10-101-464A-954
6	1360.5	27.0	990	2	US-10-101-464A-814
7	1355	26.9	984	2	US-10-101-464A-919
8	1341.5	26.6	996	2	US-10-101-464A-889
9	1341.5	26.6	996	2	US-10-101-464A-933
10	1305	25.9	998	2	US-10-101-464A-914
11	1300.5	25.8	980	1	US-08-473-553A-6
12	1293.5	25.6	985	1	US-08-473-553A-2
13	1293	25.6	999	1	US-08-473-553A-5
14	1275	25.3	1166	2	US-10-101-464A-900
15	1264.5	25.1	974	2	US-10-101-464A-921
16	1242	24.6	1133	2	US-10-101-464A-809
17	1227.5	24.3	1196	2	US-08-881-706-2
18	1227.5	24.3	1196	2	US-08-823-394-2
19	1206	23.9	919	2	US-10-101-464A-642
20	1140.5	22.6	910	2	US-09-228-986-72
21	1140.5	22.6	910	2	US-10-101-464A-72
22	1136.5	22.5	947	2	US-09-228-986-73
23	1136.5	22.5	947	2	US-10-101-464A-73
24	1133	22.5	1025	1	US-08-567-375-4
25	1133	22.5	1025	1	US-08-587-680A-4
26	1133	22.5	1026	2	US-09-623-551-18

## ALIGNMENTS

27	1112.5	22.1	1012	1	US-08-475-891A-4	Sequence 4, Appl
28	1035.5	20.5	864	2	US-10-101-464A-896	Sequence 896, App
29	999	19.8	968	2	US-09-228-986-76	Sequence 76, Appl
30	999	19.8	968	2	US-10-101-464A-76	Sequence 76, Appl
31	960.5	19.0	1112	2	US-09-353-585-3	Sequence 3, Appl
32	959.5	19.0	1112	2	US-09-353-585-2	Sequence 2, Appl
33	939	18.6	968	2	US-09-180-439-3	Sequence 4, Appl
34	937	18.6	968	2	US-09-180-439-3	Sequence 3, Appl
35	933	18.5	1016	2	US-09-180-439-8	Sequence 8, Appl
36	904	17.9	697	2	US-10-101-464A-940	Sequence 940, App
37	878	17.4	1023	1	US-08-475-891A-2	Sequence 2, Appl
38	878	17.4	1023	1	US-08-567-375-2	Sequence 2, Appl
39	878	17.4	1023	1	US-08-587-680A-2	Sequence 2, Appl
40	869.5	17.2	843	2	US-10-101-464A-893	Sequence 893, App
41	842	16.7	705	2	US-10-101-464A-894	Sequence 894, App
42	823.5	16.3	828	2	US-10-101-464A-934	Sequence 934, App
43	822	16.3	692	2	US-10-101-464A-897	Sequence 897, App
44	817.5	16.2	799	2	US-09-180-439-6	Sequence 6, Appl
45	811.5	16.1	804	2	US-10-101-464A-890	Sequence 890, App

RESULT 1  
US-10-101-464A-945  
Sequence 945, Application US/10101464A

Patent No. 6768041  
GENERAL INFORMATION:  
APPLICANT: Strabala, Timothy  
APPLICANT: Nieuwenhuizen, Nicolaas  
TITLE OF INVENTION: Compositions Isolated from Plant Cells  
FILE REFERENCE: 11000.102002  
CURRENT APPLICATION NUMBER: US/10/101,464A  
CURRENT FILING DATE: 2002-03-18  
PRIOR APPLICATION NUMBER: 09/704,302  
PRIOR FILING DATE: 2000-11-01  
PRIOR APPLICATION NUMBER: 09/228,986  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/162,866  
PRIOR FILING DATE: 1999-11-01  
PRIOR APPLICATION NUMBER: PCT/US00/00724  
PRIOR FILING DATE: 2000-01-11  
NUMBER OF SEQ ID NOS: 989  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 945  
LENGTH: 502  
TYPE: PRT  
ORGANISM: Pinus radiata  
US-10-101-464A-945

Query Match 31.1%; Score 1568; DB 2; Length 502;

Best Local Similarity 62.0%; Pred. No. 1.3e-113;

Matches 310; Conservative 75; Mismatches 107; Indels 8; Gaps 6;

QY	481	DISNNDISGIPPELNLQNTIILRLNENNLGNV-GSLANCISLTVLNVSHNLVDIP	539
DB	3	DISANOLSGIPPELNLQNTIILRLNENNLGNV-GSLANCISLTVLNVSHNLVDIP	62
QY	540	KNNPFRPDSPTIGNPGCGSWLNSPCDSTRVAVTSRAILDLAIGGVILMLVLI	599
DB	63	VTQNFRTFPESEFFGNPGGLGVWISLCSIAQPRASVSTTAVICISLASVILVCVITI	122
QY	600	AACRPHPPEFLDGLDKPVTYSTPKLVILHNMALHVEDIMRMTENLSEKTIIGGAS	659
DB	123	ALVLSQHKRFTTGSSSK-TGQSSPRLVILHNMALYMDIDIRMTENLSEKTIIGGAT	181
QY	660	STVYKCVLKNCKPVAIKRLYSHNPQGMKQFTELEMLSTIKRNLVSLQAYSLSHGSL	719
DB	182	STVYKCVLKNCKPVAIKRLYSHNPQGMKQFTELEMLSTIKRNLVSLQAYSLSHGSL	241

QY	720	FVYVLENGSLIMDLIHPETKCKTLLMDPTRIKIAVYGAAGLAIYHHDCSPRIIHRPVKSNI	779
QY	242	FVYVWNGSLIMDLIHPSSSKIKIDMNTIRIKILGAAGLAIYHHDCNRIIHRPVKSNI	301
Db	780	LIDKDLIARLTDEGIAKSLDVSCKSHSTIYVMGTIGYIDPEYARTSLTEKSDVYSYGIVL	839
QY	302	LIDDNEAHLSDDEGIAPKCI PAKTHASTIYVMGTIGYIDPEYARTSLTEKSDVYSYGIVL	361
Db	840	LELTTERKANDESNINHLIMSKTGNEIEMADPDISTCKDLCVYKVKVQALLCTKR	899
QY	362	LELTTERKAPVNDNSNIHQILISGADNMNMEVDEPVATCIDETFAKTIQALLCTKR	421
Db	900	QPNDRPTMQVTVTLGSLFM-LSEOPAPATDTSATLAGSC--VYDEY--ANIKTEPHSYNCS	954
QY	422	QPNDRPTMQVAVTLGSLPTSKQAPSSRVNQPAAANNRYRRLDEYTEGNHRDVRGASTS	481
Db	955	SMSASDAQLFIRFGQYIISON	974
QY	482	S-STSDQGLFVRGVEIVISON	500

```

RESULT 2
US-10-101-464A-931
; Sequence 931 Application US/10101464A
; Patent No. 6768011
; GENERAL INFORMATION:
; APPLICANT: Strubala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Hisingins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 931
; LENGTH: 998
; TYPE: PRT
; ORGANISM: Pinus radiata
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(998)
; OTHER INFORMATION: Xaa = Any Amino Acid
; US-10-101-464A-931

```

Query Match	28.4%	Score 1432.5	DB 2	Length 996
Best Local Similarity	36.5%	Pred. No. 1.3e-102		
Matches 361	Conservative 157	Mismatches 374	Indels 97	Gaps 19
QY	10	LGFLPCLSLVATVTS-----EEBATLLLEIKKSKFDVNNVLYDITTSPPSSDYCVARGVS	62	
Db	7	LHFLF-FCFVLTVRSCFAIRGMQDGLILQELCKRGDPDPSGAFRNNENNDSNP-CNWGTGIT	64	
QY	63	CENTFNNVVALNSDNLNDGEISPAIGDLKSLSLSIDLAGNRSLSGIIPBEIGCSSLQWLD	122	
Db	65	CDAGEKFEVEEDLSKNIIGPEPTVACRIDGKIKSLNNVNYGSIIPAGLRCHGELEYLD	124	
QY	123	LSFPELSGDIPIFSISKLEQLKLEOLIKNNQLIGIPRSTLSQIIPNLITILDQKSLGSEIIPR	182	
Db	125	LSQNLILIGGLDPISELFRLKHLIDLSGNNLSGPVPAPGRPELDQVNLVSLNLTITPIR	184	
QY	183	LIVNNEVLYQYIGLRKNNLVGNIISPLCQITGLMIVDVRNNSITGSIPEPTIGKCTAFQVLD	242	
Db	185	FVGDLPNLLOINLAVNPLTGVTPPEPLGNLKKLOINMLAGCNLVGSIPEPTIGNLSLTINLD	244	

QY	243	LSVNOITGRTIPDIEGL-OVATLISQGNQISGKTPSVGLMQLAVDLDSGNLSSGTPP	301
QY	244	LSVNOITGRTIPDIEGL-OVATLISQGNQISGKTPSVGLMQLAVDLDSGNLSSGTPP	302
Db	245	LSNMRTSSGISPSITKDLKVOIETLYONLSSGPIPVAMGELKALRPDASKNMLDGGIPA	304
QY	302	ILGNLTFETKELYHSNKLGSIPPELGMMSKLHYLELDNHLTGHIPEPEGLKTDLEDLN	361
Db	305	GLGSLNL-ESLNLVONNNVLGEIIPPELGSPFTSLKELKPSNBLTSSLEPNIGRNDLLALD	363
QY	362	VA-----NNDLGGPIPDHLSCTTNINSLNHGNKFRSGTTPR	397
Db	364	IAONLISGRLPDLCCKNKLIELISFNNEBLGNNLPESIGTCTISINRVLAGNKENGKSVPS	423
QY	398	APQKL-----ESMTYLNUNSSNNIKPPIVELSRIGNLTLD	433
Db	424	LEFGLFHVBLLEHKONVEFGPISPIDIADAKSLVIGSNLFGSLPPEISELNLSEIT	483
QY	434	LSNNKINGIIPSSIGDLLEHLKMNLSRNHITGVVPGDFGNLRSIMEIDLSNNDISGPIPE	493
Db	484	ASNNMLTGALLPSSIGLQDLGKLDLSNNQSGELPAELISSCKOLGEINLSNQSGSSIPA	543
QY	494	ELNOLONIILRLIENNLTGVNGLANCLSLTVLVNHNHVLGDI P--KNNFSRPSPD	550
Db	544	SVGTLLEVLNLYLDSDMLLTGPPISELGNLKTNPEDVSDNRLSGAVPLAFENPVYEK----	599
QY	551	SFIGNGOLCG--SWLNSPCHDSRRIRVRVISAPRALIGIAIGGLVILMLVLLAACRPHNPP	608
Db	600	SFLGNBELSCREFFNGTSCSEVRESEKAKROQMMWLLRCLFALSIITLFLVGLAIFYRRYR	659
QY	609	PFLDGSGLDPVTYSTPKVLILHMNNAULHYEDINMRTENLSEKYLIGHGASSTYYKCVLK	668
Db	660	NFANAERKKSVDKSSMMLSPH-RGPFSEYE----ILDCLDEDNVISGGAGKXYKATLS	714
QY	669	NCKPVAIKRLYSH--NPOSMKOFETLEMLTSIKRNLVSLQAYLSLHGSLLFYLYLE	725
Db	715	NGELVAIKILMWSGKTNASTDNGFOAEVDTLGKIRKHNIIVLWCCSCSKSDSNLLVVEYMP	774
QY	726	NGSLMULLGLPRTKKTLTDWDTKLAAVGAAGLYLVHSDSPRIIHDVYSSNLLDLKDL	785
Db	775	NGSLGLLELGP-KASVLDMPRIYKLTALGAAGLALHHGCVPSIVRHVDVYSSNLLDDEDY	833
QY	786	EASLTDPGIAKSL--CVSKSHTSYVMGTIGIDPEVARTSRLTEKSDVYSYGLVLEL	843
Db	834	GAHVADFGVAKFLGSGSGADSMTLAASXYLAPEVAYTLKVNKESDIYSFGVILIELV	893
QY	844	TRKAVDDESN-----LHLLINSTGTGNEWEMADPDITSTCKDLGVYKVKYFQLALL	895
Db	894	TGRRPVPDPFEGENKDLVKWLCKNKIKETKGLNEVL---DPKLVDCKE--EWTVMVKVGLL	948
QY	896	CTKRQPNDRPTMQVTRVLGVSFMLEQPP	924
Db	949	CTSVLPINRPSMRVVE-----MDEANP	972

RESULT 3  
 US-10-101-464A-895  
 ; Sequence 895, Application US/10101464A  
 ; Patent No. 6768041  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Strabala, Timothy  
 ; APPLICANT: Nieuwenhuizen, Nicolaas  
 ; APPLICANT: Higgins, Colleen M.  
 ; TITLE OF INVENTION: Compositions Isolated from Plant Cells  
 ; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling  
 ; FILE REFERENCE: 11000.1020c2  
 ; CURRENT APPLICATION NUMBER: US/10/101,464A  
 ; CURRENT FILING DATE: 2002-03-18  
 ; PRIOR APPLICATION NUMBER: 09/704,302  
 ; PRIOR FILING DATE: 2000-11-01  
 ; PRIOR APPLICATION NUMBER: 09/228,986  
 ; PRIOR FILING DATE: 1999-01-12  
 ; PRIOR APPLICATION NUMBER: 60/162,866  
 ; PRIOR FILING DATE: 1999-11-01

PRIOR APPLICATION NUMBER: PCT/US00/00724  
 PRIOR FILING DATE: 2000-01-11  
 NUMBER OF SEQ ID NOS: 989  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 895  
 LENGTH: 998  
 TYPE: PR1  
 ORGANISM: Pinus radiata  
 US-10-101-464A-895

Query Match 27.9%; Score 1404.5; DB 2; Length 998;  
 Best Local Similarity 36.0%; Pred. No. 1.9e-100;  
 Matches 347; Conservative 168; Mismatches 362; Indels 87; Gaps 24;

12 FLFLC-----SLVATVTSBEG--ATLEIKKSPKDVNNVYDMTSPSSDYCWRG 60  
 11 FIFCIFSMLVDFGVAVFAAQTOQILURKEALEDPNLRDSDSEDF--CWRG 69  
 61 VSGENVTFNVVALNLDNLDEISPAIGDKLSIDLKGNRLSGQIPDEIGDSSLQV 120  
 70 IDC-NDGAVTRIQHSSLSGRILPDCNLSLIFELDRNSLYGNFPEFSCRLSQ 128  
 121 LDLSFNLSDGIPESIKLQLEQILKNNQLIPSTTSQIPNLKILDLQKLSGE- 179  
 129 LNLSSNLNGLSP-DLSKTKALKYLDLSNNRFSGEFVSQNLNLSLSLGIIMFRR 187  
 180 IPELIVNENLYQVGLGNNLVNGLSPDLQLTGLMVFDRNNSLTSIPETIGCTAF 239  
 188 IPELWRLTSLWLYTNCFYSGIPASLSNLSLGLNLSMDLTRIPRELGLKLY 247  
 240 VLDLSYNQLTGEIPFDIGFL--QVATLSLQGNQSGKIPSYIGMQLAVLDLSGNLSGS 298  
 248 QLELFSLNLSGEIPRELGNLTLSDPDASNSLQGRIPAPGKLERHFIQVQNLSGE 307  
 299 IPIPLGNLITTEKLYHSNKLTGSIPELGNMSKLYHLENDHNLGHIPEL--GKLT 355  
 308 IPEGFGLKMLIGISMYQNLITGLPPLKGLSVSEFFNMIDVSQNNLSGPPDLCSGGLQ 367  
 356 DLDFDANVANDLGGPIPDHLSSTCNLSLNVHNGKFSGTIPRAFOKLESTMYLNSNNI 415  
 368 YIL--VLDNEFTGQIPESYGNCKSMRFRYKVKLGRIPRGIEWEPHYSILDLSSNSF 424  
 416 KGPVPELSRIGNLDLTLNNKINGIIPSLGDLLEHLKMNLSRNITVGPEDFGLNR 475  
 425 EGEIAPRIGARNLSLXYLQNGSSGLPRAIGASOLIKIDVSGNLTGAVSEIKLS 484  
 476 SIMEIDISNDISGPIPEELNQLNIIILRLNENNLTVGN--GSLANCLSLTVLNVSHNL 534  
 485 LLSLSLQENNLGSPIPAQIGCHKFLSSINLAYNELTGPIRGLGFWEVLSNLISNML 544  
 535 VGDIPL-----KNNFSPFS-----PDSFTGNPGLCGSWLNS--PCHDS 570  
 545 SGEIPNTLALKLSVDFSRNSLTGPVPIELISQTNRSFSGNPGLCGGQIGESIQPDLH 604  
 571 RRTAVRVSISPAALIGLGLV--ILLMVLIACRPHNPPLDGLDLPVYVSTGLV 627  
 605 TRDY--YGRWITGAVSGVTFFTLIGMLIRGCRLLR---RDSKNVNNRFTWEKK-- 655  
 628 ILHNNALHAYE-DIMKNTENLSEKYLIGHASSTVYKCVLKCKCPAIVRLYS----H 681  
 656 -----SFHLNPFDEHVESMODEHIIIGHGSGTVRILQDSNSESVAVKKMLCKNGH 709  
 682 NPSGM--KQETELNLSSTIKRNLVSLQAYSLHSLGLPYDYLENGSLMDLHGTTK 739  
 710 GGGGLINREKAEVETIGTIRHRIVKLYCFNSGDNMMLVEYEMPNGNLMESLHVRNG 749  
 740 KTLMDRTRLIAYGAAGLAVLHHDGSPRIIHRDVKSNIILDLDDLEARLTDFGIASL- 798  
 770 ASDMPTRYKIALGVANGLAVLHMDCPGIIHRDVKSTNILLDBENQARVADGFAKILQ 829  
 799 CVSKSHTSYVMGTIGYIDPEYARTSLTEKSDVSYGYVLELTLTRKAVDDESN---- 854  
 830 ACPGDSVAITGHYIAPEYAVASVTEKSDIYSGVVLLELTGRRPVEAEFGKND 889

QY 855 ----LHLLMSKTGNNVEMADPDITSTCKDLYGVKVFOLALCTKROPNDRPTMHQV 910  
 DB 890 IYWMISRKILTRGAREVL---DYRIYLYKQEMI--QALKIAVTRTSKLPNVRPSMREV 944  
 QY 911 TRVL 914  
 DB 945 VQML 948

RESULT 4  
 US-10-101-464A-944  
 Sequence 944, Application US/10101464A  
 Patent No. 6768041  
 GENERAL INFORMATION:  
 APPLICANT: Strabala, Timothy  
 APPLICANT: Higgs, Colleen M.  
 APPLICANT: Nieuwenhuizen, Nicolaas  
 TITLE OF INVENTION: Compositions Isolated from Plant Cells  
 TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling  
 FILE REFERENCE: 11000.102062  
 CURRENT APPLICATION NUMBER: US/10/101.464A  
 CURRENT FILING DATE: 2002-03-18  
 PRIOR APPLICATION NUMBER: 09/704,302  
 PRIOR FILING DATE: 2000-11-01  
 PRIOR APPLICATION NUMBER: 09/228,986  
 PRIOR FILING DATE: 1999-01-12  
 PRIOR APPLICATION NUMBER: 60/162,866  
 PRIOR FILING DATE: 1999-11-01  
 PRIOR APPLICATION NUMBER: PCT/US00/00724  
 PRIOR FILING DATE: 2000-01-11  
 NUMBER OF SEQ ID NOS: 989  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 944  
 LENGTH: 370  
 TYPE: PR1  
 ORGANISM: Pinus radiata  
 US-10-101-464A-944

Query Match 27.6%; Score 1393.5; DB 2; Length 370;  
 Best Local Similarity 76.7%; Pred. No. 3.2e-100;  
 Matches 270; Conservative 39; Mismatches 42; Indels 1; Gaps 1;

9 LGFLFCLSLVATVTSBEGATLEIKKSPKDVNNVYDMTSPSSDYCWRGVCENTVF 68  
 20 LVTFYFGLLSAV--SDGNTLTLAKKSRFSDSDNVLYNMIDASSDHCKRGVTCNVIF 78  
 69 NVVALNLSNDNLDEISPAIGDKLSLSTDLRGNRLSGQIPDEIGDSSLQNLDSFNEI 128  
 79 AVVALNLSHNLGGEISPIYGNKLSLESTDLKGNGLSGQIPDEIGDSSLQNLDSFNEI 138  
 129 SGDIPIPSIKLQLEQILKNNQLIPSTTSQIPNLKILDLQKLSGEIPRLIYNN 188  
 139 YGDIPIPSIKLQLEQILYNNQMLGPISLTLQIPNLKIMFADNLQSGEIPRLIYNN 198  
 189 VLOYLDRGNLVGNISPLQLTGLMVFDRNNSLTSIPETIGCTAFQVYLDLSYNOL 248  
 199 VLOYLDRGNLVGNISPLQLTGLMVFDRNNSLTSIPETIGCTAFQVYLDLSYNOL 258  
 249 TGEIPDIFGLQVATLSLQGNQSGKIPVIGIMQALAVLDLSGNLSGSIPIILGNLTF 308  
 259 TGEIPNIGFLOVATLSLQGNKLTGKIPIVIGIMQALAVLDLSGNLSGSIPIILGNLTF 318  
 309 TEKLYHSNKLTGSIPELGNMSKLYHLENDHNLGHIPELGLKTLDFL 360  
 319 TDKLYHSNNLTSIPRELGNMTKLGYLQINDNQLTGQIPRELGNLEQLEFEL 370

RESULT 5  
 US-10-101-464A-954  
 Sequence 954, Application US/10101464A  
 Patent No. 6768041  
 GENERAL INFORMATION:



221 NNSLTGSIPTGNCSTAFQVLDLSYNQLTGEIPEDIGFL-QVATLSIQGNQSGKIPSVI 279  
242 SCGEGEVIPELGLKLTHTLYLOFNLSGPPIKQOVGNLSLVNLDLSVLLTTEITFEV 301  
280 GLMOALAVLDLGNLSGSIPIPIGLNLTTEKLYHSNKLTSIPELGNNSKLYHELN 339  
302 ASLQKLVNLFNKLHGSIPOFLADPSLETALMTNNFTGVIPEDLGRNGKLQYDLS 361  
340 DNHLTGHIPPELGLTDLFDLVNANNLDEGPIPHLSSCTNLSLVNHNKQKSGTIPRA 399  
362 TNKLTGMIIPDLCSGNQKILILFNFLPGPIPALGCSHLYVVRGQYVNGSIPNGF 421  
400 -----QKLESMYLNLSNNIKGPIPELSRIGNDLT 432  
422 IYLPQKLMELQNNYLSGALPENVRSSKRAMLNELNLSNLSGPIPSLSNSNUQIL 481  
433 DLSNNKINGIIPSSGLDEHLKLNLSRNHITGVVPGDFGNLSIMEIDLSNDISGP 492  
482 RISGNQSGPLPAFTGDLQVAKLDLRQNFSGEIPEDIGNCYHLYTDLIDSONLSGP 541  
493 EBLNQLNILLLENNNLGNV-GSLANCLSLTVLVNHNVLGDI PKNNVPSRFPDS 551  
542 LTTSKPIPLSYLISRNHLNQSIPKISTWQSLTIADFSFNPSGKIPESGQFALFNSS 601  
552 FIGNPGLCGSMNSPCH-----DSRRTVRVVISRAALIGLAVILLAVLIAACRPHN 606  
602 FVGNPGLCGSVLDIKCMLTFTSTSSRIHTFKLMFAVGLLCSLATTVAILKA----- 656  
607 PPPFLDGLDKPVYTSYTPKLVILHNNALHYVEDIMKMTENLSKYLIIHGASSTVYKV 666  
657 -----RSFRKAGAGSMKMTTF-QKLEFSV-QDILECVKQNE---IGRGAGIYVHGK 705  
667 LKCKPAIRLYSHNQSM-KOPETELEMLSSIKHENVLSLOAXSLSHLSGLLFYHLE 725  
706 MPQGTBLAVKLLGFGTNSHDGRFAEIQTLGNIRHNIIVRLAFCNKEKTNLLVEYMK 765  
726 NSGLMDLHPTKKTLDMDTRLKIAVGAAGLAYLHDCSPRIIHPDVSSNILLDKDL 785  
766 NSGLGVLHG-KKGAFLGNMLRYKIAVEAAKGLCYLHDCPCPLIHHDDVSNINILNLSY 824  
786 EARLTPFGIAKSLCVS-KSHSTYVMGTGIYIDEPVARTSRLTEKSDVSYGVILLELT 844  
825 EAHVADGLAKFLVDSGSCSMVYAGYIAPEYAVTLRVDEKSDVSYFGVILLELT 884  
845 RRAVYDESNLHLIM-----SKTGNNEVEMADPITSTCDLVYKVPOLALICTK 898  
885 GRPVGDFGQGVDIQVWTKIATTNMRREATRVDPLSLVPPK--BATHVFFVAMLCVQ 942  
899 RQNDPRTHQVTRVLGSPMLSEOP---AATPSATLAGSCYVDEX 942  
943 ENSTERPTREVVOMLSEF--PRHPPREHYSSSSSSSTSSSAFAKXF 988

RESULT 7  
US-10-101-464A-919  
; Sequence 919, Application US/10101464A  
; Patent No. 6768041  
; GENERAL INFORMATION:  
; APPLICANT: Strabala, Timothy  
; APPLICANT: Nieuwenhuizen, Nicolaas  
; APPLICANT: Higgins, Colleen M.  
; TITLE OF INVENTION: Compositions Isolated from Plant Cells  
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling  
; FILE REFERENCE: 11000.1020C2  
; CURRENT APPLICATION NUMBER: US/10/101.464A  
; PRIOR FILING DATE: 2002-03-18  
; PRIOR APPLICATION NUMBER: 09/704,302  
; PRIOR FILING DATE: 2000-11-01  
; PRIOR APPLICATION NUMBER: 09/228,986  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR APPLICATION NUMBER: 60/162,866  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: PCT/US00/00724

; PRIOR FILING DATE: 2000-01-11  
; NUMBER OF SEQ ID NOS: 989  
; SOFTWARE: RastSeq for Windows Version 4.0  
; SEQ ID NO 919  
; LENGTH: 984  
; TYPE: PR  
; ORGANISM: Eucalyptus grandis  
US-10-101-464A-919

Query Match 26.9%; Score 1355; DB 2; Length 984;  
Best Local Similarity 34.5%; Pred. No. 1,4e-96;  
Matches 345; Conservative 159; Mismatches 357; Indels 138; Gaps 24;

29 TLEIKKSFQVNNVLYDMTSPSD-----YCVMGVSCENTENVVALNSDNL 80  
1 SLSLSSLRDPSTHMDPTFESNPFLQNPACWSGVCNPNQTSQTSNLSRKL 60  
81 DGEISPAIGDLKSLSIDLGRNLSGOIPDEIGDCSSLOLDLSFNEISGDIFFSISKL 140  
61 SRAIPAEIRLYTSLHLNLSGNAFDGLQPAIPETELKTLIDHNHNFSTPFMGISKL 120  
141 QEBOLIKNNQIGPIPTLSQIPNLIKIDLAONKSGEIPRIYNN-EVLYQVLGRGN 139  
121 LRAFAVNSFTGPPQELVLSQYLEYINTLGGSYEGEIPS-DYGNFPLKSLFLGNV 179  
200 LVGNISP-----DLCOITGLMYFVVRNNSLTGSIPTIGNC 235  
180 LBGPIPELGLSLQLERLBIGYQYGGIPESELALSNLRYDISANLSGSIPOELGNV 239  
236 TAFQVLDLSYNQLTGEIPEDIGFLQ-VATLSIQGNQSGKIPSVIGLMOALAVLDLSGNL 294  
240 TKLETLFLFENRALTGQISNSFSLBALQDLSDNQLSGTIPGCLSLKQLATLGLMKNN 299  
295 LSGSIPPIGLNLTTEKLYHSNKLTSIPELGNNSKLYHELNHNLGHIPELGLK 354  
300 LSGEVPTQIGVPLPBTLOLMNNSLTGILPOGGSNAKTKLDVSSNSFSGPIPPNLCG 359  
355 TDFDLVANNNDLBPPIPHLSSCTNLSLVNHNKFSGRTIPRAFOKLESMYLNLSNN 414  
360 KKLILKLSNRKLVGAIPLSLANCTSLYRLRMDNMLNSIPFGFLPVLTAADLSNNF 419  
415 IKGPIVELS-----RIGNDLTDLNKNKINGIIPSSIGDL 450  
420 FSGEIPDDLGNGVALQYLVNVSNSFGTKLPDNIWKAPNLIQIFASSSKLKGIPDFIG-C 478  
451 EHLKNNLSRNHITGVVPGDFGNLSIMEIDLSNDISGPPIPELQONIIILRLENN 510  
479 KSLYKTELADNSLNGSIPMDIGHCEKLYLNLNRSLAGIIPWEISTLPMTIVDLSRNF 538  
511 LTGNVGS-LANCLSLTVLVNHNVLGDI PKNNVPSRFPDSFIGNPGLCGSMNSP- 567  
539 LTGSIPSNPDNCTTSLFNSFNSLTGPIPSSTIRTNLHPSFIGNDGLCGVLAQPCG 598  
568 -----HDSRRTVRVVISRAALIGLAVILLAVLIAACRPHNPPF 610  
599 GCGGADAGMDSEAGQQRRTA-----GALVWIAAFAFGVLVLAGTRCFH---- 648  
611 LDGSLDKPVYTSIP-----KLVIL-HNNMALHYVEDIMKMTENLSKYLIIHGAS 659  
649 -----ATYSHRFTERGQGVGPKLTAFORLNFRTA---EDVEEC-SMSNK-IIGGSGT 695  
660 STYKCVLKNCKQVAILRYSHNQSMKOPE---TELEMUSIKHENVLSLOAXSLSHLSG 716  
696 GTYRRAEMPEGDIIAYKMLGKREKMRKRGVLAVEVULGNVRHNIYRLLGCCNREC 755  
717 SLTFDYLENGSLMDLHGTKKKTTL-DWDTRLKIAVGAAGLAYLHDCSPRIIHRV 774  
756 TMLLYEYMPGNLDDLHGKNDLNVTSWVTFYKIALGVAQICVYLHDCNVIYHRDL 815  
775 KSNIIILDKDLRLNDPGLAKSLCVSKSHSTSYVWGTIGYIDPEARTSRLTEKSDVYS 834  
816 KPSNIIILDAEMEARVADFGVAK--LIQSDSMSVYAGYIAPEYAVTLQVDEKSDIYS 873





```
Db 15 LVLPLIALSVSOGVLVLEVKELSDPNGFLGNWKAEDSP-CKWKGISCDOKSKSVG 73
QY 73 INTSDNLDEGEISPAIGDLKSLSIDRGRNLSGOIPDEIGDCSLONLDSFNEISGDI 132
Db 74 IDSSSGVLGVFVSVCNLPOLKNLSIGDNNIGSILPRNLSMCKOLRLNLSQNLFPGNL 133
QY 133 PFSISKUKOLEQILKNNQILGIPSTLSQIPNLIKILDLAONKLSGEIPRLIYWEVLOY 192
Db 134 PDFISELAIEVLDLSNNFSGSIPAGIGKLPRLQVNLCCNLNLETIPFELGVLNLSQ 193
QY 193 LGRGNLV-GNISPDLCQLTGLMYFVRNNSLTGSPETIGNCTAQVDSLNOQTGE 251
Db 194 LLAIVPFAVGVPPELGLKLAQONIMATSCNFGALPDSIGMLSTJNLDLSNQLSGI 253
QY 252 IPEDIGFL-OVATLSOGNOLSGKIPESVIGLMOALAULDSGNLSSGIPILGNLFT- 309
Db 254 IPBAITKLNQIVOELIYHNVLGRIPENNMNLVSLRFPDVTNNLNTIPEQLARLSS 313
QY 310 -----EKLVLHSNKLTSIPPELGNNSKLHYELNDNLTHGI 347
Db 314 LNLFENNVLVGTIPEAIGVPTLSLKLFTNNLNGSLPSNKGKSGLOTLDIAGNRLSGL 373
QY 348 PPELGKLTDLFDLVANNDLGEPIDHLSCTNLNSLVHGNKFSGITPPAFOKLESMTY 407
Db 374 PPLCKKXKQLQTLNIFNNNFTGQLPLQYGACLSQVRISHNEMIGQVPSFWGLPHVY 433
QY 408 LNLSSNNIKGPI-----PELSRIGNLDTLSSNNKINGII 443
Db 434 LEISNNKFPBSISSEIRNAKNLSALLISGNRFSGTSLSEGLVANLSVIDGSHNQETPL 493
QY 444 PSSIGDLLEHLKNNLSRNHITGVVPGDFGNLRISIMEIDLNNDISGPIPELNOQLIL 503
Db 494 PATLSLNTKSLKHLFQNGFSGSLTDLISNELTDLNLSNNRPSGIPRELBELVLY 553
QY 504 LRIENNNLTGVNSLANCLSLTVLVANSHNLVGDIPKNNNFSRPSDPISGPNGLC--G 560
Db 554 LDISVALTGEIPELGNLKLNSFNLSDNQLTGIVPSAFSL-SFYKSLMGNGLCSNDG 612
QY 561 SWLNSPCHDRRTVRVYSIRAAITLIGLVLMLTIAAC-----RHNPPPELDGSL 615
Db 613 LKFPKSCSDMENSGRKKCYSMWMLPFLPAGITFLVGLALFYROYREYNKAKVXD-L 670
QY 616 DKEVTSYTPKLVILHMMALHVEDIWMTEMLSEKYLIGHGASSYVYKVLKCKKPAI 675
Db 671 WR--SNKSPMLTTFRLHGFREYE---LDCIDEENVISGSGSKYKATLNGETVAI 724
QY 676 KRLYSH-NPOSMAKQ-----PETELEMLSIKHNLVSLQVYSLSHUGSLIFYLNGSL 729
Db 725 KRLMNNAGSSTSCNDNGEFAVEETLGNIRHKNIVLTMCCVNDSDSNLLVYEMPGSL 784
QY 730 WDLHGPYTKKTLDMPTRLKIAAGAAOGALYHHDGSPRIIHRDYSSNILLDKOLEARL 789
Db 785 GDILHBP-KAGDLMWPRYKIAVGAAGLALYHDDCPPIIHRDYSSNILLDADGARY 843
QY 790 TDEGIAKSLCVSCKSHTS---TYVMGTIGYIDPEYARTSRLTEKSDVYSYGVILELT 844
Db 844 ADGGLAK---VLOSYESKIDFMSAIGSYGIAPEVATYILKAKKEDYSIFGVVLELV 900
QY 845 RRRAY--DDESNLHHLIMSKT---GNNEVEMADPDITSTC--KDLGVYKVPFOLALLC 896
Db 901 GKQPVIODEEESKDVMMVTRIEKQNDGQDILDSRVWVDCPREEMAVALKV---ALLC 957
QY 897 TKQPNDRPTMHQVTVL 914
Db 958 TSALPTNRBSMRVLEL 975
```

```
RESULT 10
US-10-101-464A-914
; Sequence 914, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
```

```
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OR INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.102062
CURRENT APPLICATION NUMBER: US/10/101,464A
PRIOR FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ. ID NOS: 989
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 914
LENGTH: 998
TYPE: PR1
ORGANISM: Eucalyptus grandis
US-10-101-464A-914

Query Match 25.9%; Score 1305; DB 2; Length 998;
Best Local Similarity 33.7%; Pred. No. 1.1e-92;
Matches 339; Conservative 163; Mismatches 382; Indels 122; Gaps 24;

QY 8 VLIGFL-FCLSLVATYT-----SEEGATLEIKKSPFDVANNVYDWTSSPSSDYCWR 59
Db 1 MFLSFLSLFLLLLAGAAPALSPALSNQEGLYLHGAKSLSDPOSSSLAAMDRODSP-CGWP 59
QY 60 GVSCEVNTFNVVALNLSNDLNGEISPAIGDLKSLSIDRGRNLSGOIPDEIGDCSSIQ 119
Db 60 GVCEDRASGSVSVDSGANLGGFPFLICRLPNLTFLEFNNSIT-SLPAGVSACRSVL 118
QY 120 NLDLSFNEISGDIPEFSISKUKOLEQILKNNQILGIPSTLSQIPNLIKILDLAONKLSGE 179
Db 119 HDLIGQNLLAGDLPALADLPGLAYLDLSANNFSGDIPASFGFRPFLVSLVNNLDDGA 178
QY 180 IPRLIYWEVLOYLGRGNLV-GNISPDLCQLTGLMYFVRNNSLTGSPETIGNCTAF 238
Db 179 IPGFLNVSTLKKMLNSYNPFAGRIPPELGNLTNLEVLMLSECGLTGKIPESLIGKRL 238
QY 239 QVLDLSYNOLGEPIDIGFLQ-VATLSOGNOLSGKIPESVIGLMOALAULDSGNLSSG 297
Db 239 TDIDLAFNYLBGPIPSLSTELBSVOIEIYNNSLTGELPAGSKLYALRLDLSMNRLTG 298
QY 298 SIPIILGNLTF-----TEKLYHSNKLTSIPPELGNNSKLH 334
Db 299 TIPDELTRLPLBSLNLVENQFSGELPASTADSPNLNELFLFNNRLTGKLPKULGQNAFLQ 358
QY 335 YLELNDNLTHGIPPELGKLTDLFDLVANNDLGEPIDHLSCTNLNSLVHGNKFSGT 394
Db 359 YIDVSTNNFSGEIPALCANGELEBLMTENSFGGPIPALGRCQRLTVRLGNRRLSGE 418
QY 395 IPAPFOKLESMTYLNLSNNIKGPIPELSRIGNLDTLSSNNKINGIIPSSIGDLLEHL 454
Db 419 VPBSFNGLPVLSLELADNKLSGPIGEETARASNSVLSLSRNEFTGPPKIGITVRL 478
QY 455 KNNLSRNHITGVV-----GDFGNL-----RSIMEIDLSSNDISG 490
Db 479 DPSASENKLTGSLPESILNLGQUGRLDRSNDLSGSLPGSIRHKKLNLDELADNLSGS 538
QY 491 IPELNOQLNIILRIENNNLTGVNSLANCLSLTVLVANSHNLVGDIPKNNNFSRPSPD 550
Db 539 IPAEIGLSVLNVLDSGNQFGSKVPAEQNLKLNQNLNSYNSLGGPLPMPFTKQYK-N 597
QY 551 SFTGNPGLGSMVNSCH---DSRRTVRSISRAALGIAIGGLVLLAVLLAACRPNP 607
Db 598 SFLGNPGLCGEKKGLCNGGGBRNSGYWLRSFT--LAGLVFTGV----- 644
QY 608 PFLDQ-----SLDKPVYTPKLVILHMMALHVEDIWMTEMLSEKYLIGHG 657
```

```

Db      643  -----GMFPMYKKSPFNAGRALDCKSKWTLMSSH-----KLGSEED-----ELIDCLDENNVIGTG 634
Qy      658  ASSTVYKCVLKCKPVAIRLY-----SHN-----DSMKQFETLEMLSSIKERNLV 705
Db      695  ASQKVVKKVVLSSGSDAAVAVKKLDMDGPKKSEESHDEKKGVDODGDEPAEKVTLGKIRHNIV 754
Qy      706  SLQAVSLSHSLGSLFPDYLENGSLMDLHGPFKKTLTMDTRLKIAVGAAGLAVYLHDC 765
Db      755  KLMCSCTTDCKLVLVEYEMPNCSLGDILHS-SKGLDLMPPRYRIADAAEGLSYLHDC 813
Qy      766  SPIIRHDYKSSNIIIDKDLLEARLTDFTGIASL-CVSKSHTS-TYVNGTIGYIDPEYART 823
Db      814  VPEIVHRDVKSNIIILDADFGARVADFGAVAKVERTGTGSHSMSTVAGSCCYIAPFYAYT 873
Qy      824  SRLTEKSDVYSYGVILELLTTRKKAVDDESNHHII-----MSKGTGNNEWMAADDT 877
Db      874  LRNEKSDPTYSBEVVLLELVLTGRRPVPDPFEGKDLVKVAVCTLTLDQKGVQYI---DKLD 930
Qy      878  STCKDLGVVKKVFOALCLCTKQPNDRPMHVOYTVLGSFMLSSEP 923
Db      931  SCPEK--DVCKVANIIGLQCTSPLEPIINRPMRELVVIMLEISAENAP 974

```

RESULT 11  
 US-08-473-553A-6  
 ; Sequence 6, Application US/08473553A  
 ; Patent No. 5859338  
 ;  
 GENERAL INFORMATION:  
 APPLICANT: Meyerowitz, Elliot M.  
 APPLICANT: Clark, Steven E.  
 APPLICANT: Williams, Robert W.  
 TITLE OF INVENTION: Plant Clavatal Nucleic Acids,  
 TITLE OF INVENTION: Transformed Plants, and Proteins  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fleury, Hobbach, Test, Albrighton & Herbert  
 STREET: Four Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States  
 ZIP: 94111-4187  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Releasee #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/473,553A  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 800  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Silva, Robin M.  
 REGISTRATION NUMBER: 38,304  
 REFERENCE/DOCKET NUMBER: A-60886/RET/RMS  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989  
 TELEFAX: (415) 398-3249  
 TELEX: 910 277299  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 980 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: unknown  
 TOPOLOGY: unknown  
 MOLECULE TYPE: protein  
 US-08-473-553A-6

Query Match	25.8%	Score 1300.5	DB 1	Length 980
Best Local Similarity	35.2%	Pred. No. 2.4e-92		
Matches 348	Conservative 153	Mismatches 362	Indels 125	Gaps 27
QY	30	LEIRKKS-FKDVNNVLVWPTTSSPSD-YCWRGVSCEVNTFNVVALNLSDLNLOGEISPA	87	

```

Db 31 L1NKLSMIGKRGCHLHMWIISSSPDACHSPGVCDD- DARVILSNVFTFLFGITSPBE 89
Qy 88 IGDLSKLSIDLGRNRLSGQIPDEIGDCSSLONIDLSPN-ELSGDIPSPISK-LKOLED 145
Db 90 IGMTLHVLVTLAANPFTEGLPELEKSLTSLTKVLNISNNGNLGTFTPGCILKAMVDLEVL 149
Qy 146 ILKNNQLGPI PSTLSQIPNLKIIDLANKUSGEIPRLIYMWVEVOYGLRGNLVGNIS 205
Db 150 DTYNNNENGKLPPEMSELKTKLYLSFGGNPFSGEIPESYGDIOQSLEYGLNAGJSGKSP 209
Qy 206 PDLCOLTL-----WYFDVRNNSLGSIPETIGNCTAFCQVLDLSYNOLGTEIPFDIGFQ 260
Db 210 AFLSLKTLRMEYIGY-----NSYGVPRREGGTLKLEIDMASCTLGEIPTSLSNLK 265
Qy 261 -VAITSLOGNOQSGKIPSVIGLMQALAVLDJSGNLSGSIPI---LGNLTTEKLYHS 316
Db 266 HLHTLFTLHNLGTGHPPELSGLVSLKSLDLSINOLGTBIPQSFINTGNITL---INLFR 322
Qy 317 NKLTSIPPELGNNMKLHY-----LEANDHLHGTGHPPELG 352
Db 323 NNVLGOIPALGELKLEVEFEWENNFTLQLEPANLGRGNLTKLDVSDHMLTGLLPKXDC 382
Qy 353 KLTDLFDLVANNDGEPHPDLSSCTLNSLVNHNKFSGTIPRAFOKLESMYTLNLS 412
Db 383 RGEKLEMILSNPFPGPIPELGCKSKLTKRIKYNLNGVPAGLFVLPTVITIELD 442
Qy 413 NNKIPPIVELS-----RIG---NLDTLJLSNNKINGIIPBSLGD 449
Db 443 NEFSGELPVTSGDVLDOJLYLSNNMFSGEIPPAINFPLQTLFLDRNFRFNIPREIE 502
Qy 450 LEHLKMLSRNHTGVVPGDFGNLRSIMEIDLSNNDISGPIPEELNQCNTILRLLENK 509
Db 503 LKHLSRITSANNITGGIPDLSRCSSTLISVLSNRKINGELPKGINNVKULGTNLISGN 562
Qy 510 NLTGNGVS-LANCLSLTVLVNNSHNLVGDIPKNNFSRSPSFIQNPGLC-GSWLNSPC 567
Db 563 QLTGSIPIGIGNMSTLTLTDLSDFNLSGKPLVGGQFLVENETSPAGNTVLCJPHRVSCPT 622
Qy 568 H----DSRRIVRVSISPRALIGT-AIGGLVLLMLVLIACGPHNPPRPPLDSDLKPVTY 621
Db 623 RFGQTSDHNHTALFSPSRIVITVIAITGLTILSVAIROMNKKV-----OKSLAM 673
Qy 622 STPKLVILHMMALHVEDIDIRMENTNLEBKYIGHGASVTYKCVLKNCKPAIKRLYSH 681
Db 674 KLTAFOKLDFPS---EDVL---ECLKEENITGGGSGIVYRGSMNNVDVAIKRLVR 725
Qy 682 NP-OSMKOFETELEMSSIKRNLVLSQAYSLSHLSGLLFYDYLENGSLMDLHGEFTKK 740
Db 726 GTRGSDHGFTEIQTULGRIHRHRIVRLGYVANKOTNLLIYEMPGSLGELLHG-SKGG 784
Qy 741 TLMDTRLKIAYGAAGLAYLHDDCSPRIRHDDVSSNLLDKOLEARLTDPGIAKSL-- 798
Db 785 HLOMETTRRIVEAAKGLCYLHDDSPILHDDVSSNNLLDSDPEAHVADGLAFVLD 844
Qy 799 -----CVSKSHSTVWMTGIGYIDPEVARTSLTEKSDVYSXGIVLELLETRKAVD-- 851
Db 845 GAASECMS-----IAGSYGIAPFYATTLKVDEKSDVYSGCVULLEIACKKPGEGG 898
Qy 852 -----ESNLHLIMSKTGNNEVEMADPDITSTCKDLGVYKAVFOLALLCTKRQPN 903
Db 899 EGVDDIVRWRTNTEETITQPSDAALIVVAIVDPRLTG--YPLTSVIVHFKIAMMCVEEAAA 956
Qy 904 RPTNHOVTRVLGSPMLSEOPPAATYTS 931
Db 957 RPTMEVVA-----MLTNPCKSVANLII 979

```

RESULT 12  
US-08-473-553A-2  
Sequence 2, Application US/08473553A  
Patent No. 5859338  
GENERAL INFORMATION:  
APPLICANT: Meyerowitz, Elliot M.

APPLICANT: Clark, Steven E.  
APPLICANT: Williams, Robert W.  
TITLE OF INVENTION: Plant Clavatal Nucleic Acids,  
TITLE OF INVENTION: Transformed Plants, and Proteins  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/473,553A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Silva, Robin M.  
REGISTRATION NUMBER: 38,304  
REFERENCE/DOCKET NUMBER: A-60886/RFT/RMS  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 985 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-473-553A-2

Query Match 25.6%; Score 1293.5; DB 1; Length 985;  
Best Local Similarity 35.1%; Pred. No. 8.5e-92;

Matches 347; Conservative 153; Mismatches 363; Indels 125; Gaps 27;

QY 30 LLEIKKS-FKDVNNVLYDWTTPSPD-YCVMRGVSGENTFNNVALNLDNDGEISPA 87  
DB 36 LNLKSSMIGPKKHGHDMTHSSPDHCSFSCVSCDD-DARISLNVSTPLFGITSPS 94  
QY 88 IGDLSKLSIDRGNRLSGOIPDEIGDCSSLQNLDSFN-ELSGDIPFSISK-LKOLEDT 145  
DB 95 IGMLTGLVNLTLAANNFTGELPLEMKSLTSLKVLNISNNGLTGFPEGLKAMVDLEV 154  
QY 146 ILKNNGLIPBETLSOIPNLKILDLAONKLSGEIRLIYMNVLQYLGRNNLVGNIS 205  
DB 155 DTYNNPNFGKLPKMBELKYLKLSFGNFSGEISYGDIOSLYLGNGAGLSGKSP 214  
QY 206 PDLQQLTG----WFDVNNNSLTGSIPTIGNCTAFQVLDLSYNQLTGEIPFDIGFLO 260  
DB 215 AFLSRKLNREMYIGY----NSYTGAVREFGGLKELIDMASCTVGEITSLSNKK 270  
QY 261 -VAISLQGNQSGKIPSVIGLMOALVLDLSGNLISGSIPTI--LGNLTFTEKLYLHS 316  
DB 271 HHTTFLHNNLGHIPPELSGLVLSKSLDLSINQLTGEIPQFIMGNITL--INTLR 327  
QY 317 NKLTGSIPELGNMSTLHY------LELNDHNLGHIPPELG 352  
DB 328 NNLVGOIPPAIGELPKLEVFEEVWENNFTQLPANLGRNGLIKLDVSDNHLTGLPKDLC 387  
QY 353 KLTLDLFDLVANNDDGPIPDHLSCTNLNSLVHGNKSGTIPRAFOKLESMTYLNLS 412  
DB 388 RGRKLEMLLSNNFFGPIPEELGCKSLKIRIVNKLNGVPAALFNLPLVTIIEYLD 447  
QY 413 NNKGPVPELS------RIG---NIDTIDLSNNKINGIIPSSLD 449  
DB 448 NFESGELPVMTSGDVLDDIYLSNNMFSGEIPPAIGFNPMLQTLFDRNFRGNIPREIFE 507

QY 450 LEHLKXNLSRNHITGVVPCDFGNLRSIMEIDLSNNDISGPIPEELNOLONIILRLENN 509  
DB 508 LKLSKRINSANNITGIPDISRCSTLISVDSRRRINCEIKGINNVNGLTINSGN 567  
QY 510 NLTVNGVS-LANCLSLTVLVNHNVLVDI PKXNNFSRPSDFIGNPGLC-GSWINSPC 567  
DB 568 QLTGSIPTGIGNMSTLTLDLSFNDSLGRVPLGQGLVFNETSFAGNTYLCPLHRSVSCP 627  
QY 568 H-----DSRRYVSVISRAIIGI-AIGGLVILMLVLAACRPHNPPPLDGLDPRY 621  
DB 628 RPOGTSDBHNTALFSPSRVITVIAITGLILSVAIRQNNKKR------QKSLAW 678  
QY 622 STEPLVILHNNMALHYEDIMRWENTLSEKIIIGHGASSVYCVKCNKPAIKLYSH 681  
DB 679 KLTAPQKLPKFS----EDVL--ECLKENITGKSGSGIVRGSPNNVDAIKLVR 730  
QY 682 NP-QSMKOFETELEMLSIKHRNLVSLQAYSLSHLGSLFYDLENGSLMDLHGPTKK 740  
DB 731 GTRSDHGFIAEIQTLGRIRHRHIVRLGVVANKOTNLLLEYMPNGSLGELLHG-SKGG 789  
QY 741 TLDMDTRLKAYGAAGLAVLHDCSPRIIHRDVKSSNILLDKDLARLTDGIAKSL- 798  
DB 790 HLOMETRHRVAVAAKGLCYLHHDGCPILHRDVKSSNILLSDFEAHVADFLAKFLVD 849  
QY 799 -----CVSKSHSTGYVGTIDPEYARTSRLTESDVSXGIVLLELTRKAVDD-- 851  
DB 850 GAASECWS----IADSYGIAPBYATTLKXDESDVYSGVVLELJAGKKPGEFG 903  
QY 852 -----ESNLHLHLSKTNNEWMADPDITSTCKDLGVKKVFOALCTKROPND 903  
DB 904 EGVDIRVWRNREEITQPSDAIVAIVDPRITG--YPLTSVIVHFKLAMCVBEBA 961  
QY 904 RPTMQVTRVLSFMSLSEOPPAITDTSA 931  
DB 962 RPTMREVVH-----MLTNPKSVANLIA 984

RESULT 13

US-08-473-553A-5  
Sequence 5, Application US/08473553A  
Patent No. 5859338

GENERAL INFORMATION:

APPLICANT: Meyerowitz, Elliot M.

APPLICANT: Williams, Robert W.

TITLE OF INVENTION: Plant Clavatal Nucleic Acids,  
TITLE OF INVENTION: Transformed Plants, and Proteins

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: United States

ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/473,553A

FILING DATE: 06-JUN-1995

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Silva, Robin M.

REGISTRATION NUMBER: 38,304

REFERENCE/DOCKET NUMBER: A-60886/RFT/RMS

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 781-1989

TELEFAX: (415) 398-3249

TELEX: 910 277299

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 999 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: unknown  
 TOPOLOGY: unknown  
 MOLECULE TYPE: protein  
 US-08-473-553A-5

Query Match 25.6%; Score 1293; DB 1; Length 999;

Best Local Similarity 34.6%; Pred. No. 9.5e-92;

Matches 347; Conservative 160; Mismatches 385; Indels 112; Gaps 22;

```

13 LFCLSLVATVTS-----EEGATLL-EIKSKFDVNNVLYDWTTPSSDYCVWRGVC 63
2 LYCLILCLCSSTYLPSELNODATIRQAKLGSDPAQSSSDNNVTPCKMLGVSC 61
64 ENYTFNVALNLDNLNDEISPAIGDKSLISIDLRGNLSGQI-PDEIGDCSSLNLD 122
62 D-ATSNVAVSDLSSEFMLVGPSPSILCHLPISLHSLVYNSINGSLSDADFDYCHNLISLD 120
123 LS-----FNEISGD-----IPPSISLTKQLEQLIKNNQLIGPIP 157
121 LSENLVGSIPKSLPFLPMLKFLIEISGNNISDTIPSSFGFRLIESINLAGNLSGTIP 180
158 STLSQIENLKIDLAONKLS-GEIPRLIYMNVEVQLRGNNVIGNISPDLCQTLGLMY 216
181 ASLGNVTTLKEIKLALYVLFPSQIPSQLGNLTLEQLVLMAGCNLVGPIPELSLSLTVN 240
217 FDVNNNSLTGSI-----PETIGNCTAFOVLDISYNQLTGEI 252
241 LDTLFFNQLTSGIPSMITQKTVEQIELFNNSFSGELPESMGNNMTTLKRFDSNNKLTGKI 300
253 PFDTGFOVATLSIQGNQSGKIPSVIGLMQALAVLDLSGLLSGSI-PRILGNLTFTK 312
301 PDNLNLNLBSLNFENMLEGPPESTIRSKTISELKFNRLNLTGVLVPSQIGANSPIQVY 360
313 YLHSNKLTGSIPEPLGNMKSLEYELNDNHLTGHIPPELGKLTLPDLNVAANDLEGPIR 372
361 DLSVNRSGEIPAVVCGEGKLEYILLIDNSFSGEISNNLGCKSKLTVRSLNNKLSQIP 420
373 DILSSCTNLNSLVNHNKFSGTIPRAFQKLESMTYLVNLSNNIKGPIPELSRIGNLDL 432
421 HGFGLPRLSLLELSDNSFTGSIPTKIIGAKNLNLRISKRFSGSIPNEIGSLNGIIEI 480
433 DLSNNKINGIIPSSLDLEHLKNNLSNNHITGVVPGDFGNLRSIMEIDSNNDISGPIR 492
481 SGAENDSSEGEIPESELVYKQLSRDLSSKNQSGEIPRELKWKNNLNEINLNNHLSGEIP 540
493 EELNQLONIILRLNNNLITGNVSLANCLSLTVLVNLSHNNLVGDIKANNFSRSPDSF 552
541 KEVGLIPLVNLVLDSSNQSGEIPLELONLKTANLVNLSYNHLSGKIPPLVANKIYAHF-F 599
553 IGNGLCGSWINSFCHDSRRTVAVSISPAALIGLIGLVTL--LWVLIACRPHNPPPF 610
600 IGNGLCAVD-LDGLCRKLTTRSGKNIGYWIILTFILAGLVFVVGIVMFIACRKLRLAL-- 656
611 LDGSLDRPVYSTKLVILHNMALHYEDIMRMTENLSEKTIIGHGASSVYVCVLKNC 670
657 -----KSSTLAASKMSF--KLHFSER--EIADECLDERKNVIGFGSGKGYVVEYLRGG 705
671 KPAVKIKRL-----YSHNPOSMKOFETLEMLSSIKRNLVSLQAYVLSHLSGLLF 720
706 EVAVAVKLINKSVKGGDEYSDSLNRDVFPAAEVETLGTIRKSTIVRLMCCSSGDDCKLLV 765
721 YDVLNGLSLMDLHGPTK-KKTLDMVTRKLYAGAAGLAVLHDCSPRIIHRDVKSSNI 779
766 YEYVNPNSIADVLHGDRCGVVGLGWPERLRIALDAEGLSYLHHDCAVPIVHRDVKSSNI 825
780 LLDMDLEARLTDPGIAKSLCVSKSHT--STVYMGITIGYIDPEYARTSRLNLEKSDVYSYG 836
826 LLDSVDYGKAVDFGIAKVGQMSGSKTPBAMSGIASCYIAPEVYITLIRVNEKSDIISFG 885
837 IVLLELTTRRAKAVDDESNIHL-----IMSKTGNNVEMADPDITSTCKDLGVVKKVF 890

```

```

Db 886 VVLELVTKQKOPDSELDGDKMAKWCTALDKGCLPEVI---DPKDLKFE--EISKVI 940
Qy 891 QALLLCTCKROPNDPPTMHQVTRVLSFMLE-----QPPATDTS 930
Db 941 HIGLLCTSPILNRPMSRKVV-----IMLOEVSQAVPSSPNTS 979

```

RESULT 14

US-10-101-464A-900

Sequence 900, Application US/10101464A

Patent No. 6768041

GENERAL INFORMATION:

APPLICANT: Strabala, Timothy

APPLICANT: Nieuwenhuizen, Nicolaas

APPLICANT: Higgins, Colleen M.

TITLE OR INVENTION: Compositions Isolated from Plant Cells

TITLE OR INVENTION: and Their Use in the Modification of Plant Cell Signaling

FILE REFERENCE: 11000.1020c2

CURRENT APPLICATION NUMBER: US/10/101,464A

CURRENT FILING DATE: 2002-03-18

PRIOR APPLICATION NUMBER: 09/704,302

PRIOR FILING DATE: 2000-11-01

PRIOR APPLICATION NUMBER: 09/228,986

PRIOR FILING DATE: 1999-01-12

PRIOR APPLICATION NUMBER: 60/162,866

PRIOR FILING DATE: 1999-11-01

PRIOR APPLICATION NUMBER: PCT/US00/00724

PRIOR FILING DATE: 2000-01-11

NUMBER OF SEQ ID NOS: 989

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 900

LENGTH: 1166

TYPE: PRT

ORGANISM: Pinus radiata

US-10-101-464A-900

Query Match 25.3%; Score 1275; DB 2; Length 1166;

Best Local Similarity 30.8%; Pred. No. 3e-90;

Matches 344; Conservative 170; Mismatches 342; Indels 260; Gaps 27;

```

31 LEIKSFK----DVNNVLYDWTTPSSDYCVWRGVCENAVTNNVALNLDNLNDEIGIS 85
41 IEALQAFKASLTYPDSHALNM--DFVANHVCMNVTGVCNPHKRVLSALNNYNSLSGTTIP 99
86 PARGDLKSLISIDLRGRUSGQIPDEIG-----DCSS----- 117
100 PHIGNISFLGLVNLTLNLSFSGIIPNEIGKURLKRLSKONOLISSIPEALKDCTISRL 159
118 -----LQNLDSLFEELSGDIPPSISKTLQLEQLIKNNQLIGPIP 157
160 NLSHNNLTGTHIPSGLOGOLQNLNLSFNGLTKVPTFCNGSALLETIGSNPLSGTIP 219
158 STLSQIPNLKIDLAONKLSGEIP-----RLIYNEV-----LOY 192
220 SHLGMLARIKILSISGRNQLSGGIPEPSLNLCTELRGVLYENRLTGEIPWEIGAKLSKIEF 279
193 LGRGNLVGNISPDLCQLGLWYFDVRNNSLTGSIPTETIG----- 223
280 LSLGNSLGSIGIPEPSLNLCTELSELDELLENRLTGEIPWEIGAKLSKIEF 339
234 -----NCTAFOVLDISYNQLTGEIPDIG--FLQVATLSLQGNQSGKIPSVIGLMQAL 285
340 IPEPSLNLCTELSELDELLENRLTGEIPWEIGAKLSKIEFSLGNGQSGGIPEPSLNLCTEL 339
286 AVIDLSGNLSSGIPPLIGNL-----TFTEK----- 311
400 SELELDENSLTGGIPQSIGRLIQLDMDLDNNHLYSESSISFGALSNCNTNLQWLSLSSN 459
312 -----LYHSNKLTSIPPELGMSKLEYELNDNHLTGHIPPELG 352
460 DLKGDLPGSIDRLSQNLNLYLYLGGNRFYTKIPQMSNLTGILILDNDNLSSGGLPSALG 519

```

	Query Match	25.1%;	Score 1264.5;	DB 2;	Length 974;	
	Best Local Similarity	34.2%;	Pred. No.1.5e-89;			
	Match 335;	Conservative 161;	Mismatches 386;	Indels 97;	Gaps 23;	
Oy	14 FCLSLV--ATVTSEEGATLLEIKKSFMDYVN-VLYD-----TTPSSDYCWRG	60				
Db	22 FCLLPFSASLAGDDLVLTQRAALAPNSTALHDWVGESSSSSSPPPHCSPTG	81				
Oy	61 VSCENVTFNNVALMSLDNLDEGISPAIGDKLSISIDLRNRLSGQIPDEIGCCSIQN	120				
Db	82 VTCD-AGSRVYSMLTDVRLFGRVPREIGLRDRDVNTLVS CNSLGTLPEPLGNITELGV	140				
Oy	121 LDSLFPNELSGDIPSISIKLKQLEDILKKNNLIQPIPTSTSQIPNKLIDLAKQLSGEI	180				
Db	141 LDVDNNFTAOLPEPVGLKKLKNLANAGNFEEIPEBTVISEMSELEYLGQAANQSGRV	200				
Oy	181 PRLTYMNEVLQYLGL-RGNNLVGNISPDLCQTLTWDFVRANNLSGTSPETIGNCTAFQ	239				
Db	201 PASLAKUKNQMWLVGFNYTDSGITPAEFSGMKRLRDLASCGLSGEIPTSLEBKLD	260				
Oy	240 VLDSYNQLTGEIIPDIG-FLOVAATLSLQGNQSGKITPSVIGLMQALAVIDLSGNLSGS	298				
Db	261 SLFQNMNLMGVIPPELSKMLSLSLDNSNYTLTGVIPTAPEBKNNLTLLFNHHEQG	320				
Oy	299 IPIPLGNITFEKXYLHSNKLTGSIIPBLGMSLHYHLIELNDNHLPCHHIPBLCKLDTLF	358				
Db	321 IPBFVGPLPNLETIQVGNNGFTMMPLPAGLGNGGLVLVDVQTQNFHTGIIPRELCCRGLK	380				
Oy	359 DLVANANDLEGPIPDHLSCTNLNSLVNHGKESGITPRAPFOKL-----	402				
Db	381 TLIITNNSPFEPRIPEDEGECKSLTKVAVGNKFLDGTIPRGIFFNPQATIEIENDNLFSGE	440				
Oy	403 -----ESMTYLNSSNNTKGPIPELRSIRGNLDYDLSNNKINGII PSSLGDLERULK	455				
Db	441 LPAMGSENVIVLSTSNRRISGEIIPAIIGNFGSRTLLDLANRPSGKIPELSFSPFLLR	500				
Oy	456 MNLSRNHIITGVPCDPGNLRSIMEIDLSNDNISPIPEELNOJONILLLENNNLGNV	515				
Db	501 VNIGNSISGIPSSVGTCTSLAADLSRNNLAELINGLSLKVLVALNLSNRLLGPV	560				
Oy	516 -GSLANCLSLTLVNVSHNNVGDIPKNNNFSRFSDSFIGNPGICGSMNSP-----CHDS	570				
Db	561 PKELGIMTSINTLDTLSDFNDSGBVPHHGQPLVFGNSSFAGNQKLC-----SPGRFSC-PS	614				
Oy	571 RRTVRSISPAITIGAIIGLVITLMLVLIACRPHPNPPELDGSLDXPVTYSTPKVILH	630				
Db	615 RSSASRTSSERVITAISLVTAALLITVTYVOVLKR-----ROGSRANKLT-AFOKLGf--	667				
Oy	631 MNMALHYEIOIMRTELSKEYIIGHASASTYVKCVLONKPVAIKRLYGH--NPOSMQ	688				
Db	668 ----KAEDVLC-K--LEEENIIGKGAGIVTRGSPNPGTDAIKQLAGRGGGLSDHG	718				
Oy	689 PETELEMISSIKRHNLVSLQAYSLSHSGLSLFDYDNGLSAMDLLHGPYKKKTLDMDTRL	748				
Db	719 FSAEIQTLGTRHRNIYRLGLYLSNKTONTLLVEYMNGSLGELLHG-SKGGHQMetry	777				
Oy	749 KIAYGAAGLAVLHHDCSPRIIHRDVKSNIILLDKDIEARLTPFGIAKSL-----Cvs	801				
Db	778 RIABEAAGCYLHDCPLPIIHRDVKSNNILLSDSDEAHVADFGIAKFLODAGASECMS	837				
Oy	802 KSHSYTYVMGTIGYIDPEYARTSKLTFRKSVYSGVLYLELLRRKAVVDDESNIHLI-M	860				
Db	838 S-----VASGYGIAEYAVTLKVDKSDSVYSFGVALLBELIARKRVGGEGBDVDIRW	891				
Oy	861 SKTGNNEVME-MADPDITSTCKD-----LGVKKVFCOALLCTCRQPNDRPTMHQVTR	912				
Db	892 VKTASDPLPQPEDAVALAVIVRRLOGRYIASVINHFIAKACQVEESESSERPTRVHVH	951				
Oy	913 VLGSFMLSQPPAAATDSA 931					
Db	952 ML-----TNMPLSATTFA 964					

Thu Sep 7 09:31:08 2006

us-10-519-135-2.rai

Page 12

Search completed: September 2, 2006, 06:57:56  
Job time : 56 secs

---



GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: September 2, 2006, 06:47:45 / Search time 315 Seconds  
(without alignments)  
2866.080 Million cell updates/sec

Title: US-10-519-135-2  
Perfect score: 5043  
Sequence: 1 MALFRDVLGLFCLSLVA.....SASDAQFLRFQGVISONSE 976

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	5043	100.0	976	2	Q42371_ARATH	Q42371 arabidopsis
2	3709	73.5	978	2	Q69SP5_ORYSA	Q69SP5 oryza sativ
3	3372.5	66.9	921	2	Q8W0U9_SORBI	Q8W0U9 sorghum bic
4	3200.5	63.5	980	2	Q65867_ORYSA	Q65867 oryza sativ
5	3113	61.7	999	2	Q7X899_ORYSA	Q7X899 oryza sativ
6	3089.5	61.3	967	2	Q6XAT2_ARATH	Q6XAT2 arabidopsis
7	3079.5	61.1	966	2	Q6XAT3_ARATH	Q6XAT3 arabidopsis
8	3059	60.7	932	2	Q9LVP7_ARATH	Q9LVP7 arabidopsis
9	2967.5	58.8	938	2	Q9LVB3_ARATH	Q9LVB3 arabidopsis
10	2306.5	45.7	719	2	Q84XU6_ELAUV	Q84XU6 elaeis guin
11	2299	45.6	441	2	Q56W23_ARATH	Q56W23 arabidopsis
12	1504.5	29.8	1124	2	Q49318_ARATH	Q49318 arabidopsis
13	1489	29.5	1102	2	Q9LVP0_ARATH	Q9LVP0 arabidopsis
14	1480.5	29.4	1109	2	Q6Y777_ORYSA	Q6Y777 oryza sativ
15	1464	29.0	1250	2	Q6L315_SORBI	Q6L315 sorghum dem
16	1454	28.8	1104	2	Q7F8X5_ORYSA	Q7F8X5 oryza sativ
17	1454	28.8	1104	2	Q7X817_ORYSA	Q7X817 oryza sativ
18	1446	28.7	1232	2	Q9SN91_ARATH	Q9SN91 arabidopsis
19	1442	28.6	1232	2	Q9FIZ3_ARATH	Q9FIZ3 arabidopsis
20	1441	28.6	1109	1	RPKI_IPONT	RPKI194 ipomoea nil
21	1427.5	28.3	1029	2	Q7XZM7_ORYSA	Q7XZM7 oryza sativ
22	1412.5	28.0	1133	2	Q9SH12_ARATH	Q9SH12 arabidopsis
23	1410.5	28.0	1003	2	Q49545_ARATH	Q49545 arabidopsis
24	1410.5	28.0	1008	2	Q9LXZ6_ORYSA	Q9LXZ6 oryza sativ
25	1409	27.9	1072	2	Q69X93_ORYSA	Q69X93 oryza sativ
26	1407.5	27.9	1098	2	Q7XHS7_ORYSA	Q7XHS7 oryza sativ
27	1407.5	27.9	1098	2	Q8W5K7_ORYSA	Q8W5K7 oryza sativ
28	1401	27.8	1012	2	Q9LXZ4_ORYSA	Q9LXZ4 oryza sativ
29	1400	27.8	1123	2	Q8GZ71_ORYSA	Q8GZ71 oryza sativ
30	1399.5	27.8	1030	2	Q8H037_ORYSA	Q8H037 oryza sativ
31	1397.5	27.7	392	2	Q6ZG67_ORYSA	Q6ZG67 oryza sativ

32	1397	27.7	1123	2	Q9SSL9_ARATH	Q9SSL9 arabidopsis
33	1396	27.7	1023	2	Q6ZLK5_ORYSA	Q6ZLK5 oryza sativ
34	1393	27.6	1012	2	Q9LXZ5_ORYSA	Q9LXZ5 glycine max
35	1391	27.6	1123	2	Q8L740_ARATH	Q8L740 arabidopsis
36	1383	27.6	1010	2	Q6ZAB5_ORYSA	Q6ZAB5 oryza sativ
37	1378	27.3	1274	2	Q8L155_ORYSA	Q8L155 oryza sativ
38	1368.5	27.1	1002	2	Q9M221_ARATH	Q9M221 arabidopsis
39	1367.5	27.1	992	2	Q65440_ARATH	Q65440 arabidopsis
40	1367	27.1	1112	2	Q6ZAB7_ORYSA	Q6ZAB7 oryza sativ
41	1366.5	27.1	1040	2	Q6Z8Y3_ORYSA	Q6Z8Y3 oryza sativ
42	1365.5	27.1	1192	1	EXS_ARATH	EXS178 arabidopsis
43	1352.5	26.8	1041	2	Q9F115_ARATH	Q9F115 arabidopsis
44	1352	26.8	1117	2	Q5VQM7_ORYSA	Q5VQM7 oryza sativ
45	1345.5	26.7	1120	2	Q84RP5_ARATH	Q84RP5 arabidopsis

## ALIGNMENTS

RESULT 1  
ID Q42371\_ARATH PRELIMINARY; PRT; 976 AA.  
AC Q42371;  
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.  
DT 01-NOV-1996, sequence version 1.  
DT 07-MAR-2006, entry version 38.  
DE Putative receptor-like protein kinase, ERCTA (Putative receptor protein kinase, ERCTA).  
GN Name=ERCTA; OrderedLocustNames=At2g26330;  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC rosids; eustoids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RX MEDLINE=96206819; PubMed=8624444; DOI=10.1105/ltpc.8.4.735;  
RA Torii K.U., Mitsukawa N., Oosumi T., Matsura Y., Yokoyama R., Whittier R.F., Komeda Y.;  
RT "The Arabidopsis ERCTA gene encodes a putative receptor protein kinase with extracellular leucine-rich repeats.";  
RL Plant Cell 8:735-746(1996).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C., Skyes S.M., Kaul S., Mason T.M., Kerlavage A.R., Adams M.D., Somerville C.R., Venter J.C.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RA Town C.D., Kaul S.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.W., Quach H.U., Toriumi M., Ju G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shimizu P., Southwick A., Shinzaki K., Davis R.W., Ecker J.R., Theologis A.;  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
CC -|- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -|- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms> Distributed under the Creative Commons Attribution-NonCommercial license  
CC EMBL; U47029; AAC49302.1; -; mRNA.  
CC EMBL; DB3257; BAA11869.1; -; Genomic DNA.  
CC EMBL; AY035110; AAK59615.1; -; mRNA.  
CC EMBL; AC004484; AAC14518.1; -; Genomic DNA.

DR PIR; B84659; B84659.  
 DR HSP; P36897; 11AS.  
 DR GenomeReviews; CT485783\_GR; AT2G26330.  
 DR TAIR; At2G26330; -  
 DR GO; GO:0005739; C:mitochondrion; IDA.  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR007090; LRR\_pln.  
 DR InterPro; IPR003591; LRR\_typ.  
 DR InterPro; IPR000719; LRRNT\_2.  
 DR InterPro; IPR008271; Prot\_Kinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkin\_AS.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00560; LRR\_1; 19.  
 DR Pfam; PF00563; LRRNT\_2; 1.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR PRINTS; PR00019; LEURICHRPT.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; UNKNOWN\_1.  
 DR PROSITE; PS00101; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR ATP-binding; Kinase; leucine-rich repeat; Nucleotide-binding; Receptor; Repeat; Serine/threonine-protein kinase; transferase.  
 KW SEQUENCE 976 AA; 107334 MW; 0E51D46A4B94C8D CRC64;

Query Match 100.0%; Score 5043; DB 2; Length 976;  
 Best Local Similarity 100.0%; Pred. No. 9 6e-272;  
 Matches 976; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALFRDIVLLGFLFCLSLVATVTSEEGATLLIEIKKSFQDVNNVLYDMTTPSSSDYCVWRG 60  
 DB 1 MALFRDIVLLGFLFCLSLVATVTSEEGATLLIEIKKSFQDVNNVLYDMTTPSSSDYCVWRG 60  
 QY 61 VSCENYFNNVVALNSDNLDEGSPAIQDKSLSDIDGNRLSGQIPETIGCCSLQN 120  
 DB 61 VSCENYFNNVVALNSDNLDEGSPAIQDKSLSDIDGNRLSGQIPETIGCCSLQN 120  
 QY 121 LDISFNLSGDIPRSISKQLKQLEQLKNNQLIPISSTLSQIPNLKILDLAOKLSGEI 180  
 DB 121 LDISFNLSGDIPRSISKQLKQLEQLKNNQLIPISSTLSQIPNLKILDLAOKLSGEI 180  
 QY 121 LDISFNLSGDIPRSISKQLKQLEQLKNNQLIPISSTLSQIPNLKILDLAOKLSGEI 180  
 DB 121 LDISFNLSGDIPRSISKQLKQLEQLKNNQLIPISSTLSQIPNLKILDLAOKLSGEI 180  
 QY 181 PRLIYNEVLQYLRGNINLVGNISPDLCQITGLMYFDVNNSLTGSIPETIGNCTAFQV 240  
 DB 181 PRLIYNEVLQYLRGNINLVGNISPDLCQITGLMYFDVNNSLTGSIPETIGNCTAFQV 240  
 QY 181 PRLIYNEVLQYLRGNINLVGNISPDLCQITGLMYFDVNNSLTGSIPETIGNCTAFQV 240  
 DB 181 PRLIYNEVLQYLRGNINLVGNISPDLCQITGLMYFDVNNSLTGSIPETIGNCTAFQV 240  
 QY 241 LDISYNLTGEIPDIFLQVATLSLQGNQSGKIPSVIGLMQALAVLDISGNLSSGIP 300  
 DB 241 LDISYNLTGEIPDIFLQVATLSLQGNQSGKIPSVIGLMQALAVLDISGNLSSGIP 300  
 QY 241 LDISYNLTGEIPDIFLQVATLSLQGNQSGKIPSVIGLMQALAVLDISGNLSSGIP 300  
 DB 241 LDISYNLTGEIPDIFLQVATLSLQGNQSGKIPSVIGLMQALAVLDISGNLSSGIP 300  
 QY 301 PILGNLFTFEKLYLHSHNKLTSISIPPELGNNMSKLAHYLEINDHLLTGHIPPELGKLTDLFDL 360  
 DB 301 PILGNLFTFEKLYLHSHNKLTSISIPPELGNNMSKLAHYLEINDHLLTGHIPPELGKLTDLFDL 360  
 QY 301 PILGNLFTFEKLYLHSHNKLTSISIPPELGNNMSKLAHYLEINDHLLTGHIPPELGKLTDLFDL 360  
 DB 301 PILGNLFTFEKLYLHSHNKLTSISIPPELGNNMSKLAHYLEINDHLLTGHIPPELGKLTDLFDL 360  
 QY 361 NVANNIDEGPIPDHLSSCTNLSINLVHGNKFSGTIPRAFOKLEBMTYLNISNNIKAPIP 420  
 DB 361 NVANNIDEGPIPDHLSSCTNLSINLVHGNKFSGTIPRAFOKLEBMTYLNISNNIKAPIP 420  
 QY 361 NVANNIDEGPIPDHLSSCTNLSINLVHGNKFSGTIPRAFOKLEBMTYLNISNNIKAPIP 420  
 DB 361 NVANNIDEGPIPDHLSSCTNLSINLVHGNKFSGTIPRAFOKLEBMTYLNISNNIKAPIP 420  
 QY 421 VEISRIINLTLDISNNKINGIITSSIGDLPHLLKNNLSRHHITGVVPGDGNLSIMEI 480  
 DB 421 VEISRIINLTLDISNNKINGIITSSIGDLPHLLKNNLSRHHITGVVPGDGNLSIMEI 480  
 QY 421 VEISRIINLTLDISNNKINGIITSSIGDLPHLLKNNLSRHHITGVVPGDGNLSIMEI 480  
 DB 421 VEISRIINLTLDISNNKINGIITSSIGDLPHLLKNNLSRHHITGVVPGDGNLSIMEI 480  
 QY 481 DLSNNDISGPIPEELNQLNIILRLFENNLTGVNGSLANCLSTLVNVSHNNLVGDIPIK 540  
 DB 481 DLSNNDISGPIPEELNQLNIILRLFENNLTGVNGSLANCLSTLVNVSHNNLVGDIPIK 540  
 QY 481 DLSNNDISGPIPEELNQLNIILRLFENNLTGVNGSLANCLSTLVNVSHNNLVGDIPIK 540  
 DB 481 DLSNNDISGPIPEELNQLNIILRLFENNLTGVNGSLANCLSTLVNVSHNNLVGDIPIK 540  
 QY 541 NNNFSRSPSPSFIGNPGICGSLWNSPCHDSRRYRVVISRAAIIIGIAGIVILLAVLIA 600  
 DB 541 NNNFSRSPSPSFIGNPGICGSLWNSPCHDSRRYRVVISRAAIIIGIAGIVILLAVLIA 600  
 QY 541 NNNFSRSPSPSFIGNPGICGSLWNSPCHDSRRYRVVISRAAIIIGIAGIVILLAVLIA 600  
 DB 541 NNNFSRSPSPSFIGNPGICGSLWNSPCHDSRRYRVVISRAAIIIGIAGIVILLAVLIA 600  
 QY 601 ACRPHNPPPLDGLDKPVYTSPTKLYTLHNNMALHYVEDIMRMTENLSEKYIIIGHGASS 660  
 DB 601 ACRPHNPPPLDGLDKPVYTSPTKLYTLHNNMALHYVEDIMRMTENLSEKYIIIGHGASS 660

QY 661 TVYKCVLKNCKPVAIKRLYSHNPQSMKOFETELMSSIKGRNLVSLQAVSLSHLSGLLF 720  
 DB 661 TVYKCVLKNCKPVAIKRLYSHNPQSMKOFETELMSSIKGRNLVSLQAVSLSHLSGLLF 720  
 QY 721 YDYLENGSLMDLHGPKPKKTLMDPTRLKAYGAAGLALVHDDCPRIIHRVKSNNIL 780  
 DB 721 YDYLENGSLMDLHGPKPKKTLMDPTRLKAYGAAGLALVHDDCPRIIHRVKSNNIL 780  
 QY 721 YDYLENGSLMDLHGPKPKKTLMDPTRLKAYGAAGLALVHDDCPRIIHRVKSNNIL 780  
 DB 721 YDYLENGSLMDLHGPKPKKTLMDPTRLKAYGAAGLALVHDDCPRIIHRVKSNNIL 780  
 QY 781 LDDLEARLTDPGIASSLCSKSHSTYVWGITGYIDPEYARTSRLTESKDVSYGIVLL 840  
 DB 781 LDDLEARLTDPGIASSLCSKSHSTYVWGITGYIDPEYARTSRLTESKDVSYGIVLL 840  
 QY 841 ELLTRRAVDESNNLHLILMSKTGNNEVEMADPDITSTCKDLGVYKVFQALACTKQ 900  
 DB 841 ELLTRRAVDESNNLHLILMSKTGNNEVEMADPDITSTCKDLGVYKVFQALACTKQ 900  
 QY 901 PNDPPTMHQYTRVLGSMLESEPPAATDTSATLASCYDEYANLKTTPHVNCSMSASD 960  
 DB 901 PNDPPTMHQYTRVLGSMLESEPPAATDTSATLASCYDEYANLKTTPHVNCSMSASD 960  
 QY 901 PNDPPTMHQYTRVLGSMLESEPPAATDTSATLASCYDEYANLKTTPHVNCSMSASD 960  
 DB 901 PNDPPTMHQYTRVLGSMLESEPPAATDTSATLASCYDEYANLKTTPHVNCSMSASD 960  
 QY 961 AOLFLRFGVYISQNSE 976  
 DB 961 AOLFLRFGVYISQNSE 976

RESULT 2  
 069SP5\_ORYSA  
 ID 069SP5\_ORYSA PRELIMINARY; PRT; 978 AA.  
 AC 069SP5;  
 DT 13-SEP-2004, integrated into UniProtKB/TrEMBL.  
 DT 13-SEP-2004, sequence version 1.  
 DT 21-FEB-2006, entry version 15.  
 DE Putative receptor protein kinase.  
 GN Name=OSJNB001601.39;  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep clade;  
 OC Euharicotidae; Oryzeae; Oryza.  
 OX NCBI\_TaxID=39947;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Sasaki T., Matsumoto T., Yamamoto K.;  
 RT "Oryza sativa nipponbare (GAJ) genomic DNA, chromosome 6, BAC  
 clone:OSJNB001601.39."  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 CC -----  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NonCommercial License  
 CC -----  
 DB EMBL; AP004991; BAD35990.1; -; Genomic\_DNA.  
 DB Gramene; O69SP5; -  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0000166; F:nucleotide binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR007090; LRR\_pln.  
 DR InterPro; IPR003591; LRR\_typ.  
 DR InterPro; IPR013210; LRRNT\_2.  
 DR InterPro; IPR000719; Prot\_Kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00560; LRR\_1; 19.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF07714; Pkinase\_Tyr; 1.  
 DR PRINTS; PR00019; LEURICHRPT.  
 DR ProDom; PD000001; Prot\_kinase; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN\_1.  
 DR PROSITE; PSS0011; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
 KW ATP-binding; kinase; leucine-rich repeat; Nucleotide-binding;  
 KW Receptor; Receptor; Serine/threonine-protein kinase; transferase.  
 S0 SEQUENCE 978 AA; 106746 MW; 9F0485366B705BD2 CRC64;

Query Match 73.5%; Score 3709; DB 2; Length 978;  
 Best Local Similarity 73.6%; Pred. No. 1,5e-197;  
 Matches 713; Conservative 100; Mismatches 148; Indels 8; Gaps 4;

```

13 LFLSLVATVTSSEGATLLEIKKSFKDYNVLYDWTTSPSSDYCVWVGSCENTFENVA 72
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
13 LVALLVAVAVADDGSTLEIKKSFRRVDNVLYDMA---GDYCSYWRGVLCNDVTFVAA 69
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
73 LNTSDNLDOEISPAIGDLKSLSIDKRGRLSGQIPDEIGDSSGLONLDPNELSGDI 132
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
70 LNTSGNLGGEISPAVGRIGVSDIKSGNSGQIPDEIGDSSGLKTTLDLSPNSLDGDI 129
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
133 PFESIKLKOLEQILKKNQOLIGPIPTLSQIPNLKIDLQNKLSGEIPRLIYWEVLAQY 192
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
130 PFESVSKLKHESILKKNQOLIGVPTLSQIPNLKIDLQNKLSGEIPRLIYWEVLAQY 189
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
193 LGLRGNLVGNISPDLCQLTGLWYFDVRNNSLTGSIPEITGNCTAFQVLDLSYNTLGEI 252
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
190 LGLRGNLVGEGISPDICQLTGLWYFDVRNNSLTGSIPEITGNCTAFQVLDLSYNTLGEI 249
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
253 PPIGPIQVATLLOQNLQSGKIPSVGLMOALAVLDLSGNLSGSIPEPLISNLTFEKL 312
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
250 PFNIGFIQVATLLOQNMFPGPISPVIGLMQALAVLDLSYNTLQSGSIPEPLISNLTFEKL 309
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
313 YLHNSNKLGTSPPELGNMSKLYLELNDNLGHIPELGLKLDLPLIYANNNDLSEGP 372
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
310 YMGNKLTGIPPELGNMSTLHLELNDNLGHIPELGLKLDLPLIYANNNDLSEGP 369
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
373 DHLSSCTNLNSLVHGNKFSGITIPRAFOKLESMTYLNLSSNNIKGPIPELISNLTFEKL 432
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
370 DNISSCVNLNSFAYAGRLNGTIPPLHKLKESMTYLNLSNPISGSIPELISNLTFEKL 429
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
433 DLSNNKINGIIPBSLGLDEHLKKNLSRNHITGVPCDFGNLRSINEIDLSNNDISGP 492
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
430 DLSNNKINGIIPBSLGLDEHLKKNLSRNHITGVPCDFGNLRSINEIDLSNNDISGP 489
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
493 BELNOLQNTLLENNNLTVGNVSLANCLSTVLYNNSHNLVGDIPKNNNFSRPSDSF 552
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
490 QELQMLQNTLLENNNLTVGNVSLANCLSTVLYNNSHNLVGDIPKNNNFSRPSDSF 549
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
553 IGNPGLCGSWLNSPCHDSRRTRVVISRAAIIIGAIIGLVIILMVLIACRPNPPEFLD 612
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
550 LGNPGLCGSWLNSPCHDSRRTRVVISRAAIIIGAIIGLVIILMVLIACRPNPPEFLD 609
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
613 GSDLRKVTYTPKLVILHNNMALHYEDIRKNTENISEKTIIGHGASTYCYKVLKXCKP 672
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
610 VSVSKFVSNNPPLKLVILHNNMALHYEDIRKNTENISEKTIIGHGASTYCYKVLKXCKP 669
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
673 VAIKRLYSHNPOSKQFETELMSSIKRNLVSLQVYSHSGSLFVYLVNGSLMDL 732
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
670 VAAVKLYAHNPQSKFETELMSSIKRNLVSLQVYSHSGSLFVYLVNGSLMDL 729
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
733 LH-GPTKKTLTDVTRLKIAVGAAGLAVYHHDCSPRIIRHDVSSNILLDKLEALRLD 791
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
730 LHGGPTKKTKKLDVTRLKIAVGAAGLAVYHHDCSPRIIRHDVSSNILLDKLEALRLD 789
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
790 FGIAKSLCVSKSHTSYVMGTIGIDEVARTSLNEKSDVYSGVILTELLTGKKRPVDN 849
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
792 FGIAKSLCVSKSHTSYVMGTIGIDEVARTSLNEKSDVYSGVILTELLTRRAVDD 851
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
852 ESMLHLIMKKTGNVEMKADPDITSTCDLVGVKVRQALILCTKRONDPPTMHQVT 911
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
850 ESNLHLILSKTANNAMETVPDIDATCDLGVKKVFPALLCTKROPSSDRPTMEVV 909
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
912 RVLGSPMLSEQPPAATDTSA---TLAGSCVDEYANILKTHSVNCSGMS--ASAQOLFRLR 967
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Db 910 RVLDCLVRPDPPEKSAQOLAMPQRPAPVPSYINIEVSLRGTSLVLSANSSCTSDAEFLFK 969  
 QY 968 GOVISONSE 976  
 Db 970 GEVISONTE 978

RESULT 3  
 O8W09\_SORBI  
 ID O8W09\_SORBI PRELIMINARY; PRT; 921 AA.  
 AC O8W09;  
 DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.  
 DT 01-MAR-2002, sequence version 1.  
 DT 21-FEB-2006, entry version 24.  
 DE Putative receptor protein kinase.  
 GN Name=SB35P03.1;  
 OS Sorghum bicolor (Sorghum) (Sorghum vulgare).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Sorghum.  
 OX NCBI\_TaxID=4558;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=15466289; DOI=10.1101/gr.2332504;  
 RA Swigonova Z., Lai J., Ma J., Ramakrishna W., Liaca V., Bennetzen J.L.,  
 Messing J.;  
 RT "Close split of sorghum and maize genome progenitors."  
 RL Genome Res. 14:1916-1923(2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=15466290; DOI=10.1101/gr.2701104;  
 RA Lai J., Ma J., Swigonova Z., Ramakrishna W., Linton E., Liaca V.,  
 Tanyolac B., Park Y.J., Jeong O.Y., Bennetzen J.L., Messing J.;  
 RT "Gene loss and movement in the maize genome."  
 RL Genome Res. 14:1924-1931(2004).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Park Y.-J., Ramakrishna W., Sanmiguel P., Emberton J., Bennetzen J.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Liaca V., Young S., Kovchok S., Messing J.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 CC  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NonDerivs license  
 CC  
 CC EMBL: AF466199; AAL68842.1; -; Genomic\_DNA.  
 DR Gramene; O8W09;  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0000166; F:nucleotide binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR001611; IPR.  
 DR InterPro; IPR007090; IPR\_pln.  
 DR InterPro; IPR003591; IPR\_tyr.  
 DR InterPro; IPR013210; IPRNT 2.  
 DR InterPro; IPR000719; Prot\_Kinase.  
 DR InterPro; IPR008271; Ser\_thr\_kin\_AS.  
 DR InterPro; IPR002290; Ser\_thr\_kinase.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR Pfam; PF000560; IRR 1; 17.  
 DR Pfam; PF000569; kinase\_1.  
 DR Pfam; PF07714; kinase\_Tyr\_1.  
 DR PRINTS; PR00019; LEURICHRPT.  
 DR PRODOM; PD000001; Prot\_kinase.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN\_1.  
 DR PROSITE; PSS0011; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE; PS00108; PROTEIN KINASE ST; 1.  
 KM ATP-binding; Kinase; Leucine-rich repeat; Nucleotide-binding;  
 KM Receptor; Repeat; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 921 AA; 100740 MW; FECCD22F8744E463 CRC64;

Query Match 66.9%; Score 3372.5; DB 2; Length 921;

Best Local Similarity 68.4%; Pred. No. 7,3e-179;

Matches 666; Conservative 96; Mismatches 141; Indels 71; Gaps 8;

```

QY 13 LFCISLVATYSEGGATLLEIKKSPKDVNNVLYWTTSPSSDYCVWNGVSEANTENVVA 72
DB 9 LVALLVAVAVADGATLVEIKKSPRVNGLYVMA---GDDYCSMGVLCDDNTFAVAA 65
QY 73 LNLSDMLDGEISPAIDLSKLSIDLRGNLRSGQIPDEIDCGSSLNLDLSPNELSGDI 132
DB 66 LNLSDMLDGEISPAIDLSKLSIDLRGNLRSGQIPDEIDCGSSLNLDLSPNELSGDI 125
QY 133 PFSISKLEQLEQLIKNNQIGIPSTLSQIPNLKILDLAQNKLSGEIPRLIYNEVLYQ 192
DB 126 PFSISKLEHNLILKNNQIGIPSTLSQIPNLKILDLAQNKLSGEIPRLIYNEVLYQ 185
QY 193 LGLRGNLVGNISDLCQLTGLWFPDVRNNSLTSGIPETGNCFAFOYLDSTYNQLGEI 252
DB 186 L-----DVKNNSLTGVIPDTGNCFSFOYLDSTYNKRFPGPI 221
QY 253 PFDIGFOVATLSLQGNQSGKIPSVIGLMQALAVLDLGNLSGSIPPIGLNLTFTKX 312
DB 222 PFDIGFOVATLSLQGNQSGKIPSVIGLMQALAVLDSTYNQLSGRIPSTIGNLTFTKX 281
QY 313 YLHNSNKLTSIPPELGNSKLYLVELNDNLGHIPELQKLTDLFDLVANNDLEGP 372
DB 282 YIQGNKLTSIPPELGNSKLYLVELNDNLGHIPELQKLTDLFDLVANNDLEGP 341
QY 373 DHISSCTNLSLNHGKFKSTIPRAFOKLESMYTLWLSNNIGRIPPELSRGINDTL 432
DB 342 DNLSSCTNLSLNHGKFKSTIPRAFOKLESMYTLWLSNNIGRIPPELSRGINDTL 401
QY 433 DLSNNKNGIIPSLGDLLEHLLKNNLSRNHTGVVPGDFGNLRISIMEIDSNNDISGP 492
DB 402 DLSNNKNGIIPSLGDLLEHLLKNNLSRNHTGVVPGDFGNLRISIMEIDSNNDISGP 461
QY 493 EELNQLONILRLLENNNLTGNGVSLANCLSTLVANVSHNNLVGDIPKNNNFSRPSDF 552
DB 462 QELNQLONILRLLENNNLTGNGVSLANCLSTLVANVSHNNLVGDIPKNNNFSRPSDF 498
QY 553 IGNPGLCGSMLNSCHSRKTRVRSISRAALIGLIVLLMVLIAACRPHNPPFP 612
DB 499 IGNPGLCGSMLNSCHSRKTRVRSISRAALIGLIVLLMVLIAACRPHNPPFP 558
QY 613 GSLDKPTVSTPKLVILHMMNALHVEDIMMTEMLSEKYLIGHGASTYKCYLKNCKP 672
DB 559 VYTSKPRNAPPKVILHMMNALHVEDIMMTEMLSEKYLIGHGASTYKCYLKNCKP 618
QY 673 VAIKRLVSNPQSKQFETELMELSSIKHRLVSLQAVLSLHSGLLFYDLNGSLMDL 732
DB 619 VAIKRLVSNPQSKQFETELMELSSIKHRLVSLQAVLSLHSGLLFYDLNGSLMDL 678
QY 733 LH-GPTKKKTLDMVTRKIAVGAAGLAVLHSDSPRIIRDVKSSNILLDKDLAALT 791
DB 679 LHGSSSKKKLDMVTRKIAVGAAGLAVLHSDSPRIIRDVKSSNILLDKDLAALT 738
QY 792 FGIAKSLCSVSKSTYVMGTIGYIDEPYARTSLRTEKSDVY-----SYGVILLELTR 846
DB 739 FGIAKSLCSVSKSTYVMGTIGYIDEPYARTSLRTEKSDVY-----SYGVILLELTR 788
QY 847 KAVDDESNLHRLIMSKTGNNEVMEMADPDITSTCKDLGVKKVYFQALLCTKRPNDP 906
DB 789 -AADWQASGQRITLSTASNEVMDVTPDIDGTCXDLGEVKKYFQALLCTKRPNDP 847
QY 907 MHQVTRVLSGFMSLEQPP---AATDTSATLAGSCYVDEYANLTKPHSVNC-SSMSASDAQ 962
DB 848 MHEVVRVLDCLVNPDPKPSAHQLPOPSPAVPSVINEYVSLRGTGALSCANSTSTSDAE 907

```

QY 963 LFLRFGVVISQNSG 976  
 DB 908 LFLRFGVVISQNSG 921

RESULT 4  
 065867 ORYSA  
 ID 065867 ORYSA PRELIMINARY; PRT; 980 AA.

```

AC 065867
DT 25-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2004, sequence version 1.
DT 21-FEB-2006, entry version 13.
DE Putative transmembrane protein kinase.
GN Name=P0538C01.27; Synonym=P0493C11.1;
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BOP clade;
OC Eriactoidae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, PAC
RT clone:P0538C01."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, PAC
RT clone:P0538C01."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivative 1.0 license
DR EMBL; AP000591; BAD4800.1; -; Genomic DNA.
DR EMBL; AP000559; BAD6763.1; -; Genomic DNA.
DR Gramene; Q65867; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005524; F: ATP binding; IEA.
DR GO; GO:0000166; F: nucleotide binding; IEA.
DR GO; GO:0004674; F: protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F: transferase activity; IEA.
DR GO; GO:0006468; P: protein amino acid phosphorylation; IEA.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007090; LRR_pln.
DR InterPro; IPR003591; LRR_tyr.
DR InterPro; IPR013210; LRRNT_2.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR008271; Ser_Thr_kin_AS.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00560; LRR_1; 19.
DR Pfam; PF00069; Kinase; 1.
DR PRINTS; PR00019; LEURCHRP.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KM ATP-binding; Kinase; Leucine-rich repeat; Nucleotide-binding; Repeat;
KM Serine/threonine-protein kinase; Transferase; Transmembrane.
SQ SEQUENCE 980 AA; 106727 MW; 01AF615B3C5B557 CRC64;

```

Query Match 63.5%; Score 3200.5; DB 2; Length 980;

Best Local Similarity 65.5%; Pred. No. 2.9e-169;

Matches 624; Conservative 140; Mismatches 178; Indels 11; Gaps 7;

```

QY 26 EGATLLEIKKSPKDVNNVLYDWTTPSSDYCVWNGVSEANTENVVA 85
DB 35 EGATLLEIKKSPKDVNNVLYDWTTPSSDYCVWNGVSEANTENVVA 92

```



D 453 TIGDLEHLLELNLSKNHLDGVPAPFAGNLSVQVYIDMSNNLSGSLPELIGQLONLDSLI 512  
Q 506 LENNNLTGVN-GLSLANCLSLTVLVNHNHVGDI PKNNNFSRSPD----- 550  
D 513 LNNNNLVGEIIPAQLANCFSL-----NNLAFQEFVYIQOFLWCPDCKELLETIPNGKHL 565  
Q 551 -----SFIGNPGLCGSLWNSPCHDSRRRTVEVSIIRAILGAIAGVILLMLV 598  
D 566 ISDNOQYINHKCSFLGNPLHLHVQCDSGSHQ-RVNISKTAIACILIGFILLCVLL 624  
Q 599 IAACRPNPPEFLDGLSDKPYTSTPKLVILHNMALHVEDIRKMTENSEKTIIGHGA 658  
D 625 LAIYKTQPOPLVYKGS-DKEV-QGPKLVYLQDMAHTYEDIRKMTENSEKTIIGHGA 682  
Q 659 SSTYVYKVLKNCKRVAIKRLYSHNPQSMKOPETELEMSSIKHNLVSLQVSLSHGSL 718  
D 683 SSTYVYKELSGKAIKRLYSQYNHSLRETELETIGSIRHNLVSLHGFSLSPGNL 742  
Q 719 LFYDYLENGSLMDLHGPTKKTLMDMDTRLKIAYGAQGLAYLHSDSPRIHRDVASN 778  
D 743 LFYDYMGNSIMDLHGSPSKVKVLMNDRIRIAVGAQGLAYLHSDNPRIIHRDVASN 802  
Q 779 ILDDKDLRLTLDFGIAKSLCVSKSHSTYVMGTIGYIDPEYARTSLTEKSDYVYIGIV 838  
D 803 ILDENEFAHLSDPGIAKCVPSAKSHASTYVLTGTYIDPEYARTSLTEKSDYVYIGIV 862  
Q 839 LLELLTRKAVDDESNLHILMSKTGNNEWMEMADPITSTCKDLGVYKVFQALALCTK 898  
D 863 LLELLTRKAVDDESNLHILMSKTGNNEWMEMADPITSTCKDLGVYKVFQALALCTK 922  
Q 899 ROPNDRPTMHQVTRVLGSFMLSE--QPPATDTSATLAGSCYVDENALTKPHSNSSM 956  
D 923 RHPDRPTMHQVTRVLGSFMLSE--QPPATDTSATLAGSCYVDENALTKPHSNSSM 979  
Q 957 SASDAQFLARQCVYISONS 975  
D 980 SSSDEQMFVRFGVEVISHKT 998

RESULT 6  
Q6XAT2\_ARATH PRELIMINARY; PRT; 967 AA.  
AC Q6XAT2;  
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2004, sequence version 1.  
DT 21-FEB-2006, entry version 13.  
DE ERECTA-like kinase 2.  
GN Name=ERL2;  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC Rosids; eustoids II; Brassicales; Brassicaceae; Arabidopsids.  
OC NCBI\_TaxID=3702;  
RN [1]  
NP NUCLEOTIDE SEQUENCE.  
RP PubMed=14985254; DOI=10.1242/dev.01028;  
RA Shpak B.D., Berthiaume C.T., Hill E.J., Torii K.U.;  
RT "Synergistic interaction of three ERECTA-family receptor-like kinases  
controls Arabidopsis organ growth and flower development by promoting  
cell proliferation.";  
RL Development 131.1491-1501(2004).  
CC - CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC - SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
CC -----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NonCommercial License  
CC -----  
CC EMBL: AY244746; AAP69764.1; -; mRNA.  
DR GO: GO:0005224; F:ATP binding; IEA.  
DR GO: GO:0000166; F:nucleotide binding; IEA.  
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO: GO:0016740; F:transferase activity; IEA.  
PR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.

DR InterPro: IPR001611; LRR.  
DR InterPro: IPR007090; LRR\_p1n.  
DR InterPro: IPR003591; LRR\_typ.  
DR InterPro: IPR013210; LRRNT 2.  
DR InterPro: IPR008719; Prot\_Kinase.  
DR InterPro: IPR008271; Ser\_thr\_kin\_AS.  
DR InterPro: IPR002290; Ser\_thr\_kinase.  
DR InterPro: IPR001245; Tyr\_kinase.  
DR Pfam: PF00560; LRR\_1; 18.  
DR Pfam: PF00069; Kinase; 1.  
DR PRINTS: PR00019; LEURCHRT.  
DR ProDom: PD000001; Prot\_Kinase; 1.  
DR PROSITE: PS00107; PROTEIN KINASE ATP; UNKNOWN 1.  
DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.  
DR PROSITE: PS00108; PROTEIN KINASE ST; 1.  
KW ATP-binding; Kinase; leucine-rich repeat; Nucleotide-binding; Repeat;  
KW Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 967 AA; 106680 MW; 90096C7B67CE852C CRC64;

Query Match 61.3%; Score 3089.5; DB 2; Length 967;  
Best Local Similarity 62.2%; Pred. No. 4,3e-163;  
Matches 605; Conservative 134; Mismatches 211; Indels 23; Gaps 6;

Q 11 GLEFCLSLV-----ATTSGEATLLETKSFKQVNNVLYDWTSPSSDYCVNRGVSC 63  
D 9 GLEFCLGMVFMILGSGVSPMNEGKALMAIKAFSNVANNLMDVDVHNHDFCSMRGVFC 68  
Q 64 ENTENVVALNTLSDNLMDGEISPAIGDLKSLSIDLRGNLSGQIPDEIGDCSSLQNL 123  
D 69 DNVSLNVSLNLSNLNLNGEISSALGDMNLQSIDLGNLGGQIPDEIGNCVSLAYVDF 128  
Q 124 SFNELSGDIPFSISKQLQLEQLILKNNQLGIPSTLSQIPNLKILDLAQNKLSGEIPRL 183  
D 129 STNLRLGDIPIFSISKQLQLEQLILKNNQLGIPSTLSQIPNLKILDLAQNKLSGEIPRL 188  
Q 184 IYNNVLYQYGLGNNLVGNISPDLCQLTGLMTFVDRANSLTSISPIETGNCTAFQVLD 243  
D 189 LYNNVLYQYGLGNNLVGNISPDLCQLTGLMTFVDRANSLTSISPIETGNCTAFQVLD 248  
Q 244 SYNQLGSEIPFDIGFLOVATLSLQGNLSGKIPSVIGLMOALAVLDLSGNLSGIPIL 303  
D 249 SYNQLGTVIYNGFLOVATLSLQGNLSGKIPSVIGLMOALAVLDLSGNLSGIPIL 308  
Q 304 GNLTFTEKLYLHGNKLTGSIPELGNMSKLYLDELNDNLGHIPELGLTDLFDLNV 363  
D 309 GNLTFTEKLYLHGNKLTGSIPELGNMSKLYLDELNDNLGHIPELGLTDLFDLNV 368  
Q 364 NNDLEGPIDPHLSSCTNLNSLVNHNKFSCTIRPAQKLESMYTLNLSNNITGPIPEL 423  
D 369 NNDLVGLIPENISSCALAQNFVHGNFLSGAVPLEFRNLGSLTYLNLSSNSFGKIPAE 428  
Q 424 SRIGNLDTLNLNNKINGIIPSSIGDLEHLKNNLSRNHTGVVPGDFGLRSIMEIDLS 483  
D 429 GHIIINLDTLNLNNKINGIIPSSIGDLEHLKNNLSRNHTGVVPGDFGLRSIMEIDLS 488  
Q 484 NNDISGEIPPELNLQNLIIILRLNNNLTVN-GLSLANCLSLTVLVNHNHVGDIIPKN 542  
D 489 ENFLAGVITPELQQLQNLIIILNNKIHGKIIPDQLNCSLANLNSFNLSGIIIPMK 548  
Q 543 NFRSFPDSFTGNPGLCGSWLNSPCHDSRRRTVAVSIRAILGAIAGVILLMLVLAAC 602  
D 549 NFRSFPDSFTGNPGLCGSWLNSPCHDSRRRTVAVSIRAILGAIAGVILLMLVLAAC 607  
Q 603 RPNHPPEFLDGLSDKPYTSTPKLVILHNMALHVEDIRKMTENSEKTIIGHGASSTV 662  
D 608 KSKQKQKVLKSGSKQ--EGSTKLVILHNMALHTPDIKRVENLDEKTIIGHGASSTV 665  
Q 663 YKCVLKNCKRVAIKRLYSHNPQSMKOPETELEMSSIKHNLVSLQVSLSHGSLFLYD 722  
D 666 YKCTSKTSRRIAIKRIYQPSNFRRETELETIGSIRHNLVSLHGFSLSPGNLFLYD 725  
Q 723 YLENGSLMDLHGPTKKTLMDMDTRLKIAYGAQGLAYLHSDSPRIHRDVSSNLLD 782



Dh 726 YMENGSLMDLLHGPCKYKLDMDMETRLKIAVGAOGLAVLHHDCTPRIIHRDIKSSNILLD 785  
Qy 783 KDLLEARLTDEGIASLCSVSKSHSTYVMGTIGYIDPEYARTSRLEKSDPYVSGIVLEL 842  
Db 786 GNFPAARLSDFGIAKSLIPATKYASTYVLTGTYIDPEYARTSRLEKSDPYVSGIVLEL 845  
Qy 843 LTRKAVDDESNLHHILMSKTGNNEWMEMADPDITSTCKDLGVKVFQALALCTKROPN 902  
Db 846 LTGKKAVDNENAHQMLLSKADNTVMEAVDAEVSVCNDSGHITKTFQALALCTKRNPL 905  
Qy 903 DRPTMHQVTVLGSFMLSSEOPPAATDTSATLAGSCYVDEYANILKTPHSVNCSSMSASDAQ 962  
Db 906 ERPTMGVSRLVSLVSPSP-----KLLPSAKYQEGGERESHSSPTTT-----PQ 953  
Qy 963 LFLRFGQVTSQNS 975  
Db 954 WFOVFREDISKSS 966

RESULT 7

06XAT3 ARATH  
ID 06XAT3 ARATH PRELIMINARY; PRT; 966 AA.  
AC 06XAT3;  
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2004, sequence version 1.  
DT 07-MAR-2006, entry version 14.  
DE ERECTA-like kinase 1.  
GN Name=ERL1;  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC Rosids; eurosoid II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP NOCLEOTIDE SEQUENCE.  
RX PubMed=14985254; DOI=10.1242/dev.01028;  
RA Spbak E.D., Berthiaume C.T., Hill E.J., Toril K.U.;  
RT "Synthetic interaction of three ERECTA-family receptor-like kinases  
RT controls Arabidopsis organ growth and flower development by promoting  
RT cell proliferation.";  
RL Development 131:1491-1501(2004).  
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NonCommercial License  
CC  
CC EMBL, AY244745; AAP69763.1; -; mRNA.  
CC GenomeReviews: BA000015 GR; AT5G62230.  
DR GO: GO:0005524; F:ATP binding; IEA.  
DR GO: GO:0000166; F:nucleotide binding; IEA.  
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO: GO:0016740; F:transferase activity; IEA.  
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro: IPR001611; IPR.  
DR InterPro: IPR007090; IPR.  
DR InterPro: IPR003591; IPR.  
DR InterPro: IPR013210; IPR.  
DR InterPro: IPR008271; Ser Thr pkin AS.  
DR InterPro: IPR002290; Ser Thr pkin AS.  
DR InterPro: IPR001245; Tyr\_kinase.  
DR Pfam: PF00560; LRR\_1; 19.  
DR Pfam: PF08263; LRRNT\_2; 1.  
DR Pfam: PF00069; Pkinase; 1.  
DR PRINTS: PR00019; LEURICHPT.  
DR ProDom: PD000001; Prot\_kinase; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; UNKOWN\_1.  
DR PROSITE: PSS0011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00106; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Leucine-rich repeat; Nucleotide-binding; Repeat;  
KW Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 966 AA; 106401 MW; 2B63CF9893338D95 CRC64;

Query Match 61.1%; Score 3079.5; DB 2; Length 966;  
Best Local Similarity 62.7%; Pred. No. 1.5e-162;  
Matches 608; Conservative 140; Mismatches 205; Indels 17; Gaps 6;  
7 IYLLGFLCLSLVATVTSSEKATLLEIKKSKFVNNVNLVDMTSPSSDYCVMRVSCENV 66  
Db 12 LAWVGN--VFGVSAAMNNEKALMAIKGSFSLVNMILMDMDVHNHSDLCMRGVCFDNY 69  
Qy 67 TRNVVALNSDLNLDEGISPAIDKLSLIDLRNRLSGQIPDEIGDCSSLONLDSFN 126  
Db 70 SYSVSSINLSSILMIGEISPAIDLRNLSIDLGKMKLQGIPEDEIGNCASLYLLDSEN 129  
Qy 127 ELSGDIPEFISIKKOLBOLILKNOLIGPPTSLQIPNLKILDLAONKLSGRIPLIYW 186  
Db 130 LLYGDIPEFISIKKOLBOLILKNOLIGPPTSLQIPNLKILDLAONKLSGRIPLIYW 189  
Qy 187 NEVLYQLGLRGNLVAVNISPDLCOLGLWYFDVRNNSLTGSIPEITGNCTAFQVLDLSYN 246  
Db 190 NEVLYQLGLRGNLVAVNISPDLCOLGLWYFDVRNNSLTGSIPEITGNCTAFQVLDLSYN 249  
Qy 247 QLTGEIPFDIGLQVATLTLQGNQLSGKIPSVGLMQALAVLDSGNLSGSLPPLGLN 306  
Db 250 QITGEIPYNIQVAVATLSLOGNRLTGRIPVETGLMQALAVLDSGNELVGPPIPLGNL 309  
Qy 307 TPTKEXLYLSNKLTSISPELGNMSKLYLELDNHLTGHIPELGLTDLFDLVANND 366  
Db 310 SFTGKLYLHGNMVLTPSPSELGNMSRSLYQLNDNKLGVITPELGLTDLFDLVANNSR 369  
Qy 367 LGEPIPDHSSCTNLNSLWVHGNKFGSTIPRAFOKLESMYTLNLSNNIKGPIPELSRI 426  
Db 370 LVPIPSNLSGCAALNQPNVHGNLSGSIPLARNLSGLTYLNLSSNPFKGIPELVGHI 429  
Qy 427 GNLDITLDSNNKINGIIPSSGLDLEHLKKNLSRNHITGVVPGDFGNLSIMEDISND 486  
Db 430 INIDKDLDSGNNSGSIPLTGLDLEHLILNLSRNHLSGOLPAEFGNLSIQMIDVSNL 489  
Qy 487 ISGPIPEELNOLNIIILRLNNNLTVGN--GSLANCLSLTVLNVSHNVLGDIPOKNNS 545  
Db 490 LSGVITPELQLONLNLSLNNKHLHGKIPDQITNCFVLNVNLSRNNSGIVPEKMFNS 549  
Qy 546 RFSPDSFIGNPGLCGSLWNSPCHDSRRTVRSISRRAIGIAGLVILMVLIAACRPH 605  
Db 550 RFAPASFVGNPVLGCMWVSGIGPLPKS--RV-FSRGALICIVGLVTLDMIFLAYKSM 607  
Qy 606 NPPFLDGLDKPVTYSTPKLVILHNMALHYVEDIMRMTENLSEKTYIGHGASSTVYKC 665  
Db 608 QOKKIIQGSSEKQ--AEGLTKLVILHMDMAIHTEDDIMRVTEINERKFIIGYGASSTVYKC 665  
Qy 666 VLKCKEPVATIKRLYSHNPSOMKOFETELEMLSIKHRNLSVLAQVSLSHLSGLFYDYLE 725  
Db 666 ALKSSSPIAKRILYNOYPHNLREFETELETGSIHRNRVLSLGVALSIPGNLFLDYME 725  
Qy 726 NGSIMDLHGLPTKKKTLMDVTRLKIAVGAAGLAVLHHDSPRIIHRDVKSSNILLDKL 785  
Db 726 NGSIMDLHGLSKVGLGWETRKLIAVGAAGLAVLHHDCTPRIIHRDIKSSNILLDENF 785  
Qy 786 EARLTPGIAKSLCVSKSHSTYVMGTIGYIDPEYARTSRLEKSDPYVSGIVLELTLR 845  
Db 786 EARLTPGIAKSLIPATKYASTYVLTGTYIDPEYARTSRLEKSDPYVSGIVLELTLR 845  
Qy 846 RKAVIDESNLHHILMSKTGNNEWMEMADPDITSTCKDLGVKVFQALALCTKROPNDR 905  
Db 846 KKAVIDENANLHQLLSKADNTVMEAVDAEVSVCNDSGHITKTFQALALCTKRNPLER 905  
Qy 906 TMAQVTVLGSFMLSSEOPPAATDTSATLAGSCYVDEYANILKTPHSVNCSSMSASDAQFL 965  
Db 906 TMAEVSRLVSLVSPSQ-----VAKLPSLDHSTRKQLQGENEVANPDAAEQWVF 965  
Qy 966 RFGQVTSQNS 975  
Db 954 QFREVTSKSS 965



```
RESULT 8
Q9LYP7_ARATH PRELIMINARY; PRT; 932 AA.
ID Q9LYP7_ARATH
AC Q9LYP7
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 21-FEB-2006, entry version 28.
DE Receptor-like protein kinase.
DE Name=TL26J14_120; Order=diocunNames=At5g07180;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsie.
OC NCBI_TaxID=3702;
RN
RP NUCLEOTIDE SEQUENCE.
RA Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
RA Rudd S., Lemcke K., Mayer K.F.X.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -| CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -| SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs license
CC
CC EMBL; AL163652; CAB87274.1; -; Genomic_DNA.
DR PIR; T48489; T48489.
DR TAIR; Q005524; F:ATP binding; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007090; LRR_Pln.
DR InterPro; IPR003591; LRR_Typ.
DR InterPro; IPR013210; LRRNT_2.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR008271; Ser_Thr_kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00560; LRR_1; 18.
DR Pfam; PF00069; Kinase; 1.
DR PRINTS; PR00019; LEURICHAPT.
DR PRODOM; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; leucine-rich repeat; Nucleotide-binding;
KM Receptor; Repeat; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 932 AA; 102776 MW; F288A5F66C9F4A CRC64;
```

```
Query Match 60.7%; Score 3059; DB 2; Length 932;
Best Local Similarity 63.1%; Pred. No. 2e-161;
Matches 597; Conservative 131; Mismatches 202; Indels 16; Gaps 5;

QY 31 LEIKSEKDVNVNLYDWTSPSDYCVWGVSCENVTFNVVALNLSDLNLDGEISPAIGD 90
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 MAIKASISNVANMLDDVDVHNHFCMGRGVFCNVSLNVSLNLSNLNGEISSLAGD 60
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 91 LKSLSLIDLRGNRLSGQIPBEIGCSSLQNLIDISFNEISGDIPIPSISKLQLEQLIKNN 150
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 61 LNNLQSIDLQGNKLGQIPBEIGCVSLAYVDFSTNLFFGDIPIPSISKLQLEFLIKNN 120
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 151 QLGIPISTLSQINLKITLDAQNKLSGETIRLLTYNNEVLOYGLRGNLVGNISPLQ 210
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
PB 121 QLGIPISTLSQINLKITLDAQNKLSGETIRLLTYNNEVLOYGLRGNLVGNISPLQ 180
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
QY 211 LTGLWYFDVRNNSLGSISPETIGNCTAFQVLDLSYNQLTGEIPFDIGLQVATLSLQNG 270
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 181 LTGLWYFDVRNNSLGSISPETIGNCTAFQVLDLSYNQLTGEIPFDIGLQVATLSLQNG 240
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 271 LSGKISVIGLMOALAVLDLSGNLGSIPRILIGNTFTEKLYSHSNKLTGSPPELGNM 330
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 241 LTGRIVEVIGLMOALAVLDLSGNLGSIPRILIGNTFTEKLYSHSNKLTGSPPELGNM 300
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 331 SKLHYELNDNHTGHIPELGLTDLFDLVANNNDLEGPIDPHLSSCTNLNSLVHGNK 390
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 301 SRLSTYQLNDNDELVGKIPPELGLTDLFDLVANNNDLEGPIDPHLSSCTNLNSLVHGNK 360
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 391 FSGTIPRAFOKESMTYLNLSNNIKGPIPELSRIGNLDLTDLSNNKINGIIPSSLDGI 450
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 361 LSGAVPLEFRNLGSLTYLNLSNFPKGIPELGHIIINDLTDLSGNNSGSIPLTGLDI 420
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 451 EHLKRNLSNHTTGVPPDQGLRISIMEDLSNNDISGPIPELNOLONIILLRLENN 510
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 421 EHLIINLSNHLNGTLPAEFGNLRISIQIIVSFNPLAGVITPELQLOINSLINNNK 480
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 511 LTGNV-GSLANCLSTLVNVSHNVLGDIPIKNNNFRSPDSFIGNPGLSWLNPSCHD 569
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 481 IHGKIPDQLNCFSLANLNSFNLSGIIIPMKNTFRFPASFPFGNPFILGNWVSGICE 540
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 570 SRRTVRSISRALLIGLIGLVLLMLVLIACRPHNPPFILDGSLDKPVYSTPKLVIL 629
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 541 SLRKSQV-FTRVAVICWVLGFIILICMIFIAVYKSKQKRVLKGSSKOP--EGSTKLVL 597
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 630 HNMALHVDIRKMTENLSKKIIGHGASSTYYKCVLKNCKRVALIKRLYSHNPSQMKQF 669
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 598 HMDMAHTFDDIRKVTENLDEKIIIGVGSSTYYKCTSKTSRIAKRIYNQVPSFRFE 657
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 690 ETELEMSSIKHRNLVSLQAVSLSHGSLLFYDLENGLSMDLHGPTKKTLDMDTRLK 749
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 658 ETELETIGSRHNIIYSIHGYALSPGNNLFTYMNENGLMDLHGPCKVKLMDWETRLK 717
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 750 IAVGAAQGLAVLHHDCSPRIIRHDVKSNTLDDKLEARITDGLAKSLCVSKSHSTYV 809
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 718 IAVGAAQGLAVLHHDCSPRIIRHDVKSNTLDDKLEARITDGLAKSLCVSKSHSTYV 777
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 810 MGTIGYIDPEYARTSLTEKSDVYSGIVLELTTRKAVDSDSHLHIMSKTNGNEVM 869
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 778 LGTIGYIDPEYARTSLTEKSDVYSGIVLELTTRKAVDSDSHLHIMSKTNGNEVM 837
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 870 EMADPDITSTCKDLGVKVFQALALCTKQPNDRPTMHQVTRVLGSMFLSEOPPAATD 929
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 838 EAVDAEVSVCNDSGHIKTFQALALCTKRNPLERPTMQSVSLVSLVSPPP----- 891
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 930 SATLAGSCYVDEVANLKTPHSVNCCSMASDAQLFIRFGQVVISQNS 975
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 892 -KLLPSPAKVQGEERRESHSSDTT-----PQMFQFREDISKSS 931
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
RESULT 9
Q9LYB3_ARATH PRELIMINARY; PRT; 938 AA.
ID Q9LYB3_ARATH
AC Q9LYB3
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 21-FEB-2006, entry version 28.
DE Receptor-like protein kinase.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsie.
OC NCBI_TaxID=3702;
RN
RP NUCLEOTIDE SEQUENCE.
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
RA Tabata S.;
RL Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
```



DR Pfam; PF00560; LRR\_1; 10.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR PRINTS; PR00019; LEURICRPT.  
 DR ProDom; PD000001; Prot kinase; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE\_ATP; UNKNOWN\_1.  
 DR PROSITE; PS00011; PROTEIN KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN KINASE\_ST; 1.  
 DR ATP-binding; Kinase; Nucleotide-binding; Receptor;  
 KW Serine/threonine-protein kinase; Transferase.  
 FT NON TER 1  
 SQ SEQUENCE 719 AA; 79689 MW; 38A5F547FAC6FD02 CRC64;

Query Match 45.7%; Score 2306.5; DB 2; Length 719;  
 Best Local Similarity 63.5%; Pred. No. 1e-119;  
 Matches 466; Conservative 93; Mismatches 150; Indels 25; Gaps 9;

QY 251 EIPPDIGFLOVATISLOGNLSKIPSVIGLMQALVLDLSGNLSSIPPIGLNLTPE 310  
 DB 1 EIPVNIQFLOVATISLOGNRLTGKIPVIGLMQALVLDLSGNLSSIPPIGLNLSYTG 60  
 QY 311 KLYHSNKLGTSPPELGNNSKLHYLELDNHLTGHIPEELGKLTDFDLVANNDEGP 370  
 DB 61 KLYHGNKLGTSPPELGNNKTLSTYLOLDNKLVTIPALGKLELPELANNLEGP 120  
 QY 371 IPHLSSCTNLNSLVHGNKFGSTIPRAFOKLESMTYLNSSNNIKGPIVELSRIGNL 430  
 DB 121 IPQNISLCTALNKNFVHGNRLNGSIPIQFOKLESITLYLNFSNNPKGKVPWELGRINLD 180  
 QY 431 TLDSNNKINGIIPSSIGDLEHLKNNLSRHNGVPGDPGNRSIMEDLSNDSGP 490  
 DB 181 TLDSNNHFGSPIDSGDLEHLLELNSRNVLNGPTEGNGRSQOTIDISTNKLSPG 240  
 QY 491 IPEELNQLNIILRLENNLTGVNG-SLANCLSTLYLVNSHNNLVGDIPKNNFSRSP 549  
 DB 241 IPEELGQVQITDITLIANNNDYIGIPIQVLTNCFSSLSLNSPNNFSDVPLSKNFSPQ 300  
 QY 550 DSFTGNFGCGSWNSPCHDSRRTVRVSISSRAAIIIGAILGVLLMVLIAACRPNPP 609  
 DB 301 ESFEGNMLCGNMWLGSSCGDLSHGSKYTISRAAVVCITLGSITLSSMVLVAIYKSSQPKQ 360  
 QY 610 FLDSGLDKPVTYSPKLVIIHNNMALHVIEDIMEMTNLSEKYYIGHGASSTYKCVLKN 669  
 DB 361 FIKGS--NRTVQGPVKLVLRMDAIIHYEDIMKITNLSEKYYIGHGASSTYKCVLKN 418  
 QY 670 CKPAVAKRLYSHNPOSMAKOFETELMLSSIKRNLVLSQAVSLSHLSGLFYDYLENGSL 729  
 DB 419 SKPIAKRLYSQYRHNLFHEFETELTIGSTRHNLVLSLHGYSLSPHGNLIFYDVMENGSL 478  
 QY 730 WDLHGFTKKKTLDMTRKLIAYGAAGLAVLHHDSPRIIHRDKSSNILLDKDLRL 789  
 DB 479 WDLHGFSKKVKLDMTRKLIAYGAAGLAVLHHDSPRIIHRDKSSNILLDENFEAHL 538  
 QY 790 TDEGIAASLCVSKSHSTYVMGTIGYIDPEYARTSLTEKSDVYSVGIIVLELTLTRKAV 849  
 DB 539 SDGFIACIPAKTHASTYVLTGYIDPEYARTSLRNEKSDVYSFGIVLELTLTGKAV 598  
 QY 850 DDESNLHLIMSKTGNNEVMEMADPDITSTCKDGLGVKKVFOALALLCTKEOPNRPMTHQ 909  
 DB 599 DINSNLHQLILSKADNDTMEAVDFEVRSPAWMG-CQKAFQALA-ICAQR--SPRPMTHE 654  
 QY 910 VTRVLGFSM-----LSQOPPAATTSATLAGSCYVDEYANLKTPTSHVNCSSMSASDA 961  
 DB 655 VAVRLVSLLEVPSPKPLVPOKP--MDYAHYLAAGPDV---KIKRTHDN---SSSDG 704  
 QY 962 QLFARFGQVSONS 975  
 DB 705 QWFLRFGVSKNT 718

DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.  
 DT 10-MAY-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 6.  
 DE Putative receptor-like protein kinase (Fragment).  
 GN Name=At2g26330.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OC NCBI\_TaxID=3702;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Totsuki Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A.,  
 RA Narusaka M., Shin-I T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y.,  
 RA Kobayashi M., Toyota A., Sakaki Y., Sakurai T., Iida K., Akiyama K.,  
 RA Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J.,  
 RA Hayashizaki Y., Shinozaki K.;  
 RT "Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs";  
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC -----  
 DR EMBL; AK221866; BAD94220.1; -; mRNA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0000166; F:nucleotide binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00069; Pkinase\_1.  
 DR PROSITE; PS00107; PROTEIN KINASE\_ATP; 1.  
 DR PROSITE; PS00108; PROTEIN KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN KINASE\_ST; 1.  
 KW ATP-binding; Kinase; Nucleotide-binding; Receptor;  
 KW Serine/threonine-protein kinase; Transferase.  
 FT NON TER 1  
 SQ SEQUENCE 441 AA; 49058 MW; 3E269FC5B9CF796 CRC64;

Query Match 45.6%; Score 2299; DB 2; Length 441;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-119;  
 Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 536 GDIPKNNFSRSPDSFTGNPGICGSMWNSPCHDSRRTVRVSISSRAAIIIGAILGVILL 595  
 DB 1 GDIPKNNFSRSPDSFTGNPGICGSMWNSPCHDSRRTVRVSISSRAAIIIGAILGVILL 60  
 QY 596 MVLIAACRPNPPPELDSGLDKPVTYSTPKLVLIHNNMALHVVEDIMRMTENSEKYYIG 655  
 DB 61 MVLIAACRPNPPPELDSGLDKPVTYSTPKLVLIHNNMALHVVEDIMRMTENSEKYYIG 120  
 QY 656 HGASSTYKCVLKNCKPVAIKRLYSHNPOSMAKOFETELMLSSIKRNLVLSQAVSLSHL 715  
 DB 121 HGASSTYKCVLKNCKPVAIKRLYSHNPOSMAKOFETELMLSSIKRNLVLSQAVSLSHL 180  
 QY 716 GSLLFYDYLENGSLMDLHGPYTKKTLDMTRKLIAYGAAGLAVLHHDSPRIIHRDKV 775  
 DB 181 GSLLFYDYLENGSLMDLHGPYTKKTLDMTRKLIAYGAAGLAVLHHDSPRIIHRDKV 240  
 QY 776 SSNILLDKDLRLTPDGLAKSLCVSKSHSTYVMGTIGYIDPEYARTSLRTEKSDVYSY 835  
 DB 241 SSNILLDKDLRLTPDGLAKSLCVSKSHSTYVMGTIGYIDPEYARTSLRTEKSDVYSY 300  
 QY 836 GIVLELTLTRKKAIVDESNLHLIMSKTGNNEVMEMADPDITSTCKDGLGVKKVFOALALL 895  
 DB 301 GIVLELTLTRKKAIVDESNLHLIMSKTGNNEVMEMADPDITSTCKDGLGVKKVFOALALL 360  
 QY 896 CTRKQPNDRPTMQVTRVLGSGFMLSQOPPAATTSATLAGSCYVDEYANLKTPTSHVNCSS 955

Db 361 CTRKQPRDRMTQVTRKVLGSFMLSSEQPPATDTTSATLASSCYVDEVANLKTSPHSVNCSS 420  
QY 956 MSASDAQFLRFGQVISONSE 976  
Db 421 MSASDAQFLRFGQVISONSE 441  
RESULT 12  
049318 ARATH  
ID 049318 ARATH PRELIMINARY; PRT; 1124 AA.  
AC 049318  
DT 01-JUN-1998, integrated into UniProtKB/TrEMBL.  
DT 01-JUN-1998, sequence version 1.  
DT 21-FEB-2006, entry version 33.  
DE Putative receptor-like protein kinase.  
GN OrderedLocustNames=At2g33170;  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC rosids; eusters II; Brassicales; Brassicaceae; Arabidopsie.  
OC NCBI\_TaxID=3702;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Rounsley S.D., Ketchum K.A., Lin X., Crosby M.L., Brandon R.C.,  
RA Sykes S.M., Kaul S., Mason T.M., Kerlavage A.R., Adams M.D.,  
RA Somerville C.R., Venter J.C.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Town C.D., Kaul S.;  
RA Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC distributed under the Creative Commons Attribution-NonCommercial license  
CC -----  
DR EMBL; AC002334; AAC04906.1; -; Genomic\_DNA.  
DR PIR; B84742; B84742.  
DR HSSP; P36897; 11AS.  
DR TAIR; At2g33170; -;  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0000166; F:nucleotide binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0004668; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR001611; LRR.  
DR InterPro; IPR007090; LRR\_Pln.  
DR InterPro; IPR003591; LRR\_Typ.  
DR InterPro; IPR013210; LRR\_2.  
DR InterPro; IPR000719; Ser\_Kinase.  
DR InterPro; IPR008271; Ser\_Thr\_kin\_AS.  
DR InterPro; IPR002290; Ser\_Thr\_kinase.  
DR InterPro; IPR001245; Tyr\_kinase.  
DR Pfam; PF00560; LRR 1; 20.  
DR Pfam; PF00069; Pkinase; 1.  
DR PRINTS; PRO0019; LEUCINRPT.  
DR PRODOM; PD000001; Prot\_kinase; 1.  
DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Leucine-rich repeat; Nucleotide-binding;  
KW Receptor; Repeat; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 1124 Aa; 123723 MW; 53018CD25966777 CRC64;  
Query Match 29.8%; Score 1504.5; DB 2; Length 1124;  
Best Local Similarity 33.8%; Pred. No. 7.5e-75;  
Matches 383; Conservative 172; Mismatches 340; Indels 237; Gaps 29;  
QY 8 VILGFHFCISLVATVTFSE---EGATLLERK-KSPFDVNVNVLVDWTSSSDVCVRGVS 62  
Db 15 MFGVGLFLLTLVW-TSESLSNDGFLLELKNKGFDQSLNRLNNMGIDETP-CNMIGVN 72

QY 63 CENV-----TNNVVALNSLDLDEISPAIGDKLSIDLGRNRSQGLPDEIGDC 115  
Db 73 CSSGSSSSSSSSSLVVTSLDSSNMLSGIVSPSIGGLVNLVYLAVALNATLGDIPREIGNC 132  
QY 116 SSIQNLDLSFNEISGDIPIPSISKQ-----LEQLILKNQ 151  
Db 133 SKLEVMFLNNQGGSIPIVEINKLSQLRSPNLCNNKLSGFLPEIGDLVNLBELVAYTN 192  
QY 152 LIGIPSTL-----SQIP-----NLKILDAONKLSGEIIPR----- 182  
Db 193 LTGFLPRSLGNLNLKLTTPRAGQNDPSGNITPEIGKLNKLGLAQNFTSGELPKXIGML 252  
QY 183 -----LIYNE-----VLQYGLRGNNLVGNISPDLCQLTGLWYFDVRNNS 223  
Db 253 VKLQEVILWQNKPSGFIPIKDIGNLSTLETALVGNLGVPIPEIIGNMKSLKLYIQNG 312  
QY 224 LTGSIPTETGNCAPVLDLSYQLTGEIIPFDGL-QVATLSQNGQSGKIPSYIGLM 282  
Db 313 LNGTIPKEIKGKSKWEIDPSENLISGEIIPVELSKISERLVLFQNKLTGIIIPNELSKL 372  
QY 283 QALAVDLGSLNLSGSIPIPIGLNLTPEKLYHSNKLTSIPELGNMSTLHYLELDNH 342  
Db 373 RNIAKLIDLSNLGTGFIIPGFQNLTSMRQLQFLHNSLGVIPQGLSLYPLWVVDSENG 432  
QY 343 LTGHIPP-----ELGKL 354  
Db 433 LSGKIPPIPCQGSNLILNLGSRNIRPGNIPGVLRCKSLQLRVGNRLTQGFPELTKL 492  
QY 355 TDLFDLVANNDLEGIIPHLSSCTNLNLVHGKFGSGTIPRAFQKLSMITYLNSNN 414  
Db 493 VNLSAITELDQNFSGFLPPEIGTCQKQLRLHLAANQSSNLPELSKLNLYFNVSNS 552  
QY 415 IKGPIVELSRIGNDTLNLNNKINGIIPSSIGDLEHLKNNLSNHTGVVPGDQGNL 474  
Db 553 LGGPISELANCMQLRLSRNSFGISLPEELSGHQELIRLSNRRSGNIPFTIGNL 612  
QY 475 RSIMEI-----DLSNNDISGPIPEELNQLNILLLENN 509  
Db 613 THLTQLQMGNLFSGSIPQGLSLSLQAMNLSTYNDPFGSEIPEELGNLHLMYLSLNN 672  
QY 510 NLTVGN-GLANCLSLTVNLVSHNNLVGDIIPKNNFSRSPSGFIGNPGLCGSMLNS--P 566  
Db 673 HUSGEIPTTFENSLSLGCFNSNNLTGQLPHTQIFQNNLTLSFLGNKLCGGHLSGCP 732  
QY 567 CHD-----SRRTVRSIRALIGIAGVILLMLV-----AACRDP 605  
Db 733 SHSSWPHISSLAGSARRGRITII-----IVSVYGGISLLILAIIVHFLNVPVETAPYVH 788  
QY 606 NPPEFLDGLDKPVYSTPEKVLILHNNMALHYVEDIMRTENLSEKYIIGHGASSTVYKC 665  
Db 789 DKEPFQES-----DIYFVK-----ERFTVKQILEATKGFHDSYIVGRGACGVYKA 836  
QY 666 VLKNCQPAIKRLYS-----HNPQSMKQFETELMSSIGHRLVLSQAVSLSLGS- 717  
Db 837 VMPGKTIIVAKKLESNREGNNNSNNTDNSFRAEITLTCKIRHNRNIVRLYSFCY-HQGSN 895  
QY 718 --LTFDYLENGSLMDLHGTKKKTLMDTDLTKIAYGAAGLAVYHHCSPRIITHRDV 775  
Db 896 SNLLIYVSRSLGELHLHG-GKSHSMDPTPALAGABGLAVYHHCCKRIIHRDK 954  
QY 776 SSNILLDKLEARLNDPGLAKSLCVSKSHSTSYWGTIGYIIPPEYARTSLTEKSDVSY 835  
Db 955 SNNILIDENFEHVGDFGLAKYIDMPLSSVAVAGSYVAINPEYAYIMTKVTEKCDIYSF 1014  
QY 836 GIVLLELLTRRAV---DDESNL---HLLIMSTGNNEVEMADPDITSCKD-LGV 885  
Db 1015 GVVLELLTGKAPVPLEGCGDLATWTRNHI-----RDSLTSEIIDPYLTFKVEDVILNH 1070  
QY 886 VKKVQALCTKQKQPNRPTMHOYT-----RVLGSMISEQPPA 926  
Db 1071 MTTVTKIAVLCTKSSPSDRPTMRVAVLMLIESGERAGKIVISTTCSDDLPPA 1122

```
RESULT 13
Q9LVPO_ARATH PRELIMINARY; PRT; 1102 AA.
ID Q9LVPO_ARATH
AC Q9LVPO_
DT 01-OCT-2000. Integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000. Sequence version 1.
DT 21-FEB-2006. Entry version 27.
DE Receptor-like protein kinase.
GN OrderedLocName=At5g63930;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxId=3702;
OX RN
RX NUCLEOTIDE SEQUENCE.
RP MEDLINE=2018115; PubMed=10718197; DOI=10.1093/dnares/7.1.31;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
RA Tabata S.;
RA "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
RT clones.";
RL DNA Ref.7,31-63(2000).
CC -I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -----
CC Copyrighted under the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDeriv license
CC -----
EMBL: AB019227; BAA96896.1; -; Genomic_DNA.
DR TAIR; At5g63930; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006688; F:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007090; LRR_pln.
DR InterPro; IPR003591; LRR_typ.
DR InterPro; IPR013210; LRRNT_2.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00560; LRR_1; 16.
DR Pfam; PF00069; Kinase; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR ProDom; PD000001; Prot_Kinase; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Leucine-rich repeat; Nucleotide-binding;
KW Receptor; Repeat; Serine/threonine-protein kinase; Transferase.
SQ
SEQUENCE 1102 AA, 120477 MW, 6CDF852ADD3D54D CRC64;

Query Match 29.5%; Score 1489; DB 2; Length 1102;
Best Local Similarity 35.0%; Pred. No. 5.3e-74;
Matches 397; Conservative 168; Mismatches 350; Indels 218; Gaps 32;

QY 3 LRPDIYLGLPFLSLVATYTSF-----RCATLLLETKKSFKQVNVVLYWTTSPSSDYC 56
DB 1 MVEKMKLAVFFSLILLILISITGTINLEGQYLLEKSKFVAKONLRLWNSNDSP-C 59
QY 57 VNRGVCENVTFN--VVALNLSDLNLDEGISPAIGDKLSLISIDLGNRLSGQIPDEIGD 114
DB 60 GMTGWCSNVSSDPYLSNLSSMWLSGKLSPIGGLVHLKQDLSTNGNSGKIPKEIGN 119
QY 115 CSSLQNLDSFNLSDGIPFSISKLKQLEQLIKNNQLGPIP-----STISQ----- 162
DB 120 CSSLEIKLNKNQFDEIPVEIKGLVLENIILYNNRISGSLPVEIGNLISLQLVYNSN 179
QY 163 -----IPNK-----IIDLQNKLSGSEIPR----- 182
DB 180 NISGQLPRSTGNLKRLLTSFRAGQNMISGSLPSEIGCESLWMLGALQNMQLSGELPKYIGM 239
```

```
QY 183 -----LIYW-NEV-----LQYGLRGNNLVGNISPDLCOUTGLMYPDVRNN 222
DB 240 LKLSQVILMEBNSFGFIPREISNCTSLFTIALYKQLVGPIPKELGDLQSLFFLYLYEN 299
QY 223 SLTGSIPETIGNCTAQAQVLDLSTNQLTGEIPPDIGLQ--VAITSLQGNQSGKIPVIGL 281
DB 300 GINGTIPREIGNSVYIEIDFSENALTGEIPLEIGNIEGLELYLPEENQLTGTPVPELST 359
QY 282 MQLAVLDSGNLSSGIPPIIGNLFTFEKLYHSNKLGTSPPELGNNSKLHYLELNDN 341
DB 360 LKNLSLDSINALTPIPLGFGYLGFLMLQLFQNSLSGTIPPKLGMVSDLVLDMSDN 419
QY 342 HLTHGIPPELGLTDLFDINVANNDLEGPDPHLSSC----- 378
DB 420 HSGRIPSYLCHSNMIIINLGTNNLSGNIPTGITTCKTLVQLRLARNLVGRFPENLCK 479
QY 379 -TYNLSLNVHGNKFGSGTIR-----AFQKLE-----SMTYNLSSN 413
DB 480 QVNVTAIEIGQNRFRGSIPEVGNCSALQRLQADNGFTGELPREIGMLSQGLTNISSN 539
QY 414 NIKGPIPEVL-----SRIGN--LDTLDSNNKINGIIPESLGD 449
DB 540 KLTVGVSEIPFNCKMLQRLDMCCNNSGTLPSBEVGLYQLELLKLSNNLSGTPVALGN 599
QY 450 LERHLKMNLSRNHITGVVDFEGNLSRI-MEIDLNNDISGPIPEELNQLQNIILRLN 508
DB 600 LSRTELQNGNLFNGSIPRELGLTGLOALNLSYKLTGEIPPELSVMLEFLLNN 659
QY 509 NNLITGNV-GSLNCLSLTYLVANSHNNLVGDIPKNNNFSFSDPSFGNGGLGSMWN--- 564
DB 660 NNLISGIPSSFANLSLLQYNFSYNSLTGPILRLNISM--SSFTGNBGLCGPPLNQC 716
QY 565 --SPCHDSRRYRVSISR-----AIGIAIGLVILMLVI-----AACRPNP 607
DB 717 QTOPFAPSGSTGKPGSKMSKIIATIAVIGVSLMLILYVLMKRRPVTYASSAQDQ 776
QY 608 PPELDGSLDKPVYVSTPKLVILHMNALHYEDIMKMTENLSEKYLIGHGASVYKCVL 667
DB 777 PS--EWSLSD--IYFPK-----EGFTPOLVATQNPDES FVVGAGACGTIVKAVL 823
QY 668 KNCKPVALIKLVY-----HNPSMKQFETELMLSSIKRNLVSLQAYSLSHLS--LLEY 721
DB 824 PACTYLAIVKKLASNHGKNNVNDNSFRAEILTGINIRRNIVKLGHF-CNQGSLVLLY 882
QY 722 DYLENGSLMDLHGPKKKKTLMDRTLKTIAYGAQGLAVLHDCSPRIIHRDVKSSNILL 781
DB 883 EYMPKSLGEIILHDPK--CNLDMSKRFKIALGAAGLALVHDDCKRIFHRDIKSNMILL 940
QY 782 DKDLERLTDFGIAKSLCVSKSHSTTYVMGTIGYIDPEYARTSRLTEKSDVYSYGVILLE 841
DB 941 DKDFEAVHVDGFLGAKVIDMPSKMSGALIGSYCIAPETAYTMKVTKEKSDIYSGVLL 1000
QY 842 LLTR--KAVDDESLLHLHLSKTNNEVMEADPDITSTCKDLGVK--KYFDALL 895
DB 1001 LILGKAPVQPIIDGGGVVWVWSYI--RDALSSGVLDARLTLEDERIVSHMTLVLLALL 1059
QY 896 CTGRQPNDRPTMNVQVTRVLSFNLSEQPPAATPTTSATLAGSCVVDYKALIKTP 948
DB 1060 CTSVSVAPRPMQVVLMLIBESRSEGEQEHDT-----ELTQTTP 1102

RESULT 14
Q6Y777_ORYSA PRELIMINARY; PRT; 1109 AA.
ID Q6Y777_ORYSA
AC Q6Y777_
DT 05-JUL-2004. Integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004. Sequence version 1.
DT 07-MAR-2006. Entry version 14.
DE Putative LRR receptor-like kinase.
DE Name=BJ364A02.24;
OS Oryza sativa (Japanese cultivar-group); Embryophyta; Tracheophyta;
OC Eukaryota; Viridiplantae; Streptophyta;
```

OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC	Euphorbiaceae; Oryzae; Oryza.
OX	NCBI_TaxID=39947;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RA	Sasaki T., Matsunoto T., Katayose Y.;
RT	"Oryza sativa nippobare(GA3) genomic DNA, chromosome 7, BAC
RL	clone:B1364A02."
CC	Submitted (JAN-2003) to the EMBL/genbank/DDBJ databases.
CC	- I - CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC	Distributed under the Creative Commons Attribution-NoDerivs license
CC	-----
DR	EMBL; AP006163; BAC84715.1; -, Genomic_DNA.
DR	Giramele; G6Y777; -.
DR	GO; GO:0005524; F:ATP binding; IEA.
DR	GO; GO:0000166; F:nucleotide binding; IEA.
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR	GO; GO:0004872; F:receptor activity; IEA.
DR	GO; GO:0006740; F:transferase activity; IEA.
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR	InterPro; IPRO07090; LRR pin.
DR	InterPro; IPRO03591; LRR typ.
DR	InterPro; IPRO13210; LRRT_2.
DR	InterPro; IPRO0719; Prot_Kinase.
DR	InterPro; IPRO02871; Ser thr_pkin AS.
DR	InterPro; IPRO02290; Ser thr_kinase.
DR	InterPro; IPRO01245; Tyr_pkinase.
DR	Pfam; PF00560; LRR_1; 21.
DR	Pfam; PF08263; LRRT_2; 1.
DR	Pfam; PF00063; PKinase; 1.
DR	PRINTS; PRO0019; LEURICHRPT.
DR	PRODOM; PD000001; Prot_kinase; 1.
DR	PROSITE; PS00011; PROTEIN KINASE DOM; 1.
DR	PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW	ATP-binding; Kinase; leucine-rich repeat; Nucleotide-binding;
KW	Receptor; Repeat; Serine/threonine-protein kinase; Transferase.
SQ	SEQUENCE 1109 AA; 119195 MW; 13853B7045129011 CRC64;
Query Match	29.4%; Score 1480.5; DB 2; Length 1109;
Best Local Similarity	32.9%; Pred. No. 1.6e-73;
Matches 366; Conservative 187; Mismatches 374; Indels 187; Gaps 22;	
Oy	7 IVLGFLFCLSLVATVISSEG---ATLEIKKSKFDVNNAVLYDWTSSPS--DYCYWR 59
Dd	:::::     :::     :::     :::     :::     :::     :::     :::     :::
Oy	8 VLLAAVFFAFAAAAAAASSSAVAALMEFKTXLDVDGRLLSWDAAGSGGGCGPCGP 67
Oy	GVSCENVTFNVVALNSDLNLDEGISPAIGDKLSLTDLAGNRLLSGOIPPEIGDCSSLQ 119
Dd	:::     :::     :::     :::     :::     :::     :::     :::     :::
Oy	60 GVSCENVTFNVVALNSDLNLDEGISPAIGDKLSLTDLAGNRLLSGOIPPEIGDCSSLQ 119
Dd	68 GIAC-SAAEMEYAVTGLHGLNHGELSLAAVCALPRIALVNTSKNALAGLPGLAACRYLE 126
Oy	120 NLDSLFNE-----LSGDIPFSISKUKOLEQLILKNNOIGLP 155
Oy	VLDSTNSIHGGIPEPSLCSPISLRQLFISENPFSGEIPAIGNLTALAELEIYSNNLTGG 186
Dd	127 VLDSTNSIHGGIPEPSLCSPISLRQLFISENPFSGEIPAIGNLTALAELEIYSNNLTGG 186
Oy	156 IPSLTLSQIPNLKIIDLAKNQKLSGEIPRLIYNNEVLQYGLRGNNLVGNISPDLCOITGM 215
Dd	187 IPTTIAALQRRIIRAGLANDLSGPPIVEISAASLAIVGLAQNMNLAGEIPELTSKLKULT 246
Oy	216 YEDVRNNSLTGSIPETIGCTCAFOVLDSYNOLTGEPIDIGFL-QVATTLSLOGNOISGK 274
Dd	247 TLIIQNARLSEIPEPEDDISLEMLANDNAFTGCVGREIGALPSLKLYTYRNOLDGT 306
Oy	275 IPSYIGLMQALAVLDLSGNLLSGSIPIPLIGNLTFTEKLYLHSNKLTGSIPELG----- 328
Dd	307 IPRELGDQSAYEIDLENKLTGVIPEGELGRIPTLRLLYFPENRLOGSIPELGELTVIR 366
Oy	329 -----MSKHTYLELNDMHLGHIPPELGKLTDELDDLVANNDLEGF 370
Dd	367 RIDUSINNLTGITPMEFQNIPTDLELQIFDNQHIVIPPMIGAGSNISVLDLSDRLTGS 426

OY	371	IPDH-----	-----ISSCTNIN	382
Db	427	IIPHCKFOKILFSLGSNRLLIGNI	PBGVACRTLTQLOLGNNMLTGLSPVELLSLRRLS	486
OY	383	SLNVHGNKFSGSTIRAFQKLESMYYL-----	-----NLSSNNIKGP	418
Db	487	SLDMRRNFSCPIRPEELIGKRISIRLLSENYPFGQLP	PGIGNITKLVAFISSNQLTGP	546
OY	419	IPVELSRIGNLDTLDSLNKKINGIIIPSSGLDLEHLXMMNL	SRRNHITGVVPDGFGNLSIM	478
Db	547	IPRELACTYKQRDLDEKNSLTGTVIP	DELGLTVNLBQLKSDSNLNGTVPSSFGLSRILT	606
OY	479	EIDUSNDDISGRPEEBEENQL-----	ONIT-----LIRLENNNTG	513
Db	607	ELQMGGRSLRGQLPVELEGOLITALOIALNVSYNMKSGEIPTOLGNI	LHMLEFLYLNNNELEG	666
OY	514	NV-GSLANCLSLTYLVANSHNVLVDGDIKNNNFSP	PDSPFIENGPLGC-----SWINSR	566
Db	667	EVPSSFGELSLELCNLSYNNAALPPLEPTTL	FQMDSNSNFIGNNGLGCIKSKCSGLSGS	726
OY	567	CHDSRRTRY-RVSISRRAALIGIA--	IGSLVILLMVLVIACRPHPNPFPFLDGSLDKPYTYS	622
Db	727	AYAREEAAYOKKRLRREKITSISIVIAFVSLVIDAVCMSSIKSKI	IDVLVSNERRKTGFS	786
OY	623	TPKLVIIHMNALHV-YEDIRMTENLSEKKYIIHGASSTYVKCVL	KXCKPVAIKRLYSH	681
Db	787	GP-----HYFLKEKITFOELMKVTDSFESES	AVIGRGACGVTKAIMPDRVAVKUKCQ	841
OY	682	NPOSM-KOPETELEMLSITKHRYLVLOAVSLSHLSGL	LFYDVLBNGLMDLHGPTRK	739
Db	842	GEGSNVDRSFPAELITTLTGNAVHRNIVKL	YGCFSQDCNCLLIYEMANGSLGELLHSKD	901
OY	740	KTLMDTRLKTIAYAAOGLAWLHHDCSPRIIHDPVKSNNILL	DXLEBARLTFGSIASLTC	799
Db	902	CLMDMDRYRALGAAGAKLYHSDCPKYIHDRIKSNNILL	DEMBAHDYFGLATLID	961
OY	800	VSKHSTSYVWGTTGYIDPEYARTSLRTEKSDVSYGIVILLELIT	TRRKAVD-----DES	853
Db	962	ISNRTWSAIAGSXYIAPEYAFPMKYTEKCIDIYF	GVLLLELATVGSPIOPLEQGDDLV	1021
OY	854	NL-HHLMSTKGNNVENWEMADPDTITSCOKUGVKYIFOLALL	CTKQPDPDRPFMHQVTR	912
Db	1022	NLYVRMTNSTSTNSEIPD-SRLMNLSR-RLYEELSLVLKIAL	FACTSSPSIDRPSMRREVIS	1079
OY	913	VLGSMFLSEOPPATDTSATLAGSCYDEVANTLK	946	
Db	1080	-----MLMDARASAYDSFSPSAASAEPIDESSLK	1108	
 RESULT 15 O6LJ15_SOLVE PRELIMINARY; PRT; 1250 AA.				
ID	O6LJ15_SOLVE			
AC	O6LJ15;			
DT	05-JUL-2004,	integrated into UniProtKB/TREMBL.		
DT	21-FEB-2006,	entry version 15.		
DE	Putative receptor-like protein kinase.			
GN	ORName=RBEC407.5;			
OS	Solanan demissum (Wild potato).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicotyledons; oc asterids; lamids; Solanales; Solanaceae; Solanum.			
CC	NCBI_TaxId=50514;			
RN	(1)			
RP	NUCLEOTIDE SEQUENCE.			
RA	Bueli R., Liu J., Zaborsky J., Tallon L., Wirtz U., Wei F., Kuang H., Zhang P., Wang X., Marano M.R., Baker B.; Submitted (JUN-2004) to the EMBL/Bank/JDB databases. -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein. -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.			
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms distributed under the Creative Commons Attribution-NoDerivs License			



CC EMBL: AC149487; AAT040539.1; -; Genomic DNA.  
DR GO: GO:0005524; F:ATP binding; IEA.  
DR GO: GO:0000166; F:nucleotide binding; IEA.  
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO: GO:0004872; F:receptor activity; IEA.  
DR GO: GO:0016740; F:transferase activity; IEA.  
DR GO: GO:0006468; F:protein amino acid phosphorylation; IEA.  
DR InterPro: IPR001611; LRR.  
DR InterPro: IPR007090; LRR\_pln.  
DR InterPro: IPR003591; LRR\_ryp.  
DR InterPro: IPR013210; LRRNT\_2.  
DR InterPro: IPR00719; Prot\_kinase.  
DR InterPro: IPR008271; Ser\_thr\_pkinase.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR InterPro: IPR01245; Tyr\_pkinase.  
DR Pfam: PF00560; LRR\_1; 29.  
DR Pfam: PF00069; Pkinase; 1.  
DR PRINTS: PR00019; LEURICHRPT.  
DR PRODOM: PD000001; Prot\_kinase; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; UNKNOWN\_1.  
DR PROSITE: PS00101; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
DR ATP-binding; Kinase; leucine-rich repeat; Nucleotide-binding;  
KW Receptor; Repeat; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 1250 AA; 137493 MW; D958F1698B8C775 CRC64;

Query Match 29.0%; Score 1464; DB 2; Length 1250;  
Best Local Similarity 31.4%; Pred. No. 1.5e-72;  
Matches 394; Conservative 165; Mismatches 330; Indels 366; Gaps 28;

QY 1 MALFRDVLVGLFPCSLVAVTVTSE-EGATLLLEIKKGF-KDVNNVLYDMTTPSSDYCW 58  
Db 1 MSFENKLLLVFVTVLVGLVPSSETFEVLLEIKKSFLLDDPEVLSNM-SDKNQNCOW 59  
QY 59 RGVSCENVFNVAALNSDLNDEISPAIGDLKSLISIDLRGRNSG----- 106  
Db 60 SGVSCEDDTLVKVRNLSDCSISGISGFLHDLHLDSNLGPIPTLSNLSTL 119  
QY 107 ----- 106  
Db 120 QSLLYSNQLTGPIPNELGKLLKQLVLRIGDNVGLTGPLSSIGDLENLVTGLASCSLS 179  
QY 107 ----- 118  
Db 180 GMTPELGGKGRLENKMLQENQLENEIPSEIGNCSSLVAVSAVANNLNGSIPBELSLMK 239  
QY 119 ----- 129  
Db 240 LQVNNLANNSISQIPTQLGEMIELQVNLNLGNQLEGSIPMSLAKLSNVNRLDLSGNRLT 299  
QY 130 GDI PFSSISKUOLEQLLNKNQLGPIPSLT-----SOIP----- 164  
Db 300 GEIPGEFGNNDQLQVNLVLTSSNGGIPKTYCSSNGNSSLEHMMUSENQSGEIPVELRE 359  
QY 165 --NLKIIDLAQNKLSGEIPRLIYNNVLYQLGLRGNLVGNISPDQLTGLWYFDVRNN 222  
Db 360 CIGLKQDLNNTLNGSIPVELYELVELTDLNNTLVGVSPLIANLTNLQTLALSHN 419  
QY 223 SLTGSIFE-----TIGCTAFQVLDLSTNQLTGEIPFDIGF 258  
Db 420 SLHGNIKEIGMVENLEILFLYENQFSGELPMEIGNCSRLQIMIDFYGNAFSGRIPIITIG 479  
QY 259 L-QVATISLQGNQSGKIPSVIGLMQALAVLDLSGNLSSGIPPLINLTFTKLYLSN 317  
Db 480 LKEINFTDFRONDSSGEIPASVGNCHQKIIDLADNRSSGVPAFTGYLRALBQMLLYNN 539  
QY 318 KLTSGISPELGNNMSK----- 332  
Db 540 SLBGNLPDELINLSNLRINFSHNKNGSIASLCSSTSPISFDVTNNAFDHEVPRLGYS 599  
QY 333 --LHYLELDNHLTGHIPEELGKLTDLFDLVANNNDLEGPIPDHLSGCTNINSLNVHGNK 390

Db 600 PFLERLRIGNNRPTGEIPWTLGLIRELSLDDLSGNELTGLIIPPQLSLCRKLTDLNANNR 659  
QY 391 FSGTIPRAPOKLESMTYLNLSNNIKGPIPELRSIGNDPTLDLSNNKINGIIPSSIGDI 450  
Db 660 LYSGIIPWGLNLBGLBELKLSKFKSGPLPRELPFNSKSLVLSEDSNGTLPLEIGEL 719  
QY 451 EHLKKNLSRNHTTGVVPGDFGLRSIMEIDLSNNDISGPIPELNQLONI-ILRLENN 509  
Db 720 KSLNIINFDRNQSLGPIPSITIGLSKLYILRLSGNSLTGEIPSELQQLKNLQSLDLSFN 779  
QY 510 NLGNV-GLSLANLSTLVANVNNLVGDI PK-----NN-----NFSR 546  
Db 780 NISGQIPPSVGLTTLKETLDSNNHLTGEVPPQVGEMSSIGKLNLSYNNLQGLDKQYAH 839  
QY 547 FSPDSFIQNPGLGSMWLNPSCHDSRRTVR---VSISRAITLGAIGLVLLWVLIAA-- 601  
Db 840 WPADEFQGNRPLCGSPLON-CEVSKSNKSGSLNSTVVIISYSTVAIILMLGAALE 898  
QY 602 -----CRPHNPPFLDGLDKPVYIYTPKLVILHNNMALHYEDI 641  
Db 899 FKQREAFRSEVNSAYSSSSSGQKKPLFASVAKRDIR-----WDDI 941  
QY 642 MNTTENISEKTIIGHGASSTVYKCVLKNCKPVAIKELYSNPSQM-KQFETELEMSSIK 700  
Db 942 MEATNNLSNDFIIGSGSGSTVYAEFLIGEIVAKRIPSKDILLDSFARFKITLMRIR 1001  
QY 701 HRNLVSLQAY-SLSHLGS-LIFDYDLENGSLMDLH---GPTKKXT-LDMDTRLKIAYG 753  
Db 1002 HRLLVRLGLGVCNNSGGSNVLIEYEWNGSVWMLHKOPANNKRTKCLDMEARLKIAVG 1061  
QY 754 AAGQVLAHHDCSPRIIHRDVKSSNILLDKDLFARLTDGIAKSLCVS---KSHSTVY 809  
Db 1062 LAQGVETLHHDVCPKIHRDIKSSNILLDSNMEAHLDGFLAKAVADHNVNSYNTESNLWF 1121  
QY 810 MGTIGYIDPEYATSRKTESDVIYSYGIYVLELLTRKAYD-----DESNLHLI-----M 860  
Db 1122 AGSFGYIAPAYASSKATEKSDVYSWGIYVLMELVTGMPTDGSFGEDIDVNRWIESCIEM 1181  
QY 861 SKTGNNVEMMADPDITSTC-KDLGVKVFQALALCTKQPNDRPTMHQVTRVL 914  
Db 1182 SRE-----ELIDPVLKPLIPNESAAQVLEIALBCTKTAAPARPSRRVCOLL 1230

Search completed: September 2, 2006, 06:56:06  
Job time : 322 secs



GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 3, 2006, 18:19:15 ; Search time 381 Seconds  
(without alignments)  
13745.998 Million cell updates/sec

Title: US-10-519-135-1

Perfect score: 3176  
Sequence: 1 gttctcttcacatgagact.....actctctacatgcttctgc 3176

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 2281053 seqs, 824500224 residues

Total number of hits satisfying chosen parameters: 4562106

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications\_NA.New.\*  
1: /EMC\_Celerra\_SIDS3/prodata/1/pubpna/US09\_NEW\_PUB.seq.\*  
2: /EMC\_Celerra\_SIDS3/prodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
3: /EMC\_Celerra\_SIDS3/prodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
4: /EMC\_Celerra\_SIDS3/prodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
5: /EMC\_Celerra\_SIDS3/prodata/1/pubpna/PCT\_NEW\_PUB.seq.\*  
6: /EMC\_Celerra\_SIDS3/prodata/1/pubpna/US10\_NEW\_PUB.seq.\*  
7: /EMC\_Celerra\_SIDS3/prodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
8: /EMC\_Celerra\_SIDS3/prodata/1/pubpna/US11\_NEW\_PUB.seq2.\*  
9: /EMC\_Celerra\_SIDS3/prodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
10: /EMC\_Celerra\_SIDS3/prodata/1/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3176	100.0	3176	6	US-10-519-135-1
2	3176	100.0	3191	9	US-11-056-355B-46415
3	3176	100.0	3191	9	US-11-056-355B-48174
4	1691.4	53.3	3705	8	US-11-216-545-1706
5	1343.8	42.3	3673	6	US-10-449-902-23703
6	1117.6	35.2	2901	6	US-10-519-135-9
7	1074.6	33.8	2751	6	US-10-519-135-7
8	1050.8	33.1	2766	6	US-10-519-135-5
9	1035.2	32.6	3000	6	US-10-519-135-3
10	1022.2	32.2	2614	9	US-11-218-905-13435
11	935.2	29.4	1712	6	US-10-953-349-22716
12	901.2	28.4	2315	6	US-10-519-135-44
13	714.2	22.5	1714	9	US-11-218-305-14406
14	552.4	17.4	1688	6	US-10-449-902-2426
15	530.8	16.7	1273	6	US-10-519-135-21
16	488.6	15.4	1346	6	US-10-519-135-19
17	484.6	15.3	1514	9	US-11-218-305-421
18	480.6	15.1	1394	9	US-11-056-355B-4048
19	467.8	14.7	1881	6	US-10-449-902-6920
20	413.8	13.0	1305	6	US-10-953-349-13017
21	363.2	11.4	1116	9	US-11-218-305-422
22	306.8	9.7	683	6	US-10-519-135-36
23	306.8	9.7	683	6	US-10-519-135-43

24	299.2	9.4	636	6	US-10-519-135-11	Sequence 11, Appl
25	269.8	8.5	556	6	US-10-519-135-42	Sequence 42, Appl
26	265.8	8.4	558	6	US-10-519-135-40	Sequence 40, Appl
27	263.8	8.3	549	6	US-10-519-135-16	Sequence 16, Appl
28	260.4	8.2	719	6	US-10-519-135-18	Sequence 18, Appl
29	258.6	8.1	764	8	US-11-216-545-5919	Sequence 5919, Appl
30	248.4	7.8	3375	7	US-11-299-286-667	Sequence 667, Appl
31	237.6	7.5	634	6	US-10-519-135-39	Sequence 39, Appl
32	224	7.1	658	9	US-11-056-355B-14722	Sequence 14722, A
33	222	7.0	458	6	US-10-519-135-28	Sequence 28, Appl
34	216.6	6.8	3759	9	US-11-056-355B-44894	Sequence 44894, A
35	215.8	6.8	3141	9	US-11-056-355B-79288	Sequence 79288, A
36	209.6	6.6	429	6	US-10-519-135-41	Sequence 41, Appl
37	207.6	6.5	610	6	US-10-519-135-37	Sequence 37, Appl
38	204.6	6.4	3633	9	US-11-056-355B-88227	Sequence 88227, A
39	204.6	6.4	3633	9	US-11-056-355B-91983	Sequence 91983, A
40	203.2	6.4	3725	6	US-10-953-349-9197	Sequence 9197, Ap
41	200	6.3	1704	9	US-11-056-355B-70586	Sequence 70586, A
42	199.8	6.3	3647	9	US-11-056-355B-46296	Sequence 46296, A
43	192	6.0	3658	9	US-11-174-307B-1667	Sequence 1667, Ap
44	192	6.0	3558	9	US-11-056-355B-83028	Sequence 83028, A
45	191.8	6.0	3754	6	US-10-953-349-4748	Sequence 4748, Ap

# ALIGNMENTS

```
RESULT 1
US-10-519-135-1
; Sequence 1, Application US/10519135
; Publication No. US20060137041A1
; GENERAL INFORMATION:
; APPLICANT: The Australian National University
; TITLE OF INVENTION: METHOD OF PRODUCING PLANTS HAVING ENHANCED TRANSPIRATION EFFICIENT
; FILE REFERENCE: 94948/MEO
; CURRENT APPLICATION NUMBER: US/10/519,135
; PRIOR FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: AU P33339
; PRIOR FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 3176
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana ERECTA allele
US-10-519-135-1

Query Match      100.0%; Score 3176; DB 6; Length 3176;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTTCTTCTTCATGAGACTGTGAAGCTTTAAAGTATCTTAAAGCGAGTGTGTTTA 60
      |||
Db      1 GTTCTTCTTCATGAGACTGTGAAGCTTTAAAGTATCTTAAAGCGAGTGTGTTTA 60

QY      61 AGACTGTGTGAGAAATGCTCTGTTAGACATATGTTCTTGGGTTTCTCTTCG 120
      |||
Db      61 AGACTGTGTGAGAAATGCTCTGTTAGACATATGTTCTTGGGTTTCTCTTCG 120

QY      121 CTGACCTTAGTAGCTACTGTGCTCAAGAGGAGGAGCAAGCTTCTGAGATTAGAA 180
      |||
Db      121 CTGACCTTAGTAGCTACTGTGCTCAAGAGGAGGAGCAAGCTTCTGAGATTAGAA 180

QY      181 GTTCATTCAAGATGTGAACAATGTTCTTATGACTGACCACTTCTTGGATT 240
      |||
Db      181 GTTCATTCAAGATGTGAACAATGTTCTTATGACTGACCACTTCTTGGATT 240

QY      241 TTGTGCTGAGAGGCTGCTCTTGAAGATGACCTTCANGTGCTTAAATT 300
      |||
Db      241 TTGTGCTGAGAGGCTGCTCTTGAAGATGACCTTCANGTGCTTAAATT 300

QY      301 GTTCAGATTGAATCTTGATGAGAAATCTCACCTGCTATGAGATCTCAAGATCTCTT 360
      |||
```

```
|||||
Db 301 GTGAGATTGAATCTTGATGAGAAATCTCACCTGCTATTGSAAGATCTCAAGAGTCTCTT 360
Qy 361 GTCAATTGATCTGGAGAGTAATGCGTGTGCGACAATCCCTGATGAGATGGTGACTG 420
Db 361 GTCAATTGATCTGGAGAGTAATGCGTGTGCGACAATCCCTGATGAGATGGTGACTG 420
Qy 421 TTCTTCTTTGCAAACTTAGACTTATCTTCAATGAATTAAGTGTGACATACCGTTTTC 480
Db 421 TTCTTCTTTGCAAACTTAGACTTATCTTCAATGAATTAAGTGTGACATACCGTTTTC 480
Qy 481 GATTTCGAAGTTGAGCACTTGAGCAGCTGATTTCTGAAGATTAACCAATTGATAGAAC 540
Db 481 GATTTCGAAGTTGAGCACTTGAGCAGCTGATTTCTGAAGATTAACCAATTGATAGAAC 540
Qy 541 GATCCCTTCAACCTTTCACAGATTTCCAAACCTGAAATTCCTGACTGGACAGAAATTA 600
Db 541 GATCCCTTCAACCTTTCACAGATTTCCAAACCTGAAATTCCTGACTGGACAGAAATTA 600
Qy 601 ACTCAGTGTGAGATACCAAGACTTATTTA CTGGAAATGAAGTTCTTGAGTACTTGGGTT 660
Db 601 ACTCAGTGTGAGATACCAAGACTTATTTA CTGGAAATGAAGTTCTTGAGTACTTGGGTT 660
Qy 661 GCGAGAAACAACCTTAGTCGGTAA CATTTCCTCAGATTTGTGTCACTGAGTCTTTTG 720
Db 661 GCGAGAAACAACCTTAGTCGGTAA CATTTCCTCAGATTTGTGTCACTGAGTCTTTTG 720
Qy 721 GTATTTTGAGTAGAAGAAACAACAGTTGACTGTGATATACCTGAGACGATAGGAAATTG 780
Db 721 GTATTTTGAGTAGAAGAAACAACAGTTGACTGTGATATACCTGAGACGATAGGAAATTG 780
Qy 781 CACTGCTTCCAGGTTTGGACTTGTCTACAACTCACTAACTGATGAGATCCCTTTTGA 840
Db 781 CACTGCTTCCAGGTTTGGACTTGTCTACAACTCACTAACTGATGAGATCCCTTTTGA 840
Qy 841 CATGCGCTTCCAGGTTTGGACTTGTCTACAACTCACTAACTGATGAGATCCCTTTTGA 900
Db 841 CATGCGCTTCCAGGTTTGGACTTGTCTACAACTCACTAACTGATGAGATCCCTTTTGA 900
Qy 901 TTCATCAGTAGTGGTGTCTATGCAAGCCCTTGAGCTTGAATTAAGTGGCACTTGT 960
Db 901 TTCATCAGTAGTGGTGTCTATGCAAGCCCTTGAGCTTGAATTAAGTGGCACTTGT 960
Qy 961 GAGTGAATCTATTCCTCGAATTCCTCGGAAATCTTACTTTCACCGAGAAATTTGATTTGA 1020
Db 961 GAGTGAATCTATTCCTCGAATTCCTCGGAAATCTTACTTTCACCGAGAAATTTGATTTGA 1020
Qy 1021 CAGTAAACAAGCTGACTGGTTCAAATTCACCTGAGACTTGGAAACATGTCAAAATCCCAATTA 1080
Db 1021 CAGTAAACAAGCTGACTGGTTCAAATTCACCTGAGACTTGGAAACATGTCAAAATCCCAATTA 1080
Qy 1081 CTTGGAACTCAATGATATCATCTCAGGGTCAATATCCACACAGAGCTTGGAAAGCTTAC 1140
Db 1081 CTTGGAACTCAATGATATCATCTCAGGGTCAATATCCACACAGAGCTTGGAAAGCTTAC 1140
Qy 1141 TGACTTGTGATCTGAATGTGGCCAA CAATGATCTGGAAGGACCTTATCTGATCATCT 1200
Db 1141 TGACTTGTGATCTGAATGTGGCCAA CAATGATCTGGAAGGACCTTATCTGATCATCT 1200
Qy 1201 GAGCTTTTGCAAAATCTTAAACAGCTTAAATGTTCAATGGAAACAAGTTAAGTGCACTAT 1260
Db 1201 GAGCTTTTGCAAAATCTTAAACAGCTTAAATGTTCAATGGAAACAAGTTAAGTGCACTAT 1260
Qy 1261 ACCCGGAGCTTTCAAAGCTAGAAAGATGATGACTTAACTGATGTCGAGCAACATAT 1320
Db 1261 ACCCGGAGCTTTCAAAGCTAGAAAGATGATGACTTAACTGATGTCGAGCAACATAT 1320
Qy 1321 CAAAGGTCATCCCGGTTGAGCTATCTGATCGTAACTTAGATACATTTGATCTTTTC 1380
Db 1321 CAAAGGTCATCCCGGTTGAGCTATCTGATCGTAACTTAGATACATTTGATCTTTTC 1380
Qy 1381 CAAACAAGATTAATGGAATCATTTCTTCTTCCCTTGGTGAATTTGAGCATCTTTCAA 1440
Db 1381 CAAACAAGATTAATGGAATCATTTCTTCTTCCCTTGGTGAATTTGAGCATCTTTCAA 1440

|||||
Db 1381 CAAACAAGATTAATGGAATCATTTCTTCTTCCCTTGGTGAATTTGAGCATCTTTCAA 1440
Qy 1441 GATGAACCTTAGTAGAATCATATTAATGAGTTTCCAGGAGCACTTTGGAATCATAG 1500
Db 1441 GATGAACCTTAGTAGAATCATATTAATGAGTTTCCAGGAGCACTTTGGAATCATAG 1500
Qy 1501 AAGCATCATGAAATAGATCTTTCAAATTAATGATATCTGAGCCCAATTCAGAGAGCT 1560
Db 1501 AAGCATCATGAAATAGATCTTTCAAATTAATGATATCTGAGCCCAATTCAGAGAGCT 1560
Qy 1561 TAACCAATTAACAACAATAATTTTGGTGAACCTGGAAGAAATTAATACCTGATATGT 1620
Db 1561 TAACCAATTAACAACAATAATTTTGGTGAACCTGGAAGAAATTAATACCTGATATGT 1620
Qy 1621 TGGTTCAATAGCCAACTGTCTCAGTCTCACTGATTAATGATATTCATTAACAACCTCGT 1680
Db 1621 TGGTTCAATAGCCAACTGTCTCAGTCTCACTGATTAATGATATTCATTAACAACCTCGT 1680
Qy 1681 AGGTGATATCCCTTAAGAACAAATTAATTTTCAAGATTTTCAACAGAGCTTCATTGGCAA 1740
Db 1681 AGGTGATATCCCTTAAGAACAAATTAATTTTCAAGATTTTCAACAGAGCTTCATTGGCAA 1740
Qy 1741 TCCGTGCTTTGGGAGTGTGGCTAAACCTCAAGCTGATATTCCTGAGAACTGTAGC 1800
Db 1741 TCCGTGCTTTGGGAGTGTGGCTAAACCTCAAGCTGATATTCCTGAGAACTGTAGC 1800
Qy 1801 AGTGTCAATCTTAGAGCACTATTCCTTGGATAGCTATTTGGGGGACTTGTGATCCCTTC 1860
Db 1801 AGTGTCAATCTTAGAGCACTATTCCTTGGATAGCTATTTGGGGGACTTGTGATCCCTTC 1860
Qy 1861 CATGCTTAAATAGCAGCTTGGCGACCGCAATATCTCTCTCTTTTCTTGATGATCACT 1920
Db 1861 CATGCTTAAATAGCAGCTTGGCGACCGCAATATCTCTCTCTTTTCTTGATGATCACT 1920
Qy 1921 TGACAAACCGATACCTTATTCGACACCGAGCTGTCACTTCCTTCAATGAAACATGGCACT 1980
Db 1921 TGACAAACCGATACCTTATTCGACACCGAGCTGTCACTTCCTTCAATGAAACATGGCACT 1980
Qy 1981 CCAAGTTTACGAGATATCATGAGAAATGACAGAGAAATCTAAGTGAGAAATGATATCATTTGG 2040
Db 1981 CCAAGTTTACGAGATATCATGAGAAATGACAGAGAAATCTAAGTGAGAAATGATATCATTTGG 2040
Qy 2041 GCAAGGAGCATCAAGCATGTATTAACAATGTGTTTGAAGAAATTTGAAACCGGTTGGAT 2100
Db 2041 GCAAGGAGCATCAAGCATGTATTAACAATGTGTTTGAAGAAATTTGAAACCGGTTGGAT 2100
Qy 2101 TAAAGCGCTTACTCTCACAACCCACAGCTAATGAAGAAACGTTTGAAGCAAGATCCGAT 2160
Db 2101 TAAAGCGCTTACTCTCACAACCCACAGCTAATGAAGAAACGTTTGAAGCAAGATCCGAT 2160
Qy 2161 GCTAAGTAGCATCAAGCAAGAAATCTTGTGAGCTTAAAGCTTAAATCCCTCTCTCACTT 2220
Db 2161 GCTAAGTAGCATCAAGCAAGAAATCTTGTGAGCTTAAAGCTTAAATCCCTCTCTCACTT 2220
Qy 2221 GGGGAGCTTCTGTGTTCTATGACTAATTTGAAAAATGTAAGCTCTGGGATCTTCTTCAATG 2280
Db 2221 GGGGAGCTTCTGTGTTCTATGACTAATTTGAAAAATGTAAGCTCTGGGATCTTCTTCAATG 2280
Qy 2281 CCTACGAAAGAAAGACTTGTATTTGGGACACAGCGCTTAAATGAATGACATAGGTGAGC 2340
Db 2281 CCTACGAAAGAAAGACTTGTATTTGGGACACAGCGCTTAAATGAATGACATAGGTGAGC 2340
Qy 2341 ACAAGGTTTAGCTTATCTACACATGACTGATGTACAGAGATCATTTCAAGAAACGAGAA 2400
Db 2341 ACAAGGTTTAGCTTATCTACACATGACTGATGTACAGAGATCATTTCAAGAAACGAGAA 2400
Qy 2401 GTGTTCACACATTCCTTTGGAACAAGACTTAGAGGCTCGTTTGAACAGATTTGGAATAGC 2460
Db 2401 GTGTTCACACATTCCTTTGGAACAAGACTTAGAGGCTCGTTTGAACAGATTTGGAATAGC 2460
Qy 2461 GAAAAGCTTGTGTGTCAAAAGTCAATTAATTTGAGATTTGAGGACAGATAGGTTA 2520
Db 2461 GAAAAGCTTGTGTGTCAAAAGTCAATTAATTTGAGATTTGAGGACAGATAGGTTA 2520
```

QY 2521 CATAGACCCCGAGTATGCTCGACCTTCAAGGCTCAGTGAAGATCCGATGCTTACAGTTA 2580  
|||  
DB 2521 CATAGACCCCGAGTATGCTCGACCTTCAAGGCTCAGTGAAGATCCGATGCTTACAGTTA 2580  
|||  
QY 2581 TGGAAATAGTCTCTTCTGAGTTGTTAAACCGAAGAAAAGCGTTGATGACGAATCCAACTC 2640  
|||  
DB 2581 TGGAAATAGTCTCTTCTGAGTTGTTAAACCGAAGAAAAGCGTTGATGACGAATCCAACTC 2640  
|||  
QY 2641 CCACCATCTGATATATGTCAGAACGCGGGAACAATGAAGTATGGAATGGCAATCCAGA 2700  
|||  
DB 2641 CCACCATCTGATATATGTCAGAACGCGGGAACAATGAAGTATGGAATGGCAATCCAGA 2700  
|||  
QY 2701 CATCAATCGACGCTGTAAGATCTCGGTGAGTGAAGAAAGTTTCCAACTGGCACTCT 2760  
|||  
DB 2701 CATCAATCGACGCTGTAAGATCTCGGTGAGTGAAGAAAGTTTCCAACTGGCACTCT 2760  
|||  
QY 2761 ATGCACCAAAAAGACAGCCGAATGATCGAACCAATGCAACAGTGAATGCTGCTCGG 2820  
|||  
DB 2761 ATGCACCAAAAAGACAGCCGAATGATCGAACCAATGCAACAGTGAATGCTGCTCGG 2820  
|||  
QY 2821 CAGTTTATGCTATCGGAACAACCACTGCTGCACTGACAGCTGAGCGTGGCTGG 2880  
|||  
DB 2821 CAGTTTATGCTATCGGAACAACCACTGCTGCACTGACAGCTGAGCGTGGCTGG 2880  
|||  
QY 2881 TTGCTGCTACGAGTATGATGCAAACTCAAGACTCCATTCGTGCAATGCTCTTC 2940  
|||  
DB 2881 TTGCTGCTACGAGTATGATGCAAACTCAAGACTCCATTCGTGCAATGCTCTTC 2940  
|||  
QY 2941 CATGAGTCTTCTGATGCTCAACTGTTCTTCGTTTGAACAAGTTATTTCTGAGAACAG 3000  
|||  
DB 2941 CATGAGTCTTCTGATGCTCAACTGTTCTTCGTTTGAACAAGTTATTTCTGAGAACAG 3000  
|||  
QY 3001 TGAATGTTTTTCTGTTAGAGAGAGAACTTTAAAGGATCTTTTCTGCTGCTTAACT 3060  
|||  
DB 3001 TGAATGTTTTTCTGTTAGAGAGAGAACTTTAAAGGATCTTTTCTGCTGCTTAACT 3060  
|||  
QY 3061 GTTAGAAAAATTATATGCTCATGTAAGTATTAAGCACTGCTTATATATTAAGAACAG 3120  
|||  
DB 3061 GTTAGAAAAATTATATGCTCATGTAAGTATTAAGCACTGCTTATATATTAAGAACAG 3120  
|||  
QY 3121 TGTGTGTGTGATATATGCTTCAAGCTGAGCACTTAGACTTCTATAGTTCTTGCC 3176  
|||  
DB 3121 TGTGTGTGTGATATATGCTTCAAGCTGAGCACTTAGACTTCTATAGTTCTTGCC 3176  
|||

RESULT 2  
US-11-056-355B-46415  
; Sequence 46415, Application US//11056355B  
; Publication No. US20060150283A1  
; GENERAL INFORMATION:

APPLICANT: Brover, Vyacheslav  
APPLICANT: Alexandrov, Nikolai  
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
FILE REFERENCE: 2750-1590PUS2  
CURRENT APPLICATION NUMBER: US/11/056,355B  
PRIOR FILING DATE: 2005-02-14  
PRIOR APPLICATION NUMBER: 60/544,190  
NUMBER OF SEQ ID NOS: 119966  
; SEQ ID NO 46415  
; LENGTH: 3191  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
; FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)-(3191)  
OTHER INFORMATION: Ceres Seq. ID no. 13578685  
; NAME/KEY: misc\_feature  
LOCATION: (1)-(3191)  
OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 14316144

OTHER INFORMATION: as cited in SEQ ID NO 52397  
US-11-056-355B-46415

Query Match 100.0%; Score 3176; DB 9; Length 3191;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCTTCAATGAGAGCTGAAAGCTTTTAAAGTATCTTAAAGCAAGCGAGTCTT 60  
|||  
DB 1 GTTCTCTTCAATGAGAGCTGAAAGCTTTTAAAGTATCTTAAAGCAAGCGAGTCTT 60  
|||  
QY 61 AGACTGTGTGAGAAATGAGCTCTGTTTGAAGATATGTTCTTCTGGTTCTCTCTG 120  
|||  
DB 61 AGACTGTGTGAGAAATGAGCTCTGTTTGAAGATATGTTCTTCTGGTTCTCTCTG 120  
|||  
QY 121 CTGAGACTATGATGCTATGCTGCTTCAAGAGAGGAGCAAGCTTCTGAGATTTAAGA 180  
|||  
DB 121 CTGAGACTATGATGCTATGCTGCTTCAAGAGAGGAGCAAGCTTCTGAGATTTAAGA 180  
|||  
QY 181 GTCAATCAAGAGATGAAACAATGTTCTTATGACTGAGCAACTTCACTTCTCGGATTA 240  
|||  
DB 181 GTCAATCAAGAGATGAAACAATGTTCTTATGACTGAGCAACTTCACTTCTCGGATTA 240  
|||  
QY 241 TTGCTGTGAGAGAGTGTCTTGTGAAATGTCACTTCAATGTTGCTCTTAATT 300  
|||  
DB 241 TTGCTGTGAGAGAGTGTCTTGTGAAATGTCACTTCAATGTTGCTCTTAATT 300  
|||  
QY 301 GTCAATTTGAATCTTGAATGAGAAATCTCACTGCTTATGAGATCTCAAGTCTCT 360  
|||  
DB 301 GTCAATTTGAATCTTGAATGAGAAATCTCACTGCTTATGAGATCTCAAGTCTCT 360  
|||  
QY 361 GTCAATTTGAATCTTGAATGAGAAATCTCACTGCTTATGAGATCTCAAGTCTCT 420  
|||  
DB 361 GTCAATTTGAATCTTGAATGAGAAATCTCACTGCTTATGAGATCTCAAGTCTCT 420  
|||  
QY 421 TTCTTCTTGAACAACTTGAATCTTCAATGATTAAGTGTGATACCGTTTCT 480  
|||  
DB 421 TTCTTCTTGAACAACTTGAATCTTCAATGATTAAGTGTGATACCGTTTCT 480  
|||  
QY 481 GATTGGAAGTTGAGCAACTTGAAGAGCTGATTTGAAAGATTAACAATTGATAGACC 540  
|||  
DB 481 GATTGGAAGTTGAGCAACTTGAAGAGCTGATTTGAAAGATTAACAATTGATAGACC 540  
|||  
QY 541 GATCCCTTGAACACTTGAAGAGCTGATTTGAAAGATTAACAATTGATAGACC 600  
|||  
DB 541 GATCCCTTGAACACTTGAAGAGCTGATTTGAAAGATTAACAATTGATAGACC 600  
|||  
QY 601 ACTCAGTGTGAGATGCAAGACTTATTTACTGAAATGAAGTTCTTCAATCTTGGATT 660  
|||  
DB 601 ACTCAGTGTGAGATGCAAGACTTATTTACTGAAATGAAGTTCTTCAATCTTGGATT 660  
|||  
QY 661 GCGAGAAAACAATTAGTGTGTAACATTTCTCAGATTTGTGCAACTGATGCTTTTG 720  
|||  
DB 661 GCGAGAAAACAATTAGTGTGTAACATTTCTCAGATTTGTGCAACTGATGCTTTTG 720  
|||  
QY 721 GATTTTGAAGTGAAGAAACAAGTTGACTGTGATTAACCTGAGACAAATGAGAAATG 780  
|||  
DB 721 GATTTTGAAGTGAAGAAACAAGTTGACTGTGATTAACCTGAGACAAATGAGAAATG 780  
|||  
QY 781 CACTGCTTCCAGGTTTGTGAACTTGTCTTCAATCACTGATGAGATCCCTTTTGA 840  
|||  
DB 781 CACTGCTTCCAGGTTTGTGAACTTGTCTTCAATCACTGATGAGATCCCTTTTGA 840  
|||  
QY 841 CATCGGCTTCTGCAAGTTGCAACATTTATGATGCAAGCAATCACTCTGGGAAGAT 900  
|||  
DB 841 CATCGGCTTCTGCAAGTTGCAACATTTATGATGCAAGCAATCACTCTGGGAAGAT 900  
|||  
QY 901 TCCATGAGATTTGCTGATGCAAGCTTGTGATGATTTAAGTGGCAACTTGT 960  
|||  
DB 901 TCCATGAGATTTGCTGATGCAAGCTTGTGATGATTTAAGTGGCAACTTGT 960  
|||  
QY 961 GAGTGATCTATTCCTCGAATCTGGAATCTTCACTTCACTGGAATTTGATTTGA 1020  
|||

Db	961	GAGTGGATCTAATCTCCGCGATCTCGGAAATCTTACTTTCCAGGAAATGTGATTTGCA	1020
Qy	1021	CAGTAAACAGCTGAGGTTCATTCACCTGAGCTTGGAAACATGTCAAAACCTCCATTA	1080
Db	1021	CAGTAAACAGCTGAGGTTCATTCACCTGAGCTTGGAAACATGTCAAAACCTCCATTA	1080
Qy	1081	CCTGGAACCTCAATGATATCATCTCAGGGTCAATATACCAACAGAGCTTGGGAAGCTTAC	1140
Db	1081	CCTGGAACCTCAATGATATCATCTCAGGGTCAATATACCAACAGAGCTTGGGAAGCTTAC	1140
Qy	1141	TGACTGTGTTGATCTGAATGTGGCCAAATGATCTGGAAAGACCTTATCTGATCATCT	1200
Db	1141	TGACTGTGTTGATCTGAATGTGGCCAAATGATCTGGAAAGACCTTATCTGATCATCT	1200
Qy	1201	GAGCTCTTGCAAAATTAACAGCTTAAATGTTCATGGGAAACAAAGTTTATGGGCACTAT	1260
Db	1201	GAGCTCTTGCAAAATTAACAGCTTAAATGTTCATGGGAAACAAAGTTTATGGGCACTAT	1260
Qy	1261	ACCCGAGCATTTCAAAAGCTAGAAAGTATGACTTACCTTAACTGTCCAGCAACAATAT	1320
Db	1261	ACCCGAGCATTTCAAAAGCTAGAAAGTATGACTTACCTTAACTGTCCAGCAACAATAT	1320
Qy	1321	CAAAAGTCCAAATCCCGGTGAGCTATCTCGTATCGTAACTTGAATCATTGGATCTTTC	1380
Db	1321	CAAAAGTCCAAATCCCGGTGAGCTATCTCGTATCGTAACTTGAATCATTGGATCTTTC	1380
Qy	1381	CAACAACAAGATAAATGGAATCAATTCCTTCTCCCTGGTGAATTTGGAGCATCTTCA	1440
Db	1381	CAACAACAAGATAAATGGAATCAATTCCTTCTCCCTGGTGAATTTGGAGCATCTTCA	1440
Qy	1441	GATGAACTTGAGTAGAATCATATTAACCTGGTGTAGTTCCAGGCGCATTTGGAAATCTAAG	1500
Db	1441	GATGAACTTGAGTAGAATCATATTAACCTGGTGTAGTTCCAGGCGCATTTGGAAATCTAAG	1500
Qy	1501	AACGATCATGGAATATAGATCTTTCAAAATATGATATCTCTGGCCCAATTCAGAAAGCT	1560
Db	1501	AACGATCATGGAATATAGATCTTTCAAAATATGATATCTCTGGCCCAATTCAGAAAGCT	1560
Qy	1561	TAACCAATTCAGAACATAATTTTGGTGAAGCTGGAAATATTAACCTGACTGGTAATGT	1620
Db	1561	TAACCAATTCAGAACATAATTTTGGTGAAGCTGGAAATATTAACCTGACTGGTAATGT	1620
Qy	1621	TGGTTCATTAGCCAACTGTCTCAGTCTCAGTATTTGAAATGTATCTCATTAACAACCTCGT	1680
Db	1621	TGGTTCATTAGCCAACTGTCTCAGTCTCAGTATTTGAAATGTATCTCATTAACAACCTCGT	1680
Qy	1681	AGGTGATATCCCTTAAGAACATAATCTTCAAGATTTTCCACAGACGCTTCAATGGCAA	1740
Db	1681	AGGTGATATCCCTTAAGAACATAATCTTCAAGATTTTCCACAGACGCTTCAATGGCAA	1740
Qy	1741	TCCGTGCTTTGCGGATGTTGGCTAACTCAGCGTCAATGATCTCGTGAACCTGTAAG	1800
Db	1741	TCCGTGCTTTGCGGATGTTGGCTAACTCAGCGTCAATGATCTCGTGAACCTGTAAG	1800
Qy	1801	AGTGTCAATCTCTAGACAGACTAATCTTGGAAATAGCTAATGGGGGACTTGTGATCTTCT	1860
Db	1801	AGTGTCAATCTCTAGACAGACTAATCTTGGAAATAGCTAATGGGGGACTTGTGATCTTCT	1860
Qy	1861	CATGCTTTAATAGACACTTGGCGAATCCCTCCTCCTTTCTTGAATGGAATGACT	1920
Db	1861	CATGCTTTAATAGACACTTGGCGAATCCCTCCTCCTTTCTTGAATGGAATGACT	1920
Qy	1921	TGACAAACAGCTAATCTTATTCGACACCGAAGCTGCTGATCTTGAATGAACATGGCACT	1980
Db	1921	TGACAAACAGCTAATCTTATTCGACACCGAAGCTGCTGATCTTGAATGAACATGGCACT	1980
Qy	1981	CCACGTTTACGAGATATCATGAGATGACAGAGATCTAAGTGAAGAGTATCATTTGG	2040
Db	1981	CCACGTTTACGAGATATCATGAGATGACAGAGATCTAAGTGAAGAGTATCATTTGG	2040
Qy	2041	GACGAGGATCAAGCACTGATATCAAAATGTGTTTGAAGAAATGTAAACCGGTTGGAT	2100
Db	2041	GACGAGGATCAAGCACTGATATCAAAATGTGTTTGAAGAAATGTAAACCGGTTGGAT	2100

---

Qy	2101	TAAGCGCTTTACTCTCAACACCAAGTCAATGAACAGTTTGAACAGAACTCGAGAT	2160
Db	2101	TAAGCGCTTTACTCTCAACACCAAGTCAATGAACAGTTTGAACAGAACTCGAGAT	2160
Qy	2161	GCTAAGTACATCAAGCAAGAAATCTTGTGAGCTTCAAGCTTATTCCTCTCTCACTT	2220
Db	2161	GCTAAGTACATCAAGCAAGAAATCTTGTGAGCTTCAAGCTTATTCCTCTCTCACTT	2220
Qy	2221	GGGAGCTTCTGTCTATGACTTATGAAAAATGATAGCTCTGGAGTCTTTCATGG	2280
Db	2221	GGGAGCTTCTGTCTATGACTTATGAAAAATGATAGCTCTGGAGTCTTTCATGG	2280
Qy	2281	CCCTAAGAAAGAAAGACTCTTGATTTGGACACACCGCTTAAAGTATGATATGCTGACG	2340
Db	2281	CCCTAAGAAAGAAAGACTCTTGATTTGGACACACCGCTTAAAGTATGATATGCTGACG	2340
Qy	2341	ACAAAGTTTACCTTATCTACCAATGACTGTAGTCCAAAGATCATTCACAGAGAGCTGAA	2400
Db	2341	ACAAAGTTTACCTTATCTACCAATGACTGTAGTCCAAAGATCATTCACAGAGAGCTGAA	2400
Qy	2401	GTGTCACAATCTCTTGGACAAAGACTTAAAGGCTCGTTTGAACAGATTTTGGAAATAG	2460
Db	2401	GTGTCACAATCTCTTGGACAAAGACTTAAAGGCTCGTTTGAACAGATTTTGGAAATAG	2460
Qy	2461	GAAAAGCTTGTGTGTCAAAAGTCAATATCTTCACTTAAGTATGGGACAGTATAGTTA	2520
Db	2461	GAAAAGCTTGTGTGTCAAAAGTCAATATCTTCACTTAAGTATGGGACAGTATAGTTA	2520
Qy	2521	CATAGACCCCGAGATATGCTGCACTTCAAGGCTCACTGAGAAATCCGATGTCTACGTTA	2580
Db	2521	CATAGACCCCGAGATATGCTGCACTTCAAGGCTCACTGAGAAATCCGATGTCTACGTTA	2580
Qy	2581	TGGAAATAGTCTCTTGAAGTTTAAACCGAAGAAAGCCGTTGATGACGAATCCAACTC	2640
Db	2581	TGGAAATAGTCTCTTGAAGTTTAAACCGAAGAAAGCCGTTGATGACGAATCCAACTC	2640
Qy	2641	CCAACATCTGATATGTCAAAGACGCGGGAACAAATGAAGTATGAAATGGCAGATCCAGA	2700
Db	2641	CCAACATCTGATATGTCAAAGACGCGGGAACAAATGAAGTATGAAATGGCAGATCCAGA	2700
Qy	2701	CATCACATGCAAGCTGTAAAGATCTCGGTGTGTGAAGAAAGTTTCCAACTGGCACTCCT	2760
Db	2701	CATCACATGCAAGCTGTAAAGATCTCGGTGTGTGAAGAAAGTTTCCAACTGGCACTCCT	2760
Qy	2761	ATGACCAAAAAGACAGCGCAATGATGACCCCAATATGACACAGGTGACTGTCTCGG	2820
Db	2761	ATGACCAAAAAGACAGCGCAATGATGACCCCAATATGACACAGGTGACTGTCTCGG	2820
Qy	2821	CAGTTTATATCTATCGGAACAAACCACTGTGCGACTGACAGCTGACGCTGCGCTGG	2880
Db	2821	CAGTTTATATCTATCGGAACAAACCACTGTGCGACTGACAGCTGACGCTGCGCTGG	2880
Qy	2881	TTGCTGTATGCTGATGAGATGCAAAATCTCAGACCTCCTCAATCTGTCAATTTGCTTTC	2940
Db	2881	TTGCTGTATGCTGATGAGATGCAAAATCTCAGACCTCCTCAATCTGTCAATTTGCTTTC	2940
Qy	2941	CATGAGTCTTGTGATGCTCAACTGTTTCTTGGGTTTGAACAAGTATTTCTCAAGAACG	3000
Db	2941	CATGAGTCTTGTGATGCTCAACTGTTTCTTGGGTTTGAACAAGTATTTCTCAAGAACG	3000
Qy	3001	TGAGTATGTTTCTGTTAGAGAGAAATCTTTAAACGGTATCTTTTCTGTTGCTTAAAGCT	3060
Db	3001	TGAGTATGTTTCTGTTAGAGAGAAATCTTTAAACGGTATCTTTTCTGTTGCTTAAAGCT	3060
Qy	3061	GTTAGAAAAATTAATGCTCATGTTAAAGTATTAAGTATGACAGCTTATTAATTAAGCAAG	3120
Db	3061	GTTAGAAAAATTAATGCTCATGTTAAAGTATTAAGTATGACAGCTTATTAATTAAGCAAG	3120
Qy	3121	TGTGTGTGTGAATATGTCTTCAAGCTGCACTTAAGCTTCTATTAAGTCTTGGCC	3176
Db	3121	TGTGTGTGTGAATATGTCTTCAAGCTGCACTTAAGCTTCTATTAAGTCTTGGCC	3176

RESULT 3  
US-11-056-355B-48174  
Sequence 48174, Application US/11056355B  
Publication No. US20060150283A1  
GENERAL INFORMATION:  
APPLICANT: Brover, Vyacheslav  
APPLICANT: Alexandrov, Nikolai  
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding  
FILE REFERENCE: 2750-1590PUS2  
CURRENT APPLICATION NUMBER: US/11/056,355B  
CURRENT FILING DATE: 2005-02-14  
PRIORITY APPLICATION NUMBER: 60/544,190  
PRIOR FILING DATE: 2004-02-13  
NUMBER OF SEQ ID NOS: 119966  
SEQ ID NO 48174  
LENGTH: 3191  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(3191)  
OTHER INFORMATION: Ceres Seq. ID no. 13578685  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)..(3191)  
OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 14316144  
OTHER INFORMATION: as cited in SEQ ID NO 52397  
US-11-056-355B-48174

Query Match 100.0%; Score 3176; DB 9; Length 3191;  
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 3176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTCTCTTCATGAGACTTGAAGCTTTAAAGTATCTAATAAAGCGAGTCGTTTA 60  
DB 1 GTTCTCTTCATGAGACTTGAAGCTTTAAAGTATCTAATAAAGCGAGTCGTTTA 60  
QY 61 AGACTGTGTGAGAAATGCGTCTGTTAAGATATGTTCTTGGGTTTCTTCTG 120  
DB 61 AGACTGTGTGAGAAATGCGTCTGTTAAGATATGTTCTTGGGTTTCTTCTG 120  
QY 121 CTGAGGTTAGTGTCTGTGACTTGAAGAGGAGCAACGTTGCGATTAAGA 180  
DB 121 CTGAGGTTAGTGTCTGTGACTTGAAGAGGAGCAACGTTGCGATTAAGA 180  
QY 181 GTCATTCAAGATGTGAACAATGTTCTTATGACTGACAACTTCACTTCGATTA 240  
DB 181 GTCATTCAAGATGTGAACAATGTTCTTATGACTGACAACTTCACTTCGATTA 240  
QY 241 TTGTGTCTGAGAGGTGTCTGTGAAATGTCACTTCAATGTTGCTCTTAATT 300  
DB 241 TTGTGTCTGAGAGGTGTCTGTGAAATGTCACTTCAATGTTGCTCTTAATT 300  
QY 301 GTCAGATTGAATCTTGAATGAAGATCAACCTGCATTTGAGATCTCAAGATCTCT 360  
DB 301 GTCAGATTGAATCTTGAATGAAGATCAACCTGCATTTGAGATCTCAAGATCTCT 360  
QY 361 GTCAGATTGAATCTTGAATGAAGATCAACCTGCATTTGAGATCTCAAGATCTCT 420  
DB 361 GTCAGATTGAATCTTGAATGAAGATCAACCTGCATTTGAGATCTCAAGATCTCT 420  
QY 421 TTCTTCTTGAAGAACTTAAGCTTATCTTCAATGAATTAAGTGTGACATACCGTTTC 480  
DB 421 TTCTTCTTGAAGAACTTAAGCTTATCTTCAATGAATTAAGTGTGACATACCGTTTC 480  
QY 481 GATTTCGAAGTTGAAGCACTTGAGAGAGTGTCTGAAGAAATTAACCAATTTGATGAG 540  
DB 481 GATTTCGAAGTTGAAGCACTTGAGAGAGTGTCTGAAGAAATTAACCAATTTGATGAG 540  
QY 541 GATTCCTTCAACATTTCAAGATTCGAAATCTGAAATTTCTGACTTGGCAGAAATA 600  
DB 541 GATTCCTTCAACATTTCAAGATTCGAAATCTGAAATTTCTGACTTGGCAGAAATA 600

DB 541 GATTCCTTCAACATTTCAAGATTCGAAATCTGAAATTTCTGACTTGGCAGAAATA 600  
QY 601 ACTCAGTGTGAATATACCAAGACTTATTTATCTGAATGAAGTTCTTCAATCTGGGT 660  
DB 601 ACTCAGTGTGAATATACCAAGACTTATTTATCTGAATGAAGTTCTTCAATCTGGGT 660  
QY 661 GCGAGAAACAATTTGTCGTGAACATTTCTCAGATTTTGTCACTGATGATCTTTG 720  
DB 661 GCGAGAAACAATTTGTCGTGAACATTTCTCAGATTTTGTCACTGATGATCTTTG 720  
QY 721 GATTTTGAAGTGAAGAAACAAGTTGACTGTGATATCTGAGACGATAGAAATTG 780  
DB 721 GATTTTGAAGTGAAGAAACAAGTTGACTGTGATATCTGAGACGATAGAAATTG 780  
QY 781 CACTGCTTCCAGATTTTGAACCTTGTCTCAATACGCTAATCTGAGAGATCTCTTTTGA 840  
DB 781 CACTGCTTCCAGATTTTGAACCTTGTCTCAATACGCTAATCTGAGAGATCTCTTTTGA 840  
QY 841 CATGCGCTTCTGCAAGTTGCAACATTTATCATTTGCAAGGCAATCAACTCTGGAAGAT 900  
DB 841 CATGCGCTTCTGCAAGTTGCAACATTTATCATTTGCAAGGCAATCAACTCTGGAAGAT 900  
QY 901 TCCATCAGTATGATCTCATGCAAGCCCTTGCAAGTCTTGAATCTAAGTGCAACTTGT 960  
DB 901 TCCATCAGTATGATGATCTCATGCAAGCCCTTGCAAGTCTTGAATCTAAGTGCAACTTGT 960  
QY 961 GAGTGTATCTATTTCTCCGATTTCTGGAATCTTACTTTTACCGAATAATTTGATTTGCA 1020  
DB 961 GAGTGTATCTATTTCTCCGATTTCTGGAATCTTACTTTTACCGAATAATTTGATTTGCA 1020  
QY 1021 CAGTAAACAGCTGACTGTTCAATTCGACCTGAGCTTGGAAACATGTCAAATCTCATTA 1080  
DB 1021 CAGTAAACAGCTGACTGTTCAATTCGACCTGAGCTTGGAAACATGTCAAATCTCATTA 1080  
QY 1081 CCTGGAATCTAATGATATATCTCAAGGTCATATACCAACAGCTTGGAAAGTTAC 1140  
DB 1081 CCTGGAATCTAATGATATATCTCAAGGTCATATACCAACAGCTTGGAAAGTTAC 1140  
QY 1141 TGAATTTTGAATCTGAATGTGGCAACATGATCTGGAAGACCTTATCTGATCTCT 1200  
DB 1141 TGAATTTTGAATCTGAATGTGGCAACATGATCTGGAAGACCTTATCTGATCTCT 1200  
QY 1201 GAGCTCTGCAACAATCTAATACGCTTAAATGTTCAATGGAACAAGTTTGGCACTAT 1260  
DB 1201 GAGCTCTGCAACAATCTAATACGCTTAAATGTTCAATGGAACAAGTTTGGCACTAT 1260  
QY 1261 ACCCGAGCAATTCGAAAGCTAAGATGATGACTTACCTTATCTGTCCAGCAACAATAT 1320  
DB 1261 ACCCGAGCAATTCGAAAGCTAAGATGATGACTTACCTTATCTGTCCAGCAACAATAT 1320  
QY 1321 GAAAGTCCAAATCCGCTGAGCTATCTGTATCGGTAACTTGAATGATGATCTTTC 1380  
DB 1321 GAAAGTCCAAATCCGCTGAGCTATCTGTATCGGTAACTTGAATGATGATCTTTC 1380  
QY 1381 CAACCAACAATGAAATGAAATCAATCTTCTTCCCTTGGGATTTGAGAGATCTTCTCA 1440  
DB 1381 CAACCAACAATGAAATGAAATCAATCTTCTTCCCTTGGGATTTGAGAGATCTTCTCA 1440  
QY 1441 GATGAACCTGAGTGAATATATATCTGTGATGTTCCAGGCACTTTGGAATCTTAAG 1500  
DB 1441 GATGAACCTGAGTGAATATATATCTGTGATGTTCCAGGCACTTTGGAATCTTAAG 1500  
QY 1501 AAGCATCAATGAAATGATCTTCAATATATCTGTGAGCCCAATTCGAAAGGCT 1560  
DB 1501 AAGCATCAATGAAATGATCTTCAATATATCTGTGAGCCCAATTCGAAAGGCT 1560  
QY 1561 TAACCAATTAACAATATTTGCTGAGACTGAGAAATTAATACCTGATCTGATATGT 1620  
DB 1561 TAACCAATTAACAATATTTGCTGAGACTGAGAAATTAATACCTGATCTGATATGT 1620  
QY 1621 TGGTATTAATGCAACTGTCTCACTGATCTGATGATGATATCTGATTAACAACCTCGT 1680  
DB 1621 TGGTATTAATGCAACTGTCTCACTGATCTGATGATGATATCTGATTAACAACCTCGT 1680

1681 AGGTGATATCCCTAAGAACAACTTCTCAAGATTTTCCAGACAGCTTCATTTGGCAA 1740  
1681 AGGTGATATCCCTAAGAACAACTTCTCAAGATTTTCCAGACAGCTTCATTTGGCAA 1740  
1741 TCCGTGCTCTTGGCGGAGTGGCTAACTCACCGTGTCAATGATTTCTGTCGAACTGTACG 1800  
1741 TCCGTGCTCTTGGCGGAGTGGCTAACTCACCGTGTCAATGATTTCTGTCGAACTGTACG 1800  
1801 AGGTGATATCCCTAAGAACAACTTCTCAAGATTTTCCAGACAGCTTCATTTGGCAA 1860  
1801 AGGTGATATCCCTAAGAACAACTTCTCAAGATTTTCCAGACAGCTTCATTTGGCAA 1860  
1861 CATGCTTTAATAGCACTTGGCGAAGCTTCCTCTCTCTTCTTGTGATGATCACT 1920  
1861 CATGCTTTAATAGCACTTGGCGAAGCTTCCTCTCTCTTCTTGTGATGATCACT 1920  
1921 TGACAAACCAAGTAACTTATTCGACACCGAAGCTGTCTATCTTCAATGAAATGACACT 1980  
1921 TGACAAACCAAGTAACTTATTCGACACCGAAGCTGTCTATCTTCAATGAAATGACACT 1980  
1981 CCAAGTTTAAAGAGATATCATGAGATGACAGAACTCTAAGTGAAGATATCATTTGG 2040  
1981 CCAAGTTTAAAGAGATATCATGAGATGACAGAACTCTAAGTGAAGATATCATTTGG 2040  
2041 GCAAGGAGATCAAGCACTGTATCAAAATGCTTTGAAGATTTGTAACCGGTTGGAT 2100  
2041 GCAAGGAGATCAAGCACTGTATCAAAATGCTTTGAAGATTTGTAACCGGTTGGAT 2100  
2101 TAAAGCGCTTACTCTCAACCAAGTCAATGAAACAGTTTGAACAGAACTCGAGAT 2160  
2101 TAAAGCGCTTACTCTCAACCAAGTCAATGAAACAGTTTGAACAGAACTCGAGAT 2160  
2161 GCTAAGTATGATCAAGCACTGTATCAAAATGCTTTGAAGATTTGTAACCGGTTGGAT 2220  
2161 GCTAAGTATGATCAAGCACTGTATCAAAATGCTTTGAAGATTTGTAACCGGTTGGAT 2220  
2221 GGGGAGCTCTTCTGTATGACATTTTGAAGATTTGTAACCGGTTGGAT 2280  
2221 GGGGAGCTCTTCTGTATGACATTTTGAAGATTTGTAACCGGTTGGAT 2280  
2281 CCTTACGAAAGAAAGCTCTTGTATGAGACACCGGCTTAAATGATGATGTCAGC 2340  
2281 CCTTACGAAAGAAAGCTCTTGTATGAGACACCGGCTTAAATGATGATGTCAGC 2340  
2341 ACAAGTTTAAAGAGATATCATGAGATGACAGAACTCTAAGTGAAGATATCATTTGG 2400  
2341 ACAAGTTTAAAGAGATATCATGAGATGACAGAACTCTAAGTGAAGATATCATTTGG 2400  
2401 GTGCTCCAACTTCTTGGACAAAGCTTGAAGGCTCGTTTGAAGATTTTGGAAATAGC 2460  
2401 GTGCTCCAACTTCTTGGACAAAGCTTGAAGGCTCGTTTGAAGATTTTGGAAATAGC 2460  
2461 GAAAAGCTTGTGTGTCAAAAGTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 2520  
2461 GAAAAGCTTGTGTGTCAAAAGTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 2520  
2461 GAAAAGCTTGTGTGTCAAAAGTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 2520  
2521 CATAGACCCCGAGATGCTGCACTTCAAGGCTCACTGAGAAATCCAGATGTCAGATTA 2580  
2521 CATAGACCCCGAGATGCTGCACTTCAAGGCTCACTGAGAAATCCAGATGTCAGATTA 2580  
2581 TGAATAGTCTCTTGTGTCAAAAGTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 2640  
2581 TGAATAGTCTCTTGTGTCAAAAGTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 2640  
2641 CCACCATCTGATATGTCAAAGACGGGGAACAATGATGATGAAATGGCAATCCAGA 2700  
2641 CCACCATCTGATATGTCAAAGACGGGGAACAATGATGATGAAATGGCAATCCAGA 2700  
2701 CATACATCGACGTGTAAGATCTCGGTGTGTGTAAGAAAGTTTCCAACTGGCACTCT 2760  
2701 CATACATCGACGTGTAAGATCTCGGTGTGTGTAAGAAAGTTTCCAACTGGCACTCT 2760

2761 ATGACCAAAAAGACAGCCGATATGACACCAATGACACAGATGACTGTGTTCTCGG 2820  
2761 ATGACCAAAAAGACAGCCGATATGACACCAATGACACAGATGACTGTGTTCTCGG 2820  
2821 CAGTTTATGCTATCGGAACCAACCACTGCTGCACTGACAGCTGACGACGCTGCTGG 2880  
2821 CAGTTTATGCTATCGGAACCAACCACTGCTGCACTGACAGCTGACGACGCTGCTGG 2880  
2881 TTGCTGCTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2940  
2881 TTGCTGCTAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2940  
2941 CATGAGCTCTTCTGATGCTCACTGTTCTTCTGCTTGAAGATTTTCTGACAAAG 3000  
2941 CATGAGCTCTTCTGATGCTCACTGTTCTTCTGCTTGAAGATTTTCTGACAAAG 3000  
3001 TGAGTATGTTTGTGTAAGGAGAACTTTTAAACGATCTTTGTCGTTAAAGCT 3060  
3001 TGAGTATGTTTGTGTAAGGAGAACTTTTAAACGATCTTTGTCGTTAAAGCT 3060  
3061 GTTAAAGAAATTAATGCTCATGTAAGATTAATGACAGCTTATTAATTAAGCAAG 3120  
3061 GTTAAAGAAATTAATGCTCATGTAAGATTAATGACAGCTTATTAATTAAGCAAG 3120  
3121 TGTGTGTGTGTAATGATGCTTCAAGCTGCACTTGAACCTTCTAATGATTTCTTCC 3176  
3121 TGTGTGTGTGTAATGATGCTTCAAGCTGCACTTGAACCTTCTAATGATTTCTTCC 3176

RESULT 4  
US-11-216-545-1706  
Sequence 1706, Application US/11216545  
Publication No. US20060135758A1  
GENERAL INFORMATION:  
APPLICANT: MONSANTO Technology, LLC  
APPLICANT: McLeod, Paul L  
APPLICANT: tao, Nengbing  
APPLICANT: Wu, Kunsheng  
TITLE OF INVENTION: Single Nucleotide Polymorphic Markers and Methods of Genotyping  
FILE REFERENCE: 38-21 (53659)B  
CURRENT APPLICATION NUMBER: US/11/216,545  
CURRENT FILING DATE: 2005-08-31  
PRIOR APPLICATION NUMBER: US 60/606,062  
PRIOR FILING DATE: 2004-08-31  
NUMBER OF SEQ ID NOS: 8783  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1706  
LENGTH: 3705  
TYPE: DNA  
ORGANISM: Glycine max  
US-11-216-545-1706

Query Match 53.3%; Score 1691.4; DB 8; Length 3705;  
Best Local Similarity 74.2%; P-Value 0;  
Matches 2204; Conservative 0; Mismatches 731; Indels 34; Gaps 4;

68 GTGAGAAATGAGCTGTTAGAGATATGTTCTTGGGTTTCTTCTGCTGAGC 127  
505 GTTGCACCTATGACATTTGCAATTTGAGAGTCTTATTTCTTCTGCTGAGC 553  
128 TTAAGTACTGATGATTTGAG 187  
564 --TGTCAATCTGTGAGATCTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 621  
188 AAGATGTAACAATGTTCTTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 247  
622 AGGATGTGATATGATGTTCTTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 681  
248 TGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 307  
682 TGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 741



QY	308	TTGAATCTTGTATGAGAAATCTCACCTGCTATTTGGAGATCTCACAAGTCTCTTGCAATT	367
Db	742	TTGAATCTTGTATGAGTGAATTTCACTGCAATGAGAACTTCAACAGTTTGCTCTTAAT	801
QY	368	GATCTGCGAGGGTAATC-GCTGTCTGGACAATCCCTGATGAGATTTGGGACGTGTTCTTC	426
Db	802	GACCTTCAGAGAAAACAGTTATCAAGGGCAGATACCGATGAGATTGGTACTGTCTTC	861
QY	427	TTTGCMAAATTAGACTTATCCCTCAATGAATTAAGTGTGACATACCGTCTTTCGATTTTC	486
Db	862	TTTAAAGAACCTGAGACTTATCATTTAATGAATTAAGAGGGGATATACATTTTCTAATTC	921
QY	487	GAACTTGAAGCACTTGAGCAG-----CTGATCTGGAAGATTAACCAATT	531
Db	922	TAAGTGTAACAGATGAGAAATCTGGCTGGAGAAATCTGATTTTGAAGAACACCAATT	981
QY	532	GATAGACCGATCCCTTCAACCTTTCACAGATTTCCAAACCGAAATTTCTGGACTGGC	591
Db	982	GATTGACCAATTCCTTCAACTTTGTCTCAGATTCCTGTGTTTGAAGATTCTAGACCTGGC	1041
QY	592	ACAGATAAATCTCAGTGTGAGATACCAAGACTTTATCTGGAATGAAGTCTTCAGTA	651
Db	1042	TCAAAATATCTTAOGGAGAAATCCAAGGCTTATATATGGAACGAAGTTTGCAATA	1101
QY	652	TCTTGGGTTCGAGAGAAACAATTAGTGGTAACATTTCTCCAGATTTGTCAACTGAC	711
Db	1102	TCTAGGCTTGAAGAGGAAACAATTTGTTGTTCACTATCACAGACATGTGCAGTAAAC	1161
QY	712	TGCTCTTTGGATTTTGAACGTAAAGAAACAAGTTGACTGTAATATACCTGAGACAT	771
Db	1162	TGGGTGTGGTATTTTGTATGTAGAAACAATGCTGACGGAATATTTCCAGAAACAT	1221
QY	772	AGGAATATGCACTGCTCCAGAGTTTGGACTTGTCTCAATCACTGACTAACGTGGAGAT	831
Db	1222	AGCAATTTGTACTGCTTCAGAGTCTTGGATTATCTTAACAACAATTACTGAGAGAT	1281
QY	832	CCCTTTTGACATCGGCTTCTCGCAAGTTGCAACATTAATCTTGAAGCAATCACTGC	891
Db	1282	ACCATTCAATATTTGATTTCTTSCAAGTAGCAACTTTGTCTTGGCAAGCAATTAACCTGC	1341
QY	892	TGGGAAGATTCATCAGATGATTGGTCTCATGCAACCTCTGCACTTAAGATCTAACTGG	951
Db	1342	TGGACATATTCACCGGTATCGGTCTATGTCAMACACTGTGCTCTAAGCTTAAGCTG	1401
QY	952	CAACTGTTGAGTGAATCTAATCCTCCGATTTCTGGAATCTTAATTTCAACGAGAAAT	1011
Db	1402	CACTGTTTAAGTGAATGATCCCTCTCTATCTTGGAAATTTGACTTACACGAAAAAT	1461
QY	1012	GTATTTGACAGTAACAAGCTGACTGTTCAATTCACTGACCTTGGAAAAATGTCAAA	1071
Db	1462	GTACTTGCATGGAACAAGCTGACTGGCTTCAATCCCCCAAGGCTTGGAAATATGTCAAA	1521
QY	1072	ACTCATTAACCTGGAATCAATGATATATCTACCGGTCAATATCAACAGAGCTTGG	1131
Db	1522	GCTTCACTAATTTGGAACGTGAATGATACATTTTAAGTGACATATCCGCCGAGCTTGG	1581
QY	1132	GAACTTACTGACTGTTTGTGATCTGAATGTGGCCAACATGATCTGGAAGAACCTATACC	1191
Db	1582	AAAGCTTACTGATCTGTTTGACTTAAATGTTTCTAACACAACTCTCGAGGGCCAAATTC	1641
QY	1192	TGATCATGTAGCTTTCACAAATCTAAACAGCTTAATGTTTCAATGGGAACAAGTTTNG	1251
Db	1642	TAGTAAATCTTAGCTCATGTAABAAATCTCAACGCTCATATGTCATGCAACAACTTGA	1701
QY	1252	TGGCACTATACCCCGAGCATTTCAAAAGCTGAAGATGACTTAACCTTAATCTGTCCAG	1311
Db	1702	TGGATCAATTCCTCCCTTTCTTGGCAAGCTTGAAGAGCATGACCTTTTGAATCTTCTTC	1761
QY	1312	CAACAAATATCAAAGGTCCAATCCGGTGTAGGTAATCTGTATCCGTAACCTTAAGATTA	1371
Db	1762	CAACAAATCTTCAGGGGCGCAATTTCAATAGAACTGTCCGGGATTTGGCAATTTGGATAC	1821
QY	1372	GGATCTTTTCAACAACAAGATTAATGAAATCTTCCTTCTTCCCTTGGTGAATTTGGACA	1431

Db	1822	GGATATTTCCAACATATACTTAGTTGGTTCATCCCTTCCCTGGTGACTTGGAAACA	1891
Oy	1432	TCTTCTCAAGATGAACTGAGTAGAATAATCATATACTAGTGTAGTTCAGAGCGACTTGG	1491
Db	1892	TCTTCTGAAGTTGGAATCTTAGCAGAAACAATTTAAACAGAAATTAATTCAGCAGAAATTGG	1941
Oy	1492	AAATCTAAGAACATCATAGAAATAGATCTTTCAAATAATGATATCTCTGGCCCAATTCC	1551
Db	1942	AAATCTTAGAAGTGTATGAGAAATTGATCTTTCAAATATATCAATCTCTGGCTGATTTCC	2001
Oy	1552	AGAAAGCTTAAACAATTACGAACATPATTTTGTCTGAGACTGGAATAATACTGCAC	1611
Db	2002	TGAATGAACCTTAGAGCTTCAAAAACATGATATCTTGAGACTTTGAAAATAACAAATTGAC	2061
Oy	1612	TGATPATTTGGTTCAATAGCCCAACTGTCAGTCTCACTGATTTGAATGATCTCATTA	1671
Db	2062	TGGCGATGTGGCACTACCTTTCAAAATGTGATTAAGTCTCTCTACTPATATGTGTCTATA	2121
Oy	1672	CAACCTGTAGTGATATCCCTAAGAAACAATACTTCTCAAGATTTTCAACGACGTT	1731
Db	2122	CAACTATTTTGGTGTATTCCTCCACGAGTAACAATTACAGGTTTCCCTCGACAGTTT	2181
Oy	1732	CATTGGCAATCTGTGTCTTTGGCGTAGTGGCTTAACTACACCGTGTATGATTTCTCGTC	1791
Db	2182	CATTGGAACCTGTGTGTGTGTATGTGCTAAATTTGCCGCTCATGTGTGTCTGCC	2241
Oy	1792	AACTGTACGATGTCAATCTCTAAGACGCTAATCTTGGAAATACCTPATTTGGGGACTGT	1851
Db	2242	TTCAAGCGAATTAACATTAATCTTAAGCGCTGCCATTTCTTGGAAATTAATCTTGTGTGCCCTTGT	2301
Oy	1852	GATCCCTTCTCATGCTCTTTAATAGCAGCTTGGCGACGCGATATTCCTCTCTTTCTTGA	1911
Db	2302	GATCTCTTATATGATATTTGCTGTGGACGTGGCAACAATAGTCCCTCTCTTTTCCGTA	2361
Oy	1912	TGATCACTTGACAAACCAAGTAATTAATTGACACCGAGTGTCTATCTTCAATAGAA	1971
Db	2362	TGGAATCAATTTGACAAACCAAGTAATTTTCTCCCCCAAGCTAGTGAATCTTCAATAGAA	2421
Oy	1972	CATGGCACTCCAGCTTTTACAGAGATATCATGAGAAATGACAGAAATCTAATGTGAAAGTA	2031
Db	2422	TATGGCACTACATGTGTATGAAAGATATCATGAGGATATCTGAAACCTGAGTGGAAAGTA	2481
Oy	2032	TATCATTTGGGACCGAGCATCAACACTGTATACAAATGTGTTTTGAAGATTTGTAAC	2091
Db	2482	TATATTTGGAATATGAGAGATCAATCAAGTTTAAATATGTGTCTTAAGAAATTCAGACC	2541
Oy	2092	GGTTGCGATTAGCGGCTTTACTCTCAACCCACAGTCAATGAACAAGTTTGAACAGA	2151
Db	2542	GGTGGCTATCAGAGAGATCTAATCTCACTATCCCAATGTATTAAGAAATTTGAACTGA	2601
Oy	2152	ACTGAGATGCTAATGTAGCATCAAGCAACAGAAATCTTGTAGCGCTAAGCTTATTCCT	2211
Db	2602	ACTTGAGACGGTGTGGACATCAACGACCGGAATCTGTCTCAAGGTTATATTCCT	2661
Oy	2212	CTCTCACTTGGGGAGTCTTCTGTCTTATGACTAATTTGGAAATGTAGCCTCTGCGATCT	2271
Db	2662	GTCCCAATATGGGATCTCTGTGTTTATGACTACATGGAATATGGCAGTGTATGGATCT	2721
Oy	2272	TCTTCATGGCCCTTACGAGAAAAAGACTCTTGATTTGGGACACACGCGCTTAAGATAGATA	2331
Db	2722	TCTTCATGSACTTACCAAGAAAAAGCTTGACTGGAGACCTGTGCTTAAAAATAGCACT	2781
Oy	2332	TGGTGACGACAAAGTTTAGCTTATCTACACCAATGATGCTAGTATCCAGAGATCATTTCCAG	2391
Db	2782	TGGAGCAGCACAGAGGCTGTGCTTATCTACACCAATGATGCTGTCTTGAATCATCTCCAG	2841
Oy	2392	AGAGGTAAAGTCGCCAAACTCTCTTGGAACAAAGACTTAAAGGCGCTTGTGACAGATTT	2451
Db	2842	AGATGTAAAAATCTATAACTTCTAATTTGATGCGACACTTGAAGCTCATCTCACTGATTT	2901
Oy	2452	TGGAATAGCGAAAAGCTTGTGTGTGTCAAACTCATATCTTCAACTTACGTTAGTGGCAC	2511



Db	2502	TGGCATTTGCCAAAAGTCTCTGCGCCCTCAAAGTCCCATCTTCTACTTACATATATGGGCAC	2961
Qy	2512	GATAGGTTACATAGACCCCGAGTATGCTCGCACTTCACGGCTCACTGAGAAATCCGATGT	2571
Db	2562	AATTGGCTATATAGACCTGTAGTATGTAGAACTTACGCTCTCACTGAGAAAGTGTGATGT	3021
Qy	2572	CTACAGTTATGGAATAGTCTCTTTGAGTTGTAAACCGAAGGAAAGCCGTTGATGACGA	2631
Db	3022	GTAACGTTACGGTATATGTTTTACTTGAGTTGCTAACCTGGAAGAAAGCTGTTGCAATGA	3081
Qy	2632	ATCCAAATCCACCACTGATATATGTCAAAGCGGGGAAACAATGAAAGTATGGAATGGC	2692
Db	3082	ATCCAACTCCACCACTGATATTTTGTCCAAAGGACMAACAATGCAAGTATGAGAAACGT	3141
Qy	2692	AGATCCAGACATCACATCGAGCGTGTAAAGATCTCGTGTGTGAGAAAGTTTCCACT	2751
Db	3142	TGATTCAGACATTACTGCGACATGMAAGACCTTAGAGCTGTAAAAAGTTTATCACT	3201
Qy	2752	GGCACTCCCTATGCAACCAAAAGACAGCCGAATGATGACCCCAATGACCCAGGTGACTCG	2811
Db	3202	TGCTCTATTATGCAAAAGAGGACGACGCTGATAGCGCGCAATGACGAAATGACAGC	3261
Qy	2812	TGTTCTCGGCGAGTTTATGCTATC-----GGAAACAACACTGCTGCTGCAC	2856
Db	3262	TGTACTCGGAAGCCTTGTGCTGTCAAAACCCCAACCAAGCAACTAGTGTGACCAACC	3321
Qy	2857	TGACACGTCAGACGACGCTGGCTGTGTGCTGACTGATGAGTATGCAAAATCTCAAGAC	2916
Db	3322	TGCTTCAAAATCAATCTGCGCAAAAGTCCATGCTACGTGATGATGATGCAAACTTCAGAC	3381
Qy	2917	TCTCATTTCTGTCAATTGCTCTTCCATGAGTGTCTGATCTCAACTGTTCTTCGGTT	2976
Db	3382	TCCACACTTGGTGAACGTGCCCTCAATGAGCACCTCAATGTCAACTTCTCTCAAGTT	3441
Qy	2977	TGACAAAGTTATTTCTCAAAACAGTGAAT	3005
Db	3442	TGGAGAGTAATCTCTCAAAACAGTGAAT	3470

RESULT 5  
US-10-449-902-23703  
; Sequence 23703, Application US/10449902  
; Publication No. US20060123505A1

APPLICANT: National Institute of Agrobiological Sciences.  
 APPLICANT: Bio-oriented Technology Research Advancement Institute  
 APPLICANT: The Institute of Physical and Chemical Research.  
 APPLICANT: Foundation for Advancement of International Science.  
 TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF  
 FILE REFERENCE: MOA-A000571-US  
 CURRENT APPLICATION NUMBER: JP/10/449, 902  
 CURRENT FILING DATE: 2003-05-29  
 PRIOR APPLICATION NUMBER: JP 2002-203269  
 PRIOR FILING DATE: 2002-05-30  
 PRIOR APPLICATION NUMBER: JP 2002-383870  
 PRIOR FILING DATE: 2002-12-11  
 NUMBER OF SEQ ID NOS: 56791  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 23703  
 LENGTH: 3673  
 TYPE: DNA  
 ORGANISM: *Oryza sativa*  
 PUBLICATION INFORMATION:  
 DATABASE ACCESSION NUMBER: AK073793  
 DATABASE ENTRY DATE: 2001-12-06  
 JS-10-449-902-23703

	Query Match	42.3%	Score 1343.8	DB 6	Length 3673
	Best Local Similarity	67.6%	Pred. No. 0		
	Matches 1969	Conservative 0	Mismatches 917	Indels 25	Gaps 5
Qy	112 TCCTCTTCGCTTGA	CTTAGTACGTAC	TGTGACCTTCA	GAGAGGAGCA	ACCTTCTGGA

[illegible]

OY	1252	TGGGCACTATACC	CGAGGATTTTCAA	AAGCTGAAAGTATG	CTACCTTAATCTGTCAG	1311
Db	1358	TGGGCACTATCCT	CTTCAATTCGATTA	AACTTGAGAGCATATG	ATTGGAATTTGTCTATC	1597
OY	1312	CACAAATATCAA	AGGTCCCAATCC	GGTTAGCTATCTGTAT	CCGGTAACTTAAGATACAT	1371
Db	1598	AAATTTCTTA	AGTGTTCTAAT	TCATTTAGAGCTAT	CGAATTCACAAATTTGGAC	1657
OY	1372	GGATCTTTTCAA	CAACAAAGATTAAT	TGGAATCATTTCTTCTT	CCCTTGSTGATTTGGAGCA	1431
Db	1658	GGATTTATCC	CTGTAAACATGAT	TTCAGGCCCAATTC	CATCAACCAATGGAGATTTGGAGCA	1717
OY	1432	TCTTCTCAAGAT	TGAACCTTGAGTA	AAATCATATAACGTGAT	GTAGTTCAGGCGCACTTTGG	1491
Db	1718	TCTATTAAGACT	TAACTTGAGCA	CAATGTGCTT	AGATTCATCTTCGCAAAATTTGG	1777
OY	1492	AAATCTAAGAA	GCATCATGA	AAATAGATCTTTCA	AAATATATATCTTGGCCCAATTC	1551
Db	1778	CAACTTGAGAG	GTATCATGAGAT	TGATATATGCCA	CAATCATCTTGGCGGTTGATTC	1837
OY	1552	AGAAAGCTTA	CAACCAATTA	CCGAATATTTTGCT	GTAGACTGGAAAAATATTAAC	1611
Db	1838	TCAAGAACT	CGAAATGCTGCA	AAATCTGATGTTTAA	TATCTCAAAACAAACATTAAC	1897
OY	1612	TGATTAATG	TGTTGCTCAT	TAGCAACTGTCT	CAGTCTCACTGATTTGAATGATCT	1671
Db	1698	TGGGGATGTCT	CTTCACTGATGA	AACTGCTTCA	AGCTCAATCTTAATATGATCT	1957
OY	1672	CAACCTGTAG	GTATATCCTTA	GAACATTAATCTTCA	AGATTTTACCAGACGCTT	1731
Db	1958	TAAATTTGGCT	GTGTGTGTACT	CACTGATTAACAT	CTTCCACGGTWTTCGCTCGACAGCTT	2017
OY	1732	CATTGGCAAT	CTGTGCTTTT	CGGGATGTGGCT	TAAACCTCACCGGTATATGATCT	1791
Db	2018	TTTGGGTAT	CTCAGACCTTT	GTGGATATATG	AGCTTGTCTTCGTGCGCTTATCT	2077
OY	1792	AACGTACAG	ATGTCAATCTCT	TAAGCAGCTAAT	CTTTGGAAATAGCTATTTGGGGAC	1851
Db	2078	TCAACAGAA	ACCACTAATCTCA	AAAGGCTGCAAT	ACTTGGAAATTCGCGGGGTGGGCTTGT	2137
OY	1852	GATCCTTCT	ATGATGCTTAAT	ATAGCAGCTTGG	CCGACCGATATATCTCTCTCTTTCTTGA	1911
Db	2138	TATCCTCT	CTGATGATCTTA	GTAGGGGTCTG	AGGCTCATATGTCACCTGTTTCAAGA	2197
OY	1912	TGATATCA	CTTACAAACAC	AGTAATCTTAT	TTCGACACCGAGCTCGTCAATCTCTTATGAA	1971
Db	2198	TGTCTGT	GTATGCAAAAC	AGTACGAATGTTCC	CCCAAGCTGGTATCTTCAATGAA	2257
OY	1972	CATGGCACT	CAAGTTTAC	GAAGATATCAT	GAGATGACAGAAATCTTAAGTGAAGTA	2031
Db	2258	CCTTTCCCT	CTTGTATACG	AGATATATATAC	ATGACTGAAAAACCTGAGTGAAGTA	2317
OY	2032	TATATTTGGG	CAGGAGCATCA	ACACATGATTA	CAATATGTTTGAAGATTTGTAAC	2091
Db	2318	CATATAT	TGGGTAGAG	AGCATCAGACGGT	TATTAATATGTTTTCGAAGAACCCGAAC	2376
OY	2092	GGTTGCAAT	TAAAGCGCTT	TAATCTCA	CAACCCACAGTCAATGAAACAGTTTGAAGAGA	2151
Db	2377	AGTGGCAGT	AAAAAGCTAT	ATGCCCACAT	TCCACAGAGCTTCAAGAAATTTGAACTGA	2436
OY	2152	ACTGAGAT	TGTAAGTAG	CATCAAGAC	ACAGAAATCTTGTAGGCTTACAAGTTATTCCT	2211
Db	2437	GCTTGAG	CTGTGTGAT	GCATCAACACCG	GAATCTATGTCAGTCTTCAAGGATATTCCT	2496
OY	2212	CTCTACCT	TGGGAGCTTCT	GTCTATGAT	CTATTTGGAATATGTAAGCTCTG	2271
Db	2497	ATCTC	GTGGAATCTTCT	CTTCTAGAT	TATCATGGAATATGGAAGCCTCTG	2556
OY	2272	TCTTCA	T---GGCC	CTACAGAAAAA	AGACTCTTGATTTGGACACAGCGCTTAAGATAGC	2328
Db	2557	TTTGCAT	TAAGAGTCA	CTAATAAGAAAAA	CTTGATTTGGAAAACTGCTACGAATTTGC	2616

OY	2329	ATATGTGCGACGAAGAGTTAGCTTATCTACACCAATGCTGTATGCCAAGATCATTTCA	2388
Db	2617	TCATAGTGGCGGCCCAAGGCCCTTGTCTTATCTTCATCCATGACGTATAGCCACAGGATTAATCA	2676
OY	2389	CAGAGACGTGAAGTGCCTCCAACTTCTCTTGAGCAAAAGACTTATAGAGCTCGTTTACAGA	2448
Db	2677	CAGGGAATGTGAATTCAAAAATATATCTCTTGATTAAGATTTATAGGCACATCTTACAGA	2736
OY	2449	TTTTGGAATAGCGAAAAGCTTGTGTGTGTCAAACTCACATACTTCAACTTACGTATGGG	2508
Db	2737	CTTTGGCATTTGTAAAGATTGTGTGTATTAAAAAATCACACGTCCACTATATGTCATGGG	2796
OY	2509	CAGCATATGTTACTATAGACCCCCGATATGCTCGCACTTACAGGCTCATCTGAATCCGA	2568
Db	2797	AACATATGGCTATATTCATCTCTGATATGCTCGCACCTCCCGTCTCATATGAATTAAGTCTGA	2856
OY	2569	TGCTTACAGTTATCGAATATGCTCTTGTGTGATTTTAAACCGAAGAAAGCCGTTGATGA	2628
Db	2857	TGCTTACAGCTATAGGACATGTCTTGTGTGTGAGCTGTACCGGAAAAAAGCCAGTGCATA	2916
OY	2629	CGAATTCGAATCTCCACCATCTGATTAATGTCAAAACGGGGAAACAATGAAGTATGATAAT	2688
Db	2917	CGAATGCATATCTCATATCACTTGTATCTTGTCAAAAGCGGCTAAACATCTGTTCATATGGAC	2976
OY	2689	GGCAGATCCAGACATCAATCGACGTGTAAAGATCTCGTGTGTGTGAAGAAAGTTTTCCA	2748
Db	2977	AGTCGACCCCGACATGTGCAGACACTTCCAGAGATCTTGGTGAAGTCAAGAAAGTGTTCCA	3036
OY	2749	ACTGGCACTCTCTATATGCACCCAAAAGACAGCCGATGATTCGACCCACAATGCAACCAAGTGAC	2808
Db	3037	GCTGGCCCTCTCTTGTGCACCAAGAGACAAACATCGGATCGGCCGACAAATGACAGAGTGTGT	3096
OY	2809	TCGTGTTCTGGGCAAGTTTTATNGCATATGGAAACAACCACTGTGTGC-----GACTGA	2859
Db	3097	GCGCGTCTTGGACTGCTCTAGTTGTCTCCGACCCGCCACCAAGTCCGCAACAGACAGCTGGC	3156
OY	2860	CACGTCAAGCAGCGCTGAGCTGATTCGTGTGCTACGTGTGATGATATGCAAAATCTCAAGACTCC	2919
Db	3157	CATCCCGCAGAGGCGCTGTCTGTCCCGAGCTACATCAACGAGTATATGTCAGTTTAAAGAGCAC	3216
OY	2920	TCATTTCTGTCAATTGCTC---TTCCATGAGTGCTTCTGATGCTCACTGTCTTCTTCGGTT	2976
Db	3217	CAGCGTGTCTCTCGCGCCCAACTCGTGTGTACTTCCGATGTGAGCTGTCTTCTCAAGTT	3276
OY	2977	TGGAACAAGTATTTCTCAGAAACAGTAGATAG	3007
Db	3277	TGGGAGGTCAATTTCTCAGAAACAAGATAG	3307

```

RESULT 6
US-10-519-135-9
; Sequence 9, Application US/10519135
; Publication No. US20060137041A1
; GENERAL INFORMATION:
; APPLICANT: The Australian National University
; TITLE OF INVENTION: METHOD OF PRODUCING PLANTS HAVING ENHANCED TRANSPIRATION EFFICIENCY
; TITLE OR INVENTION: PLANTS PRODUCED THEREFROM
; FILE REFERENCE: 94348/MRO
; CURRENT APPLICATION NUMBER: US/10/519,135
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: AU PS3339
; PRIOR FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 2901
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana ERECTA homolog
US-10-519-135-9

Query Match      35.2%; Score 1117.6; DB 6; Length 2901;
Best Local Similarity 64.0%; Pred. No. 0;
Matches 1741; Conservative 0; Mismatches 964; Indels 15; Gaps 3;

```

131 GTAGCTCTGAGCTTCAGAGGAGGAGCAAGTTGCTGGAGATTAGAGTCATTCAAA 190  
64 GTTGCTTCGGCTATGAGCAAGAGGAGAAAGCTGTGATGGCATTAAGAGCTTTTACG 123  
191 GATGTGAACAATGTTCTTTATGACTGAGCAACTTCACCTTTCTGGATTATGTGTG 250  
124 AACTTATGATATGCTTTTGGATTGGGACGATGTTCAACAAGTACTGTGTCTTGG 183  
251 AGAGTGTGCTTGTGAAAAATGTCACTTCATGTTGTGTCTTATTTGTGAGATTGG 310  
184 CGAGGTGTTTTTGGGCAACGTTAGCTACCTGGTGTCTCTGGAATTTGTCCAGTGG 243  
311 AATCTTGATGAGAAATCTCACTGCTATTGAGAGATCTCAAGAGTCTCTTGTCAATGAT 370  
244 AATCTTGAGAGGAGATATCTCCAGCTATTGGAGACTTACGGAATTTGCATCAATGAC 303  
371 CTGCGAGGTAATCGCTGTGTGCAAAATCCCTGATGAGATTGGTGAAGTCTTCTTGG 430  
304 TTGCAAGTAAATAACTAGACAGGTCAAAATCCAGATGAGATTGGAACTGTGCTTCTT 363  
431 CAAAATTAAGCTTATCTCTCAATGAAATTAAGTGTGACATACCGCTTTTGTGCAAG 490  
364 GTTATCTGATTTGTCCGAAATCTGTATATGAGACATACCTTTCTCAATCTTAA 423  
491 TTGAGCAACTGAGCAGCTGATCTGAGAAATTAACCAATGATAGGACGATCCCTTCA 550  
424 CTCAGAGAGCTTGAACCTGAAATCTGAAGACAAATGACCTCACAGGTTCTGTACAGCA 483  
551 ACACTTTACAGATTCGAAACCTGAAAAATTTGAGACTTGGCAGAAATTAATCTCAGTGT 610  
484 ACCTTAACCCAGATTCGAAACCTTAAGAGACTTGTATCTGTGCAATCAATCAAGGTT 543  
611 GAGATACCAAGACTTATTTACTGGAATGAAATCTTCAATCTTGGGTTGCGAGAAAC 670  
544 GAGATATCGAGATTGCTTACTGGAATGAAATTTTGAATCTTGAATTAACGAGGAAAT 603  
671 AACTTATCGGTAACATTTCTCGAGATTGTTGTCACATGACTGTCTTTGGTATTTTAC 730  
604 ATGTTGACTGGAACGTTATCTTGTGATATGTGTAGCTAACCGGTTGTGTACTTTGAT 663  
731 GTAAGAAACAACAGTTTGAAGTGTAGTAATCTGAGACGATAGGAAATTTGACCTTCT 790  
664 GTGAGAGAAATATCTAATCTGGAACCATCCGAGAGCAATCGAAATTTGACAAAGCTTT 723  
791 CAGGTTTGGACTTGTCTTACATCACTACTGTGAGATCCCTTTTGAATGTGCTTC 850  
724 CAATCTCGACATATCTTATATCAATTAACAGAGAGATTCCTTCAATATGAGCTTC 783  
851 CTGCAAGTTGCAACATATCATCTGCAAGGCAATCACTCTGCGGAAGATTCATCAGTG 910  
784 CTCGAACTGTCTACTCTGTCACTTCAAGGAAACAGATTTGACGGGTAGAAATTTCCGAAAT 843  
911 ATTGTTCTCATGCAAGCCCTTGCAGTCTTGAATCTAAGTGGCACTTGTGAGTGAATCT 970  
844 ATTGTTTAAATGACAGGCTCTGCTTTTGGATTGAGTGAATGAGCTTGTGTGCT 903  
971 ATTCTCTCGATTTCTGGAATCTTACTTTACCGAGAAATTTGATTTTGCACAGTAACAG 1030  
904 ATCCCAACCGATCTTGGCAATCTCTCAATTAACCGAAAGTTGTATCTTCAATGGAATATG 963  
1031 CTGAGCTGTTCAATTCACCGTGAAGCTTGGAAACATGTCAAAATCCCATTTACCTGGAATCTC 1090  
964 CTCACCTGTCAATCCCTCTGAGCTTGGGAATATGTCAAGTCTCAGCTATTTGACAGCTA 1023  
1091 AATGATTAATCATCTCAGGAGTCATATACCAAGAGCTTGGGAAGCTTACTGATCTTGT 1150  
1024 AAGCAAAATAACTAGTGGGAATATTCACCTGAGCTTGGAAAGCTGAGCAATTTGTT 1083  
1151 GATCTGATGTGGCAACATGATCTGAGAGAGCTTATCCTGATCATCTGAGCTTTGCT 1210  
1084 GAACTGAATCTTGGCAACACCGTTTATGAGGCGCCATACCATCAACATTAATGATCAATGT 1143

1211 ACAATCTAAACAGCTTAAATGTTTATGGAACAGTTTATGAGCATATATACCCGAGCA 1270  
1144 GCAGCTTGAATCAATTCATATGTTTATGGAACCTCTGAGTGTGATCTATTCACCTGGCG 1203  
1271 TTTCAAAAGCTAAGAAATGATGACTTACCTTAAATCTGTCCAGCAACAATATCAAGTCCA 1330  
1204 TTTTCGAAATCTCGGAGCTTGAATCTGAAATCTTGTGCGAAACAATTTCAAGGAGAAA 1263  
1331 ATCCGGTGAAGCTATCTGATCGGTAATCTTGAATACATTTGATCTTTCAACAACAG 1390  
1264 ATACCACTGAGCTTGGACATATATCAATCTTGACAACTGAATCTGTCTGGCAATAC 1323  
1391 ATAAATGAATCATCTCTCTCTCTGATTTGAGAGATCTTCAATGAATCTTGA 1450  
1324 TTCTCAGGAGTCTATACCATTAACGTTGGGATCTTGAACACCTTCAATTAATCTT 1383  
1451 AGTGAATATATTAATGTGTAGTTCAGGGGACTTTGGAAATCTAAGAACATCATG 1510  
1384 AGCAGAAACCATCTTATGTGACAAATTAACCTGACAGAGTTGGGAACCTTGCAGACATTCAG 1443  
1511 GAATATGATCTTTCAAAATATGATATCTGAGCCCAATTCAGAGAGCTTAACCAATTA 1570  
1444 ATGATTTGATATATCATTCATCTGCTCTCCGAGTTATTCACATGAACTTGGCCAAATGG 1503  
1571 CAGAACATTAATTTTGTGAGACTGAAAAATTAATTAACCTGATGTAATGTT---GGTTCA 1627  
1504 CAGAAATTTAACTTTTAAATTTGAACACACAGAGCTTATGGAATTTCCAGATCAG 1563  
1628 TTAGCCACTGTCTCAGCTCACTGATTTGAATGATATCTATTAACAACCTGTGATGAT 1687  
1564 CTTACGAAACGCTTCACTCTTGTCAATCTGAATGTCTCTTCAACAATCTCTCGGATA 1623  
1688 ATCCCTAAGAACATTAATCTCTCAAGATTTTACAGACAGCTTCAATGGAATCTGAT 1747  
1624 GTCCACCAATGAAAAATCTTCACTGTTTGTCTCCAGCCAGCTTTGTGGAATTCATAT 1683  
1748 CTTTGGGTAGTTGGCTTAACTCAACCGTGTATGATTTCTGTGAACTGTACAGATGTCA 1807  
1684 CTTTGTGGAACAGTGGGTGATCTAATTTGTGTGCTTTACGAAATCTGCA-----GTA 1737  
1808 ATCTCTAGACAGCTATCTTGAATATGCTAATTTGGGGAATTTGTGATCTTCTCATGTCT 1867  
1738 TTCTCCAGAGCTCTTGTGATCTGATTTGTCTTGGGTATCACTCTCTATGATGATTT 1797  
1868 TTAATGCACTTGGCCGACCGCAATATCTCTCTTTCTGATGATCACTTGACAA 1927  
1798 TTCTTGCAGTTTAACAATTAATGACAGAGAAAGTTTACAAAGCTC-----CTCA 1851  
1928 CCAATTAATTTTGCACCCGAGCTGTGATCTTCTATATGAACATGGCACTCAAGTT 1987  
1852 AACAAGCTAAGAGTTTAAACAGCTAGTATCTCCACATGACATGGCAATTCATATCA 1911  
1988 TAGAGGATATCATGAGATGACAGAGATCTAAGTGAAGATATCATTTGGGACGGA 2047  
1912 TTTGATGATATCAATGAGAGCTGAGAAATCTTAAGAAAGTTTATTAATGATATGAT 1971  
2048 GCATTAAGCACTATTAACAATGTGTTTGAAGAATTTGTAACCGGTTGGATTTAAGCGG 2107  
1972 GCTTCTAGCAGGATTAACAATGTGATTAAGTTTCCGACCTATTTGCAATTAAGCGA 2031  
2108 CTTTACTCTCAACACCACAGTCAATGAACAGTTTGAACAGAACTCGAGATGCTAATG 2167  
2032 CTCTACATCAATATCCGATTAACCTTGGGGAATTTGAGACAAACTGTGACCAATTTGG 2091  
2168 AGCATCAAGCAAGAAATCTTGTGAGCTTACAAAGCTTATTCCTCTCTCACTTGGGAGT 2227  
2092 AGCATTTAGGCAAGAAACATATGACGCTTGCATGATATGCTTGTCTCTACTGCGAAC 2151  
2228 CTTCTGTTCTATGATATTTGGAATGTAAGTGTGAGCTGATCTTCTTCAATGGCCCTACG 2287  
2152 CTTCTTTCTATATCATATGAGAAATGATCACTTTGGGACCTTCTTCAATGGGCTATTG 2211  
2288 AAGAAAAAGACTTGTGATTTGGGACACAGCGCTTAAGATACATATGTTGACAGCAAGGT 2347

Db 2212 AAGAAAGTGAAAGCTTGATGGGAGCAAAAGTTGAAGTAAGCCGTTGGAGCTGCACAAGGA 2271

Qy 2348 TTAGCTTACTACACCATGACTGTATGTCCAAGGATCATTTCAAGAGACGTGAAGTCGCC 2407

Db 2272 CTAGCCTATCTTCAACCAAGATTGTACTCTGGAATCATTTCAACCGTGAATCAAGTCATCG 2333

Qy 2408 AACATTTCTTGGACAAAGACTTAGAGCTCGTTGAACAGATTTTGGAAATGCGAAAAGC 2467

Db 2332 AACATACCTTCTGAAGAAATTTCCAAACACATTTATCTGATTTTCGGATTTGCTAAAGGC 2391

Qy 2468 TTGTTGTGTCAAAGTCAATCACTTCAACTTACGTATGGGACAGATAGTTACATAGAC 2527

Db 2392 ATACAGGTAGCAAAAACCATGCCCTGCACCTTATGTTTGGGAAACAATTGGTTATATAC 2453

Qy 2558 CCCGAGTATGCTCGCATTCCAGGCTCATGGAATCCGATGTCTACAGTTTGAATA 2587

Db 2452 CCAGAGTATGTCTGACTTTCAGATCAATGAGAAATCCGATATATACAGCTTCGGTATT 2511

Qy 2588 GTCTCTTCTTGAAGTTTAAACCGAAGAAAGCCGTGATGACGATTCATCTCCACAT 2647

Db 2512 GTTCTTTCTTGAAGCTTCTCACTGGGAAAGAGCATGTATACGAGACTTACTGATATA 2571

Qy 2648 CTGATATATGTCAAAGACGGGAAACAATGAATGATGAATGGCAGATCCACAATCA 2707

Db 2572 CTGATATATGTCAAAGGCTGATGATATATCTGATGAGAAGCAGTTGATCCAGAGGTTACT 2633

Qy 2708 TCGACGTGTAAGATCTCGGTGTGTTGAAGAAAGTTTCCAACTGGGACTCTATATGACC 2767

Db 2632 GTGACTTGTATGGAATTTGGGACATATCCAGGAAGACATTTTCAGCTGGCTCTTATGACA 2691

Qy 2768 AAAAGACACGCGAATGATCGAACCCACAATGCAACAGGTACTCGTGTCTCGGACGTTTT 2827

Db 2692 AAGGAAACCTTTTAGAGAGACCCACAATGCTGTGAAGTCTTAAGGTTCTGCTCTCTTT 2753

Qy 2828 ATGCTATGGAACAACACC 2847

Db 2752 GTCCCATCTCGAAGTAGC 2771

RESULT 7  
 US-10-519-135-7  
 : Sequence 7, Application US/10519135  
 : Publication No. US20060137041A1  
 : GENERAL INFORMATION:  
 : APPLICANT: The Australian National University  
 : TITLE OF INVENTION: METHOD OF PRODUCING PLANTS HAVING ENHANCED TRANSPIRATION EFFICIENCY  
 : FILE REFERENCE: 94948/MRO  
 : CURRENT APPLICATION NUMBER: US/10/519.135  
 : CURRENT FILING DATE: 2004-12-22  
 : PRIOR APPLICATION NUMBER: AU P53339  
 : PRIOR FILING DATE: 2002-07-02  
 : NUMBER OF SEQ ID NOS: 45  
 : SOFTWARE: PatentIn version 3.1  
 : SEQ ID NO 7  
 : LENGTH: 2751  
 : TYPE: DNA  
 : ORGANISM: *Arabidopsis thaliana* ERRECTA homolog  
 US-10-519-135-7

Query Match	33.8%	Score 1074.6;	DB 6;	Length 2751;
Best Local Similarity	64.0%	Pred. No. 1.3e-11;		
Matches 1717; Conservative	0;	Mismatches 904;	Indels 60;	Gaps 4;

QY 168 TGGAGTTAAAGACGATTCGAAAGTGTGAAACAATGTCCTTTATGACGTGACCACTTCAC 227

Db 2 TGGCGATTAAAGCGCTTCATTCACGACACGTCGGCAATATGCTCTTATGTTGGAGCAGATGTC 61

QY 228 CTTCCTCGATTATTTGTGCTCGAGAGGTGTGCTTGTGAAATGTCACTTCATGTTG 287

Db 62 ATAAACACGACCTTTTGTTCTTGAGAGAGGTGCTCTTGAGTAACGTTAGGCTCCATGTTG 121

QY	288	TTGCTCTTAATTTTGTCAGATTTGAATCTTGATGGAAGAAATTCACCTGCTATTGGAATC	347
Db	122	TCTCTCTTAATCTGTCAAACTCGAATCTTGGTGAGAGATATCATCTGCCCTTGAGATT	181
QY	348	TCAAGAGCTCTGTCATTTGATCTGGAGGTAATGCGTTGTCTGGACAATTCCTGATG	407
Db	182	TGATGAATCTGCAAATCAATAGACTTGGAGAAGAAATTAATTTGGGTGTCAAAATTCAGATG	241
QY	408	AGATTGTGACGTGTTCTTCTTTCGAAAAGTTAGACTTATCCTTCATAGAAATTAAGTGTG	467
Db	242	AGATTGGAAATCTGTGTTTCTCTTGCTATTATGATGATTTCTCACCAATTTGTTGTTGGAG	301
QY	468	ACATATCCGTTTTCGATTTTCGAGTTGAAGCACTTGAGACAGCTGATTTCTGAAGATAAAC	527
Db	302	ACATATCCGTTTTCATCTTAATCTCAAAACAGCT-----	335
QY	528	AATTGATGAGACGATCCCTTCAACAGTTTCAGATTTCCAAACCTGAAAATTCGAGCT	587
Db	336	-----GACCTTAATCAGATTTCCAAACCTTAAGACCTTGGACC	373
QY	588	TGGCAGAGATTAACCTGAGTGTGAGATACCAAGACTTAATTTACTGGAATGAATTCCTTC	647
Db	374	TTCGAGAAACCAACTTAAGTGTAGATACCAAGATTAAGTCTACTGGAATGAATTCCTTAC	433
QY	648	AGTATCTTGGTTTCGAGAGAAACAATTAGTCGTAACAATTTCTCCAGATTTGTGTCAAC	707
Db	434	AGTATCTCGGTTTACGTGGGAATATGTTAACTGSGGACATGTCTCTGATATGTTGTACG	493
QY	708	TGACTGTGCTTTGGTATTTTGAACCTTAGAAACAAGTTGACGTGATATTAAGTATACCTGAG	767
Db	494	TGACGGGTCTGTGTACTTGTGATGTGAGAGCAACAACCTTACTGGAACATAATCCACAGGA	553
QY	768	CGATAGGAATTTGACATGCTTCCTCCAGGTTTTCGACTGTCTTACAAACAGCTTAACCTGATG	827
Db	554	GCATTGGCAATTTGACACAAGCTTTGAGATCTTGGATGTATCTTATATACAGATTTACCGGAG	613
QY	828	AGATCCCTTTTGAATCGGCTTCTCTGCAAGTTGACACATTATCTTTCGAAGCAATCAAC	887
Db	614	TTATATACCTTAATATTTGGTTTCTCTCCAGTAGTCTACTGTCACTTCAAGGAATAACAGT	673
QY	888	TCTCTGGGAAGATTTCCATCAGTGAATGCTGTCTCATGCAAGCCCTTGACGTCTTAGATCTAA	947
Db	674	TGACTGTGCAAAATTCGGAGATGATGTGTCTGAAGCAGGCTCTTGTCTGTATTTGAAATTTGA	733
QY	948	GTGGCAACTTGTGATGATGATCTAATCTCTCGATTTTCGGAATCTTAAGTTTCCACGAGA	1007
Db	734	GTGCAAAATGAATTAATCTGGGCTTAATTCACCAATACTTGGGAATCTGTCAATTCACCTGGA	793
QY	1008	AATTGTATTTGACAGATTAACAAGCTGAATGTTCAATTTCAACTGAGCTTGGAAACAATGT	1067
Db	794	AATGTATCTCATAGGCAACAAGCTCACTGGACAAATCCACCCGAGCTAGGCAATATGT	853
QY	1068	CAAAATCTCAATTAAGTGGAACTCAATGATATATCATCTCAAGGGTCAATATACACACAGAC	1127
Db	854	CACAGCTCAGCTAATTTTCAACTAATATATATGAATCAATGAGGAAGAAATCCCACTGAGC	913
QY	1128	TTTGGAAAGCTTACTGACTGTTGTTTATCTGATGATGAGGCAACAATGATCTGGAAGACCTTA	1187
Db	914	TTTGGAAAGCTGGAACAATTTGTTGCAACTGAAATCTTGGAAACAAACAATCTTGTAGGCGTGA	973
QY	1188	TACCTGATTCATCTGAGGCTCTTTCGCACAAAATCTAAACAAGCTTAAATGTTCAATGGAACAAGT	1247
Db	974	TTCATCTAATCAATTAAGTTTCCGTGCTGCTGCTGATTAATCAATTTCAATGTTCAATGGGAACTTCT	1033
QY	1248	TTAATGGCACTATACCCCGAGCAATTTCAAAAGCTAGAAAGTATGACTTAATCTATCTGT	1307
Db	1034	TGAGTGAAGCTGTACCACTTGAATTTCCGGAATCTTGGAAACCTTGAATCTTAATCTTAATCTTT	1093
QY	1308	CCAGCAACAATATCAAAAGGTCACATCCCGGTAGAGCATCTCGATAGGGTAACCTTAAGATA	1367
Db	1094	CTTCAAAACAGTTTCAAGGCAAAATTAATCTGCTGAGCTGTGGCCATATATCATATCTTGATTA	1153
QY	1368	CATTGATCTTTCCACAACAAGATTAATGAAATCATTTCTTCTTCCCTGTGATATTGG	1427

1154 CATTGATCTGTCTGGCAAAATTTCTCAGGCTCAATTCATTTAAACCTTGATCTTG 1213  
1428 AGATCTTTCAAGATGAATCTTGATGAAATATATATACGTGGTAGTCCAGGGACT 1487  
1214 AGATCTTCTCATCTTAACCTTGAGCAAAATATCGAATGGCACTTCCAGCAAAAT 1273  
1488 TTGGAATCTTAAGAGCATCATGGAATAGATCTTTCAAAATATGATATCTTGCCCA 1547  
1274 TCGGGAACCTCCAGAGATTCAGATCATCATGTGTCTTAATTTTCTTGCCGGTCTTA 1333  
1548 TTCCAGAGAGCTTTAACCAATTAAGAAATATATTTGCTGAGACTGGAATATATACC 1607  
1334 TTCCAACTGAACCTTGCCAGATGGCAAGAAATAACTCTGATCTGAAACAAACAAGA 1393  
1608 TGACTGCTATGT---TGCTTCACTTACCACTGCTCAAGTCTCACTGATATGAAATAT 1664  
1394 TTGATGGAAAATCCCTGATCAAGTAACTAATGCTTCAAGTCTTCCAAATCTGAACATCT 1453  
1665 CTCATAACAACCTCTGATGATATCCCTAAGAAACAATTAATCTTCAAGATTTTCAACAG 1724  
1454 CTTCAATTAATCTTTCTGGAATATATCCCACTATGAAAGAACTTTACACGTTTTCCCGG 1513  
1725 ACAGCTTCATTTGCAATCTGCTGCTTTGCGGTAGTGGCTAAACTCAACGCTGCATGAT 1784  
1514 CCAGCTTCTTTGGAATCCATTTCTGCGGGAACCTGGGTGATCAATCTGTGGCCAT 1573  
1785 CTGCTGCAACTGTACAGATGCAATCTCTAGAGACGATTTCTTGGAATGCTATTTGGGG 1844  
1574 CTTTACCTAAGTCAAGAT---ATTACACAGAGTGGCGGATTTGATGGTCTTCGGTT 1630  
1845 GACTTGTGATCTTCTCATGCTGTTAATAGACGCTTCCAGCCGATATATCTCTCTT 1904  
1631 TCATCACTCTCATATGATATATATCTTGCGTTTCAAGTCAACAGAGAAACAG 1690  
1905 TTCTGTGATGATCACTGACAAACCACTAATTTGCAACCGAGCTGCTATCTTTC 1964  
1691 TCTTGAAGGCTCTTCAAAACAC-----CTGAAGGCTCAACGACGCTGATCTTTC 1744  
1965 ATATGAACTAGGCACTCCAGTTTACAGAGATATGAGAAATGACAGAGATTTAGTG 2024  
1745 ACATGCACTAGGCTATTCACAGCTTATGATATCAAGAGATTAAGAAACCTCGATG 1804  
2025 AGAATATATCATTTGGCAGCAGACATCAAGCACTGTATACAAATGTTTTGAAGAT 2084  
1805 AGAATATCATATTTGATAGCGGTCTTCTAGCAAGTTTACAGTTCACACCTCCAAACT 1864  
2085 GTAAACCGGTGCGATTAAAGCGCTTATCTCTCAACCCACAGTCAATGAACAGTTTG 2144  
1865 CCCGACCTATTTGCCATTAAAGCAATCAATCAATCTCCAGCAACTTCCGCGAGTTTG 1924  
2145 AAACAGAACTCGAATGCTAATAGCATCAAGCAGAGAAATCTTGAGGCTCAACACT 2204  
1925 AAACAGAGCTCGAATGCAATTTGGAGCATCAGACACAGAAATATGTAAGCTTGCACGAT 1984  
2205 ATTCCCTCTCTCACTTGGGAGCTTCTGTTCTATGATATTTGGAATATGTAAGCTCT 2264  
1985 ACGCTTATATCTCTTTGGCACTCTCTTCTTACGATCATGGAATATGGGCTCTCTTT 2044  
2265 GGGATCTTCTCATGCGCTTACAGAAAGAAAGACTTTGATTTGGAACAACGCGTTTAA 2324  
2045 GGGATCTTCTCATGCGCTTGGGAGAGAAAGGTAAGTGAAGTGAAGGCTGTAAGA 2104  
2325 TAGATATGATGAGCAAGAGTTTACTTATCTAACACATGACTGTAGTCAAGATCA 2384  
2105 TAGCTGTGAGAGCTGCGCAAGAGCTTGCAATCTTCCACATGACTGCAACATGAGATA 2164  
2385 TTGACAGAGAGCTGAGATGCTTCAACATTTCTTGTGACAAAGACTTGAAGGCTGTTGA 2444  
2165 TCCATGAGAGATCAATGATCAAAATATCTCTTGTGAGGAATTTGGAAGCGGTTTGT 2224  
2445 CAGATTTTGAATGCAAAAGCTTGTGTGTCAAAAGTCAATATCTTCAACTTACGTTGA 2504

2225 CAGATTTTGGATTGGCCAGAGCATACAGCCACCAAACTTATGCTTCAACTATGTTTC 2284  
2505 TGGGACAGATAGGTTACATATGAGCCCGAGATGCTGCATTCAGGCTCACTGAGAAAT 2564  
2285 TTGGAACCATGATATATTTGAGCCAGAGTATCTGAACTTGCGCTGTAACGAGAGAT 2344  
2565 CCGATGCTTACAGTTATGGAATAGTCTTCTTGAAGTTTAAACCGAAGGAAGCGTTG 2624  
2345 CTGATATCTACAGTTTCGGATATGTCCTTCTTGAAGCTTTCACCGGCAAGAGGCTGTG 2404  
2625 ATGACGAATCAATCTCCACATCTGTATATGTCAAAGAGCGGGAACAATGAAATGATG 2584  
2405 ATACAGAGGCAATGTCATCAATATATCTTACAAAGCGGAGTATTAACACGTAATG 2464  
2685 AAATGGCAGATCCAGATCATCATGACGCTTAAAGTCTCGGTGATGTAAGAAATTT 2744  
2465 AAGCTTGTGATGAGAGGTTCTAGTATCTTGATCTGAGACACATTAAGAAAAAT 2524  
2745 TCCAACTGGCACTCTATGACCAACAAAGACGCGAATGATGACCCCAATGACACAG 2804  
2525 TTCAGGTAGCTCTTGTGACCAAGCAAAATCTTTGAGAGAACCAACATGACGAGAG 2584  
2805 TGACTGCTGTTCTCGGCACTTTATGCTATGGAACAACA 2845  
2585 TCTTGAAGGTTCTGCTTCACTTGTCCCGTCTCACCTTCA 2625

RESULT 8  
US-10-519-135-5  
; Sequence 5, Application US/10519135  
; Publication No. US20060137041A1  
; GENERAL INFORMATION:  
; APPLICANT: The Australian National University  
; TITLE OF INVENTION: METHOD OF PRODUCING PLANTS HAVING ENHANCED TRANSPIRATION EFFICIENCY  
; TITLE OF INVENTION: PLANTS PRODUCED THEREFROM  
; FILE REFERENCE: 94948/MPO  
; CURRENT APPLICATION NUMBER: US/10/519,135  
; PRIOR FILING DATE: 2004-12-22  
; PRIOR APPLICATION NUMBER: AU PS3339  
; PRIOR FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 5  
; LENGTH: 2766  
; TYPE: DNA  
; ORGANISM: sorghum ERECTA  
US-10-519-135-5

Query Match 33.1%; Score 1050.8; DB 6; Length 2766;  
Best Local Similarity 63.4%; Pred. No. 1.8e-304;  
Matches 1845; Conservative 0; Mismatches 882; Indels 185; Gaps 8;

112 TCTCTTCTGCTTGAAGTCTAGTACTGTCGACTTCAAGAGAGGAGCAAGTGTGCTGA 171  
24 TCTGTGCGCCCTCTCTCTGCGCGCTGCGCGAGAGAGGAGCGAGCTGCTGGA 83  
172 GATTAGAAGTCAATCAAGATGTAACAATGTTCTTATAGCTGAGCAACTTACCTTC 231  
84 GATCAAGAAATCTCTCCGCAAGCTCGGCAACGTACTGTAAGATTTGGCGCGGCAAC----- 138  
232 TTGGATATTTGTCTGAGAGAGTGTCTTGTGAATATGTCACCTTCAATGTTGTTC 291  
139 ----GACTACTGCTCTGCGCGCGCGCTCTGTGCAAGTACATTTCCGCTGCTGC 194  
292 TCTTAATTTGCAATTTGAATCTGATGGAAGAAATCTACCTGCTATTTGGAATGCA 351  
195 GCTCAACCTCTGCGCTCAACTTGAGGCGAGATCTTCCACGCGTGGGCACTTCA 254  
352 GAGCTCTTGTCAATGATCTGAGAGTATTCGCTTGTGACAAATCCCTGATGAGAT 411  
255 GAGCTCTGCTTCAATGATCTGAAGTCAATTTGGGCTATTCGGGCAAGATCTCTGATGAGAT 314  
412 TGGTACTGTTCTTTTGGCAAAACTTAAGCTTATCTTCAATGAATTAAGGTGACAT 471





QY	2628	ACGAATCCAAATCTCCACCATCTGAATTAAGTCAAAAGACGGGGAAACAATGAATGGAAA	2667
Db	2394	ACGAAATCC-----TATGGAAGACGGCAAGCAACAGGTCAATGGATA	2434
QY	2688	TGGCAGATCCAGACATCATCGACGTGTAAAGATCTGGTGTGTAAGAAAGTTTCC	2747
Db	2435	CCGTGGAACCTCGACATCTGGGGGACACTGCAAGAACTCGGGAGGTGAAGAAGCTTTCC	2494
QY	2748	AACATGGCACTCTTATGCACCAAAAAGACCCGAAATGACCCCAATGCAACCAAGTGA	2807
Db	2495	AGCTGGCGCTCTTTGACCAAGCGGCAACCTCGGACCGAACGATGACAGCGAGTGG	2554
QY	2808	CTCGTGTCTTCGGCAGTTTATGCTATGGGAACAACAACCTGTGTCGACTG-----	2858
Db	2555	TGCCCGTCTTGAGACTGCTGTGTGAACCCGGACCCGCGCCAAAGCCGTGGCGCACAGC	2614
QY	2859	ACAGTCACGACAGCTGGCTGTTCGTGCTACGTGATGAGATATGCAATCTCAAGACTC	2918
Db	2615	TGCCGCAACCGTCTGCCCAAGCCGTGCCAAGCTACATCAACGAATACGTCAAGCTTGGGGCA	2674
QY	2919	CTCATTTCTGCAATTGCTC---TTCCATGAGTGCCTTGTGATGCTCAACTGTTCCTTCGGT	2975
Db	2675	CCGCGCGCTCTCTCCGCGCAACTGCACCAACACTCTGGACGCGAGCTGTTCCTCAAGT	2734
QY	2976	TTGGACAAGTATTTCTCAAGAACATGAGTAG	3007
Db	2735	TCGGCAGAGGCATCTCCGCAAAACATGAGTAG	2766

RESULT 9  
US-10-519-135-3  
; Sequence 3, Application US/10519135

```

? publication NO. US20060137041A1
?
? GENERAL INFORMATION:
? APPLICANT: The Australian National University
? TITLE OF INVENTION: METHOD OF PRODUCING PLANTS
? TITLE OF INVENTION: PLANTS PRODUCED THEREFROM
? FILE REFERENCE: 94948/MRO
? CURRENT APPLICATION NUMBER: US/10/519,135
? CURRENT FILING DATE: 2004-12-22
? PRIOR APPLICATION NUMBER: AU PS3339
? PRIOR FILING DATE: 2002-07-02
?
? NUMBER OF SEQ ID NOS: 45
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 3
? LENGTH: 3000
?
? TYPE: DNA
?
? ORGANISM: rice ERECTA
? JS-10-519-135-3

```

Query Match	32.6%	Score	1035.2	DB	6	Length	3000
Best Local Similarity	63.8%	Pred	No. 9.1e-300				
Matches 1687, Conservative	0	Mismatches	888			Indels	69
						Gaps	5

QY	234	CGGATTAATTGTGTCTGGAGAGTGTGTCTTGTAAGAAATGTCACCTTCAATGTTGTCTC	293
Db	179	CCGACCCTGGCGGTGGCGCGCGCTCACTCCGCAACAGCCTCTTGTGGCCCTCTCGCC	238
QY	294	TTAATTGTCAGATTGNAATCTTGATGAGAGAAATCTCACTGTATTGAGANTCTCAGA	353
Db	239	TGAACCTGTCAAATCTMAAACCCTAGAGGTTGATCTCGCCGGCCATCGAGAGCTCAAGA	298
QY	354	GTCCTTGTCMAATGATCTGCGAGATATGCTGTCTGGCAACATCCGTATAGATTG	413
Db	299	ATCTACAGTTCGTTGATCTCAAGGGAAACAAGCTCATCTGGCCAAATCCCAATATAGATTG	358
QY	414	GTACTGTGTTCTTTGGCAAACTTAGACTATCTTCATGAAATTAAAGTGTGACATAC	473
Db	359	GGGACTGCATCTCTTAAATAATTGGATTGTCTGGCAACTCTGTATGGAACATATCC	418
QY	474	CGTTTTCGATTTCGAAGTGAAGCAACTTGGACAGCTGATTTCTGAAGATMAACCAATTGA	533

Db	419	CCCTTCATCTCCAGAGCTCAAGCAGCTTGAGGAGCTGATTTTGAAGAACACAGCTCA	478
OY	534	TAGAGCGATCCCTTCAACACTTTCAAGATTCCAACCTGAAAATTCGTGGCAC	593
Db	479	CGGAGCCCATCCCTTCCACATTTGTCCTCAAAATTCCAAGACATTTGACCTGGAC	538
OY	594	AGAAATTAACCTGAGGTGAGATPACCAACAATTATTTACTGGAAATGAAGTTCTTCAGTATC	653
Db	539	AGAACCAAGCTTACAGGCGATATCCCAAGGCTCATATACCTGAATGAATGTTCTGCAAATACC	598
OY	654	TTGGGTTGCGAGAAACAATTAGTCGGTTAACATTTCTCCAGATTGTGTCACTGACTG	713
Db	599	TAGGTTTAGGGGTAACTCACTGACTGAACTTTGTCACTGACATGTGGCAACTGACTG	658
OY	714	GTCTTTGGTATTTTGAAGCTAAGAAAACAACAGTTGACTGTGATGATATACCTGAGACGATAG	773
Db	659	GCGTGTGGTACTTTGATGTAAAGGGGAAAACAATCTCACAGGAGCCATTCACAGAGACATAG	718
OY	774	GAATTTGACTGCGCTTCCAGGTTTTTGGACTTTGTCTCAATACAGTAACTGTGATATCC	833
Db	719	GGAACTGACACAGCTTTGAGATTCGTGACATTTGTGTAAACCAATCTCTGGAGAAATAC	778
OY	834	CTTTTGAACATCGGCTTCTCGCAAGTTGGCAATTATCAATTGCCAAGGCAATCACTCTG	893
Db	779	CTTACAACTATAGGCTTTCTTCAAGTAGCACACTGTCACTTCCTCAAGAAATATAGACTGACTG	838
OY	894	GGAAAGTTTCCATCAGTAGTGTGTCTCATGCAAGCCCTTGCAGTCTTATGATCTTAAGTGCA	953
Db	839	GGAAATTTCCAGATGTGATGTGGCTGATGCAAGCTCTTGCTGTCTAAGCCGTGAGTGA	898
OY	954	ACTTTGAGTGAAGTATTAATCTCTCCGATCTCCGAAATCTTAATCTTACCGAGAAATGT	1013
Db	899	ACGAGCTGTAGGGCCCAATCTCTTCTAATACGTGGGAATCTATCTCAATCTGAAAACTAT	958
OY	1014	ATTTGACACAGTAACAGCTGACTGGTTCAATTCCACCTGAGCTTGGAAACAATGTCAAAAC	1073
Db	959	ATTTACATGGGAACAAACTTACTGTGAGTCATACCCCGAGCTTGGGAACATGAGTAAAC	1018
OY	1074	TCCATTACTGGGAATCAATGATATATCATCTCACGGGTCAATATACCAACAGACTTGGGA	1133
Db	1019	TTAGCTACTCTCAACTGAATGATATGAAATGTGGGGCAACATTCACAGAGCTTGGCA	1078
OY	1134	AGCTTACTGACTTGTTTGATGTGAATGTGGCCAACTAGATCTGGAAAGACTTATCCTG	1193
Db	1079	AACCTGGAAGACTTTTGAACATAATCTTGGCAACAACTTCCMAAGTCTTATCTCTG	1138
OY	1194	ATCATCTGAGCTCTTGCACAAACTTAAACAGCTTAAATGTTCAATGGGAAACAAGTTATAG	1253
Db	1139	CAAACTACATGTTCTTGCATGCTGCTTAAACAATTCATATGTTATATGCAATATAGCTAATG	1198
OY	1254	GCACATATACCCCGACATTTCCAAAAGCTGAAAAGTAGACTTACCTTATATGTCTCAGCA	1313
Db	1199	GTTCTATTTCCGTGGTTTCCAGAAAGTTGGAGAAGTCACTTACTTGAAACCTATCTTCA	1258
OY	1314	ACATATTCAAAGGTCCAAATCCCGGTGAGCTATCTCGATGGGTAACTTAAATATACATTGG	1373
Db	1259	ACAATTTCCAAAGGCAATATTCCTTCTGAGCTTGGTCAATCATCAACTTGGACACATTTGG	1318
OY	1374	ATCTTTCCAAACAAGATTAATGGAATCATTTCCCTCTTCCCTTGGTATTTGGAGCATC	1433
Db	1319	ATCTTTCTCAATGAATTTCTCTGACCAAGTTCTCTGCTTACCATTTGGTATCTAGACACCC	1378
OY	1434	TTCTCAAGATGAAGTGTGAGTAAATATATATATATGATGATCTCTGGCCCAATTTCCAG	1493
Db	1379	TTCTTGAACGAAATTTGTGATGAAGACATCTGTATGGGCCAGTTCTGTGATGTTTGGAA	1438
OY	1494	ATCTTAAGAAGCATATGGAATAAGATCTTTCAAAATATGATATCTCTGGCCCAATTTCCAG	1553
Db	1439	ACTTGAGAAGGTCCAAAGTATTTATATGTGCCAACACAACTTATCTGGTATGTGCTGCCG	1498
OY	1554	AAGAGCTTAAACCAATTCAGAAACATTAATTTTGTGAGACGTGGAAAAATTAATAACGACTG	1613
Db	1499	AGGAACTTGGACAATTCAAAACCTTGATAGCCTGATTTCTTAACAACAATTTTGGTTG	1558



1614 GTAATGT---TGGTTCATTAGCCCAAGTGTCTGAGTCTCA-----CTGATTTGAAT 1660  
1559 GGGAGATCCCTGCTCAATGGCCACAGCTTCACTTAAATTAACCTTGCAATTCAGGAAT 1618  
1661 GATATCTTAAACAACCTGAGTGTATCTTAAAGAACATTAATCTTCAAGATTTTCA 1720  
1619 TTGTGATACAAACAATTTATCTGAGCATGTCCGATGGCAAGAACTTCTGAAATTTCCA 1678  
1721 CCAGA-----CAGCTTCA 1733  
1679 ATGGAAGACATCTTCTAATTTCTGATTCGAACAGTACATAAATCATAAATGACGCTTCT 1738  
1734 TTGGCAATCTGGCTTTGGGTAGTGGTAAACGACGGTGCATGATTCGTGGA 1793  
1739 TGGGTATTCATTAATCTGATGATTTACTGCAAGATTCAGCTGTGACACTCTCATGA- 1797  
1794 CTGTACAGAGTGTCAATCTTGAAGCAGCTATTTCTTGAATAGCTATTTGGGGGAACTGTGA 1853  
1798 --CAAGAGTTAATATTTCAAAGCAGCAATGCTTGCATTAATCTTGAAGCTTATATCATAT 1855  
1854 TCTTCTCATAGTCTTAAATAGCAGCTTCCGACCGCATATCTCTCTCTTTCTTGATG 1913  
1856 TGTCTGCTGCTTGTGCTGTGCTATATATTAACAAATCAACCAAGCCACTTGTCAAG 1915  
1914 GATCACTTGAACAACAGTAACTTATGACACCGAAGCTGTCATCTTCATATGACA 1973  
1916 GATCCCATTAAGCCAGTCCAGAC-----CTCAAAAGCTAGTGTTCCTCAGATGAGCA 1969  
1974 TGGCACTTCAAGTTCAGAGATATCATGAGAAATGACAGAAATCTAAGTGAAGATATA 2033  
1970 TGGGTATTCATTAATGAGGACATCATGAGGCTGACAGAAATTTAGGAGAAATACA 2029  
2034 TCAATGGGCAACGAGATCAAGCATGTATCAAAATGTTTGAAGATTTGAACCG 2093  
2030 TCATTTGGCTTGGGGCTTCAAGCATCTGTCTCAAAATGTAATCAACAGCGGCAAGCCCA 2089  
2094 TTGGCAATTAAGCGCTTATCTTCAACCAACGATCAATGAAACAGTTTGAACAGAAC 2153  
2090 TTGCTGTCAAGCGCTTAAAGTATGATTAACATGAGAAATGTTCTTGGGATCTTC 2149  
2154 TCGAGATGCTAAGTATGATCAAGACAGAAATCTTGAAGCTTCAAGCTTATTCCTCT 2213  
2150 TAAAGCAATTTGGAGATACGAGCATACGAGAAATCTTGTATCCCTCAAGGCTTCTCGTAT 2209  
2214 CTCACTTGGGAGTCTTCTGTCTATGATCAATTTGAAAAATGTAAGCTTCTGGATCTTC 2273  
2210 CTCCACATGGAATCTGCTCTTCTATGATTAATGAAAAATGTTCTTGGGATCTTC 2269  
2274 TTGATGGCCCTTAAAGAAAGAAAGCTTGAATGGGACACAGCGCTTAAATGATGATG 2333  
2270 TCCAGGCTCATTAAGAAAGTGAAGTCAACGAGCAACAGCTGAGATGCGGCTG 2329  
2334 GTGACAGCAAGGTTAGTATCTATCTACACCATGAGTGTAGTCCAGGATCTTCAAGAG 2393  
2330 GAGCTGCAAGAGGCTGCTATCTCCACATGACTGCAACCTCGATATATCAAGAG 2389  
2394 AGCTGAAGTGTCTCAACATCTCTTGAACAAGCTTGAAGGCTGTTTGAAGATTTTG 2453  
2390 ATGTCAAGTCTCTCAACATCTGCTCAAGCAAGCTTGAAGGCGCACTTCAGATTTTG 2449  
2454 GAAATAGGAAGCTTGTGTGTGCAAGTCACTTCACTTGAATGAGTGGGACGA 2513  
2450 GCAATAGCAATATGTCTCTGCTCAAGTCCAGTCTCACTTATGTCTAGGAACCA 2509  
2514 TAGGTTACATAGACCCGAGTATGCTGCACTTCAAGGCTCACTGAGAAATCCGATGCT 2573  
2510 TCGGCTATCAATGATCCGAGATATCCAGGACTTCAAGGCTCAATGAGAAATCTGATGT 2569  
2574 ACAGTTATGGAATAGTCTTCTGATTTGAACCCGAGAAAGCGGTGATGAGCAAT 2633  
2570 ACAGCTTGGGATCTGCTCTTCTGGAATTTGCTCAAGGAAAGGCGGTGACACGAAT 2629

2634 CCAATCTCCACATCTGATATATGTCAAAGACGGGGAACAATGATGATGAATGAGCA 2693  
2630 CGAATCTGATCAATGATATCTCTCAAGCTGATGACAAACAGTCAATGAGGAGCTG 2689  
2694 ATCCAGACATCAATGAGCTGTAAAGATCTCGTGTGTGAAGAAATTTTCAACTGG 2753  
2690 ACTCGAGGATGACAGACGTCGACGACATGGGACTGGTCAGAGGAGGCTTCACTCG 2749  
2754 CACTCTTATGACCAACAAAGACCGCAATGATGACCCCAATGACACGAGTACCTG 2813  
2750 CCTCTTGTGTCACCAAGGACCTTTCAGACCGGCTGACCATGACGAGTTGCAAGG 2809  
2814 TTCT 2817  
2810 TGCT 2813

RESULT 10  
US-11-218-305-13435  
; Sequence 13435, Application US/11218305  
; Publication No. US20060141495A1  
; GENERAL INFORMATION:  
; APPLICANT: MONSANTO TECHNOLOGY, LLC  
; APPLICANT: McInaird, Paul L.  
; APPLICANT: Tao, Nengbing  
; APPLICANT: Wu, Kunsheng  
; TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping  
; FILE REFERENCE: 38-21 (53660)B  
; CURRENT APPLICATION NUMBER: US/11/218,305  
; CURRENT FILING DATE: 2005-09-01  
; PRIOR APPLICATION NUMBER: US 60/606,880  
; PRIOR FILING DATE: 2004-09-01  
; NUMBER OF SEQ ID NOS: 25043  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 13435  
; LENGTH: 2614  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-11-218-305-13435

Query Match 32.2%; Score 1022.2; DB 9; Length 2614;  
Best local Similarity 68.6%; Pred. No. 6,7e-296;  
Matches 1424; Conservative 0; Mismatches 648; Indels 3; Gaps 1;

776 AATTCAGTCTGCTTCCAGGTTTGGACTGTCTTCAATTCAGTAACTGATGATCCCT 835  
32 AACTGATCAAGTTTTCAGGCTTGGATTGTCTTCAACCGCTTATCTGACCAATCCCA 91  
836 TTGACATGGGCTTCTGCAAGTGTGCAATTAATCAATGCAAGGCAATCAACTCTGGG 895  
92 TTCAACATGGTTTCTTACAAAGGCTTACATATCTCTTGAAGGAAACAATTCACCTGG 151  
896 AAGATTCATCAAGTATGATGCTCATGACAGCCCTTGCAGTCTTGAATCTAAGTGCAC 955  
152 CCAATTCCTTCAAGTATTTGGCTTATGACAGGCTCTGCTGCTTCAATCTGATGATCA 211  
956 TTGTTGATGATCTATTTCTCCGATTTCTGGAATCTTAATCTTCAACGAGAAATGTAT 1015  
212 CAATTAATGCTGCTTATTAATCTATTAATGAGCACTTGAATCAATCAATGAGGCTG 271  
1016 TTGACAGTAAAGAGCTGCTGATCAATTCACACGAGCTTGAAGAAATGCAAAATCT 1075  
272 ATGCAAGGCAATATGTTAATCTGATGATACCAAGAGCTGAGAAATATGTCACACTT 331  
1076 CAATTAATGAGTCAATGATATATCAATCTCAAGGCTCATATACCAAGAGCTTGGAG 1135  
332 CAATTAATGAGTCAATGATATATCAATCTCAAGGCTCATATCAAGAGCTTGGAG 391  
1136 CTTAATGATCTTGTATGATGATGATGAGCAATGATGATGAGAGAGCTTATCTGAT 1195  
392 CTAAAGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 451

QY 1196 CATCTGAGCTCTTGCACAAATCTAAAGCCTTAAATGTTCTAGCGGAACAAGTTTAGTGC 1255  
 Db 452 AACCTAAGTTCATGTGGAATCTCAATAGCTTAATGGCAACAAGTTAAATGGA 511  
 QY 1256 ACTATACCCCGAGCATTTCAAAAGCTGAAAAGTATGACTTACCTTAATCTGTCCAGCAAC 1315  
 Db 512 ACCATTCCTCGTGGCTGCGCGGAACTTGAAAGCATGACCTAATTTAAATCTCTCCCTCAAT 571  
 QY 1316 AATATCAAGGTCCAATCCCGGTTGAGCTATCTGTATCGGTAACTTAAGATACATTTGGAT 1375  
 Db 572 TTCTAATAGTGCTCTATTTCTATTGAGCTATCGAGATCAACAATTTGGACACCTTGGAC 631  
 QY 1376 CTCTTCAACAACAAGATTAATGGAATCACTCTTCTCTCTGTTGATTTGGACATCTT 1435  
 Db 632 TTATCTGTAACTGATGACGGGTCAATTCATCATCTTGGCAACCTTGAACATCTA 691  
 QY 1436 CTCAAGATGAATCTGATGAATAATCATTAATCTGTGATGTTCCAGGCGACTTTGGAAAT 1495  
 Db 692 TTGAGGCTTAACTTGACCAAGAAATGATCTAGTTGGAATTCATCCCTGCGGATTTGGTAA 751  
 QY 1496 CTAAAGACATCATGGAATAGATCTTTCAAATATGATATCTCTGCGCCAAATCCAGAA 1555  
 Db 752 TTGAGAAAGTGCATGAGATGATTTATCTTAATCATCTTGGTGGCTGATTTCTCA 811  
 QY 1556 GAGCTTAAACCAATTACAAACATTAATTTGCTGAGACTGAAAAATTAACCTGACTGT 1615  
 Db 812 GAACCTTGAATGCTGCAAAACCTGATGTGTTAAACTGGAAAACAAATATATACCTGGC 871  
 QY 1616 AATTTGGTTCAATAGCAACTGTCTCAGTCTCAGTATGATATCTCATTAACAAC 1675  
 Db 872 GATGTCTCTTCTCTGATGAATGCTGCTCAGCTCAATATCTTAAATGTGTCTAACAATAT 931  
 QY 1676 CTGCTAGGATATATCCCTAAGAAACATTAATCTTCAAGATTTTCAACGACAGCTCAT 1735  
 Db 932 TTGGCTGTGCTGCTCTTACGACAACTTTCACAGGTTTTCATGACGATTTTAA 991  
 QY 1736 GGCATATCTGTCTTGGCGGATGTTGGCTTAACTCACCGTGTCAATGTTCTGTGAAT 1795  
 Db 992 GGTATATCTGGAATCTGTGGAATTTGGCTTGGTTCTTCAATGCTTCACTGGCCACGA 1051  
 QY 1796 GTACGATGTCAATCTCTAAGCAGCTATCTTGGAAATAGTATTTGGGGGACTTGTGATC 1855  
 Db 1052 GACAAACCGGCAATCTCAAAAGCGCCATTAATGTGTGTGTGGGGGACTTGTATC 1111  
 QY 1856 CTCTCATGCTCTTAATAGCAGCTTGGCGACCGCATATCTCTCTTCTTCTAGTGA 1915  
 Db 1112 CTCTGTATGATCTTAATAGTGTATGACGAGCAACATCACTGCTTTTAAAGATGCC 1171  
 QY 1916 TCACTTGACAAACGATTAATTTGACACCGAAGCTGTCTATCTTATATGAACATG 1975  
 Db 1172 ACTGTAGCAAGCCAGTGAAGCAATGATGCCAACCAAGCTGGTATCTTCAATATGAACATG 1231  
 QY 1976 GCACTCAACGTTTACGAGATATCATGAAATGACAGAAATCTTAAGTGAACATATATC 2035  
 Db 1232 GCTCTTATATGCTTGTATGATATATAGATGACTAGAACTTGAGTGAATATCATC 1291  
 QY 2036 ATTGGGACGAGAGATCAAGCATCTGTATACAAATGTGTTTGAAGATTTGAAACCGGTT 2095  
 Db 1292 ATTGGATACGGGGGATCAAGTCAAGTTTAAATGTGTTTAAAGAAATTCGAAACAGTG 1351  
 QY 2096 GCGATTAAGCGGGCTTTACTTCAACACCCAGTCAATGAAACAGTTTGAACGAAATC 2155  
 Db 1352 GCATTAATAAAAGCTGTATGCCCCACTACCTCAGAGCCTTAAGAAATTTGAAACGAGCTC 1411  
 QY 2156 GAGATGTATGATGATCAAGACAGAAATTTGTGAGCTTCAAGCTTATCTCTCTCT 2215  
 Db 1412 GAAGCTGTGTGATCAACACCGGAATCTAGTCAAGCTTCAAGGATCTCTCTGTCA 1471  
 QY 2216 CACTTGGGAGATCTTCTGTCTATGATCTATTTGAAATGTTAGCCTCTGGGATCTTCTT 2275  
 Db 1472 CCGTGTGGAACTCTCTCTTTATGATATATGAGAGTGGCAGCTTATGGAATGTTTAA 1531  
 QY 2276 CAT--GGCCCTACGAAGAAAGAACTCTTGATTTGGACACAGGCTTAAGATGATAT 2332

Db 1532 CATGAAGCTCATCAAGAAAGAACTTGACTGGGTGACTGGCTTACGATCGCTCTT 1591  
 QY 2333 GGTGACGACAAAGTTTAGCTTATCTACACATGACCTGTATGTCAGAGATCATTTCCAGA 2392  
 Db 1592 GGTGACGACAAAGCTTGTGCTTACCTTACATGATGACGACCAAGAAATTTACCGG 1651  
 QY 2393 GAGCTGAAGTGTGTCAACATTTCTTGGACAAAGACTTGAAGGCTCGTTTGACAGATTTT 2452  
 Db 1652 GAGCTAATTAACAAAGAAATATATCTCTGACAAAGATTATAGGCCCATCTTACAGCTTC 1711  
 QY 2453 GGAATAGCAAAAGCTTGTGTGTCAAGTCAATATCTTCAACTTACGTGATGGGACG 2512  
 Db 1712 GGCATCGCTAAGACTTATGTCTCGAAGACTTCAACGTCACCTACGTCATGCGGACT 1771  
 QY 2513 ATAGGTACATPACACCCGAGTATGCTCGGACTTCAACGCTCATGAGAAATCCGATGTC 2572  
 Db 1772 ATTGTTACATTAATCCCGATACGCCGACCTCCGCTCAACGAAAGCTTGAATGTC 1831  
 QY 2573 TACAGTTATGAATTAATCTTCTTGAATGTTTAAACCGAAGAAAGCCGTTGATGACGA 2632  
 Db 1832 TACAGCTAACGGATCTGTCTGTGAGCTGTGACCGGCAAGACAGTGAACAACGAG 1891  
 QY 2633 TCCATCTTCAACATCTGATTAATGTCAAGACGGGGAACAATAAGTATGAAATGCA 2692  
 Db 1892 TGCAATCTCCATCATTTGATCTATCGAAGACGGCGACAGCATGAGGACGCTG 1951  
 QY 2693 GATCCGACATCATGACAGTGTAAAGATCTGGGTGTGTAAGAAAGTTTCCAACTG 2752  
 Db 1952 GACCCGACGTTGGAGACACTTCAAGAGACTGTGGGAGGTGAAGAGCTGTTCAGCTG 2011  
 QY 2753 GCACTCTATGACCAAAAGACAGCCGAAATGATGCAACCAATGACCAAGTGAATCTGT 2812  
 Db 2012 GCGCTCTCTGACCAAGGCGAGCCCTCGGACCGGCGACATGACAGAGGTGTGCGC 2071  
 QY 2813 GTTCTGGCAGTTTATGCTATGGAACAACACC 2847  
 Db 2072 GTCTTGACTGCTGTGTGAACCGGAGCCGCC 2106

RESULT 11  
 US-10-953-349-22716  
 ; Sequence 22716, Application US/10953349  
 ; Publication No. US20060107345A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ALEXANDROV, Nikolai et al.  
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
 ; FILE REFERENCE: 2750-1579PUS2  
 ; CURRENT APPLICATION NUMBER: US/10/953,349  
 ; CURRENT FILING DATE: 2004-09-30  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 22716  
 ; LENGTH: 1712  
 ; TYPE: DNA  
 ; ORGANISM: Glycine max  
 US-10-953-349-22716

Query Match 29.4%; Score 935.2; DB 6; Length 1712;  
 Best Local Similarity 73.5%; Pred. No. 7.1e-270;  
 Matches 1214; Conservative 0; Mismatches 423; Indels 15; Gaps 1;

Db 1369 ATTGATCTTCCAAACAAGATTAATGGAATCATTTCTTCCCTTGGTATTTGA 1428  
 1 ATTGATATTTCAACAATTAATTAATGTTGCTTCAATCCCTTCTTCCCTGTGATTTGA 60  
 QY 1429 GCATCTTCCAAAGATGAATCTTGAAGAAATCATATTAATCTGTATGTTCCAGCGCAT 1488  
 Db 61 ACATCTTCTGAAGTTGAACCTGAGCAAGAAACATTTTAACGAGATTTATTCACAGAT 120  
 QY 1489 TGAATCTTAAGAACATCATGGAATATGATCTTTCAATATGATATCTTGGCCCAAT 1548

Db 121 TGGAAATCTTGAAGATGTATGAAATTCCTTCAGATATATCAGCTCTCTGGCTTCAT 180  
 QY 1549 TCCGAAGAGCTTAAACCAATTAGCAACATTAATTTTCTGAGACTGGAAAAATTAACCT 1608  
 Db 181 TCTGAAGAACTTATAGTTCAGAAACATGATATCTTGAGACTTAAAAACAATTT 240  
 QY 1609 GACTGTATATGTTGGTTCATTATAGCCCACTGCTCAGTCTCAGTATATGATATCTCA 1668  
 Db 241 AACTGGGAGTATGGCGTCACTTTCAAGTGTCTTCTCTCTCTACTATATGTTGTCTA 300  
 QY 1669 TAACAACCTGTGATGATATATCTTAAAGAACATTAACCTTCAAGATTTTCCACGAC 1728  
 Db 301 TAAACAACCTATTTGTGTATATCCCAAGATTAACAATTAACAGTTTCCCTGACAG 360  
 QY 1729 CTTCATTTGGCAATTCCTGCTTTTGGGCTAGTGGCTTAACTCAGCCGTCTATGATTTCTG 1788  
 Db 361 TTTTATTTGAAACCTTGGTCTTTGTGTGTAATTTGGCTAATTTGGCAATGATGTTGCTG 420  
 QY 1789 TCGAATCTGACGATGTCATATCTCTAGAGAGCTATTTCTGGAAATAGCTATTTGGGGAGCT 1848  
 Db 421 TCTTTGAGAGGAGTATCATTTATTTAGAGCTGCCATTTCTGGAAATTAATTTGGGTGCTT 480  
 QY 1849 TGTGATCTTCTATAGTCTTAAATAGCAGCTTGGCCGACCGATATATCTCTCTTTCT 1908  
 Db 481 TGTGATCTTCTATAGTATTTGTGTGAGCTTGGCCGACACAGCCCTCTCTTTTCC 540  
 QY 1909 TGTATGATCTTGTACAAACCAAGTAACTTATTTGACACCGAGTCTCTATCTTTCTAT 1968  
 Db 541 TGTATGATCTTGTACAAACCAATTAATTTCTCCCTCCAAAGCTATGATTTCTTCTAT 600  
 QY 1969 GAACATGCACTCAGCTTACGAGATATCATGAGAAATGACAGAAATCTTAAGTGAAG 2028  
 Db 601 GAATATGCACTCATATGTATGAAATATCATGAGATATCTGAAAACTTAAGTGAAG 660  
 QY 2029 GTATATCATTTGGGACGAGCATTCAGCACTGTATACAAATGTGTGTTGAAGATTTGAA 2088  
 Db 661 GTATATCATTTGATGATGTGTCATCAAGTAACTGTTATTAATGTCTCTTAAGATTTGAA 720  
 QY 2089 ACCGTTTGCATTAAGGGCTTAACTCTCTCAACCCAGCTCAATGAAACAGTTTGAAC 2148  
 Db 721 GCGGTGGCTATACAGGATCTAATTTCTCACTATCCCAATGATTAAGAAATTTGAAAC 780  
 QY 2149 AGAATCTGAGATGCTAAGTATGACATCAAGCAAGAAATCTTTGTGAGCTTAAAGCTTATTC 2208  
 Db 781 TGAATCTGAGATCTTGGCAGCATCAAGCAGCCGAATTTTGTCTCTCAAGGCTATCTC 840  
 QY 2209 CCTCTCTCACTTGGGAGTCTTCTGTCTATGATATTTGAAAAATGTAGCCCTTGGGA 2268  
 Db 841 CTGTCTCCCATATGGCCATCTCTGTTTATGATCATGGAATAATGGCAGTCTATGGGA 900  
 QY 2269 TCTTCTTCAATGAGCCCTTACGAAGAAAAAGACTCTTGTATGGGACACAGGCTTAAAGATAGC 2328  
 Db 901 TCTTCTTCAATGAGCCCTTACGAAGAAAAAGCTTGTAGGAGCTGCTGTAAAAAAATAGC 960  
 QY 2329 ATATGGGAGCAACAAGTTAGCTTATCTACACCATAGATAGTATGCAAGATCAATTTCA 2388  
 Db 961 ACTTGGAGCAACAAGCTTGTATCTACACCATAGATAGTCTGTCTGAATCATCTCA 1020  
 QY 2389 CAGAGAGTGAAGTCTCTCAACATTTCTTGGACAAAGACTTGAAGGCTGTGTGACAGA 2448  
 Db 1021 CAGGAGATGAATCATCTAATCATATATTAATGAGAGACTTGAAGCTCATCTCATCTGA 1080  
 QY 2449 TTTTGGAAATGCGAAAAAGCTTGTGTGTCAAGTCAATTAATCTTCAATGATGGG 2508  
 Db 1081 TTTTGGAAATGCGAAAAAGCTTGTGTGTCAAGTCAATTAATCTTCAATGATGGG 1140  
 QY 2509 CAGCATGTTAATAGTACACCCGAGTATGCTGCACTTCAAGGCTCTGAGAAATCGA 2568  
 Db 1141 CACATATGGCTACATAGACCTTGATGTCTAGAACTTGGATCTCTGAGAAAGTCTGA 1200  
 QY 2569 TGTCTACAGTTATGAAATAGTCTTCTTGAATGTTTAAACCGAAGAAAGCCGTGATGA 2628  
 Db 1201 TGTGTACAGTTATGAAATAGTCTTCTTGAATGTTTAACTGAGAAAGAAAGCTGTGACAA 1260

QY 2629 CGAATCCAATCTCCACCATCTGATAATGTCAAGAGCGGGAACAATGAGTATGGAAT 2688  
 Db 1261 TGAATCCAACCTCCACCATCTTATTTTGTCTCAAGGAGCAACCAATGCTGTATGAAAC 1320  
 QY 2689 GGCAGATCCAGACATCAATCGACGTATAAAGATCTCGTGTGTGTAAGAAAGTTTCCA 2748  
 Db 1321 AGTTGATCCGAGATTAATAGTCCCATGCAAGAGCTTAAGAGCTGTAAAAAGTTTATCA 1380  
 QY 2749 ACTGGACCTCTTATGCAACCAAAAGACCGGAATGATTCAGCCCAATGACCAAGTATG 2808  
 Db 1381 GCTTGTCTATTTATGCAAAAGAGGAGCGACGTGATAGGCTCAACATGACCAAGTATG 1440  
 QY 2809 TCGTGTCTCGGAGTTTATATGCTATC-----GGAACAACCACTGCTGTC 2853  
 Db 1441 ACGTGTATCTGGAAAGTCTGCTGCATTAAGATCCCAACCAACCACTGCTATCC 1500  
 QY 2854 GACTGACAGCTCAGCAGCGCTGCTGTTCTGCTACTAGTCAATGATGATGCAATCTCA 2913  
 Db 1501 ACGTGTCAATATCAATCTGCCAAAGTGCATCTAGTGAATGATGCAAACTCA 1560  
 QY 2914 GACTCTCATTTCTGTCAATTTGCTTTCATGAGTCTTGTATGCTCAACTGTTCTTCG 2973  
 Db 1561 AACCACCACTTATGATTAAGTCCCTCAATGAGCACTTGAAGTCTCAACTTCTCTCA 1620  
 QY 2974 GTTGGACAAATTTATTTCTCAGAACAGTAGT 3005  
 Db 1621 GTTGGAGAAATATCTCTCAAAACAGTAGT 1652

RESULT 12  
 US-10-519-135-44  
 ; Sequence 44, Application US/10519135  
 ; Publication No. US20060137041A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: The Australian National University  
 ; TITLE OF INVENTION: METHOD OF PRODUCING PLANTS HAVING ENHANCED TRANSPIRATION EFFICIENCY  
 ; TITLE OF INVENTION: PLANTS PRODUCED THEREFROM  
 ; FILE REFERENCE: 94948/MEO  
 ; CURRENT APPLICATION NUMBER: US/10/519,135  
 ; CURRENT FILING DATE: 2004-12-22  
 ; PRIOR APPLICATION NUMBER: AU PS3339  
 ; PRIOR FILING DATE: 2002-07-02  
 ; NUMBER OF SEQ ID NOS: 45  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 44  
 ; LENGTH: 2315  
 ; TYPE: DNA  
 ; ORGANISM: maize ERECTA  
 US-10-519-135-44

Query Match 28.4%; Score 901.2; DB 6; Length 2315;  
 Best Local Similarity 68.6%; Pred. No. 1.4e-259;  
 Matches 1258; Conservative 0; Mismatches 573; Indels 3; Gaps 1;

QY 1017 TGCACAGTAAACAGCTGATCTGTTCATTTCCACTTGAAGTGAACATGTCAAACTCC 1076  
 Db 4 TGCAGTCAACAGGTTAACTGATCATACCAAGAGCTGAGAAATATGTCAACCTTC 63  
 QY 1077 ATTACCTGGAATCAATGATTAATCATCTCAGGGGTATATACCAAGAGCTGGAAGC 1136  
 Db 64 ATTACCTGGAATCAATGATTAATCATCTCAGGGGTATATACCAAGAGCTGGAAGC 123  
 QY 1137 TTAAGTATTTGATCTGATATGATGGAACAATGATCTGGAAGGACTTAATCTGATC 1196  
 Db 124 TAAACAGCTTTGATGACTGAACCTTGGCAATTAACAACCTTGAAGGACCAATCTGACA 183  
 QY 1197 ATCTGAGCTCTTGAACAATAATCTTAACAGCTTAAATGTTATGAGGAACAAGTTAGTGA 1256  
 Db 184 ACCTAAGTTATATGTGAATCTCAATAGCTTCAATCTTAATGGAACAAGTTAAATGGA 243  
 QY 1257 CTATACCCGAGCATTTCAAAAGCTGAAAGATATGATTAATCTGTCCAGGACAA 1316

Db 244 CCATTCCTCGTCCGCGGAACTTGAAAGCATGACCTATTGTAATCTTTCATCAAAATT 303  
Qy 1317 ATATCAAAAGGTCGAATCCCGGTGAGCTATCTCGTATCGGTAACCTATGATATGATGATC 1376  
Db 304 TCATTAAGTGGCTCTATTCTATTAGAGCTATCAAGATCAACAAATTTGAGACGTTGACT 363  
Qy 1377 TTTTCAACAAACAGATAAATGGAATCATTCCTTCTCCCTTGTGATTTGGAGCATCTTC 1436  
Db 364 TATCTGTAACATGATGACGGGTCATTCATCATCATGAGCACTAGAGCATCTAT 423  
Qy 1437 TCAGATGAATCTTGAATGAAATCATATATAGTGTAGTTCGAGGAGCATTTGGAATC 1496  
Db 424 TGAGGCTTAACCTTGAGCAAGAAATATCTAGTGAATTCATCCGCGAGTTTGTATTT 483  
Qy 1497 TAAAGACATCATGGAATATAGATCTTCAATTAATGATCTCGGCCCAATTCAGAAAG 1556  
Db 484 TGAGAGTGTATGAGATTTGATTTATCTTATATCATCTTGGTGTCTGATTTCTCAAG 543  
Qy 1557 AGCTTAAACCAATTAAGAAACATTAATTTGCTGAGACTGGAATATATTAACCTGAGTA 1616  
Db 544 AACTTGAATGCTGCAAAACCTGATGTTGCTAAACCTGGAACAAACAAATTAACCTGCG 603  
Qy 1617 ATGTTGGTCTATTAGCCCACTGCTCAGCTCAGCTGATTAATGATATCTCATATAACACC 1676  
Db 604 ATGCTCTCTCTGATGAACTGCTTCAAGCTCAATATCTTAAATGTCTCATATAATATT 663  
Qy 1677 TCGTAGGTATATCCCTTAAGAAACATTAATCTTCAAGATTTTCAACGAGCTTCAATG 1736  
Db 664 TGGCTGTGCTGTCT 723  
Qy 1737 GCAATCTCTGTCTTTCGCGTAGTGTGCTTAACTGACCGTGTATGATTTCTGCGAACTG 1796  
Db 724 GTATCTCTGAGCTCTGAGATATGCTGTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 783  
Qy 1797 TACAGATGTCAATCTCTAGAGCACTATCTTCTGAATAGCTATTTGGGGAATTTGTATCC 1856  
Db 784 ACAAACCGCCATCTCAAAAGGCTCCCAATATGTTGTTGTTGTTGTTGTTGTTGTTGTT 843  
Qy 1857 TTCTCATGCTTCTTATAGCACTTGGCGACCGCAATATCTCTCTCTCTCTCTCTCTCTCTCT 1916  
Db 844 TCTGATGATTTTATAGTATCTGATATGAGGCAACACATCTCTCTCTCTCTCTCTCTCTCT 903  
Qy 1917 CACTTGAACAAACAGTAACTTATTCAGACCGAAGCTGTGATCTTCTCATATGAACATGG 1976  
Db 904 CTGTAGACAGCCAGTGAAGTGTCCACCAAGCTGTGATCTCTCTCTCTCTCTCTCTCTCT 963  
Qy 1977 CACTTCAAGCTTATAGAGATATCATAGAAATGACAGAGATCTTGAAGAGATATCA 2036  
Db 964 CTCTTCAATGCTTGTATGATATTAATGAGATGAGTGAACCTTGAAGAGAAATATCA 1023  
Qy 2037 TTGGGCAACGAGCATCAAGCACTGTATCAATGATGTTTGAAGAAATTTGTAACCGGTTG 2096  
Db 1024 TTGGATACGGGGCATCAAGTACTGTTTATTAATGTGTTCTTAAAGATTTGCAACCAAGTG 1083  
Qy 2097 CGATTAACGGGCTTACTCTGCAACCCCAAGTCAATGAACAGTTTGAACAGAACTCG 2156  
Db 1084 CAATTAACAAAGCTGTATGCTCAGTACCTGAGAGCTTGAAGAAATTTGAACAGCTCG 1143  
Qy 2157 AGATGCTAAGTATGATCAAGACAGAAATCTTGTAGAGCTTCAAGCTTATCCCTCTCT 2216  
Db 1144 AGACTGTGTGATGATCAAAACCGGAATCTAGTCAAGCTTCAAGGGGACTGTTGTAC 1203  
Qy 2217 ACTTGGGAGTCTCTGTTCTATGATATTTGAAAAATGAGGCTCTGGATCTTCTCTC 2276  
Db 1204 CTGTTGGGAACCTCTCTTTTATGCTTATATGAGAGAGTGGAGCTTATGGATGTTTAC 1263  
Qy 2277 AT---GGCCTACGAAGAAAAAGACTTTGATTGGGACACAGGCTTAAATGATGATATG 2333  
Db 1264 ATGAAGGCTCTCAAGAAAGAAACAACTTGAAGTGGTGAATCGCCTACGAGTTCCTCTG 1323  
Qy 2334 GTGAGACAGAGTTTATGCTTATCAACCATGACTGTATGTCGAAGATCAATTCACAGAG 2393  
Db 1324 GTGAGCTCAAGGCTCTGCTTACCTTCAACATGACTGAGGCCCAAGAAATATTCACCGGG 1383

Qy 2394 ACGTGAAGTGTCCCAATCTCTTGGACAAAGACTTAGAGGCTGTTGACAGATTTTG 2453  
Db 1384 ACGTAAATCAAGAAATATCTCTCGACAAAGATTATAGGGGCACTTACAGACTTG 1443  
Qy 2454 GAATAGCAAAAGCTGTGTGTGTCAAGTCACTACTTAACTTACGTATGAGGACCA 2513  
Db 1444 GCAATCGTAAGACTTATGTGTCTGAAAGCTCAACAGTCAACCTTACGTATGAGGAC 1503  
Qy 2514 TAGGTATCATAGACCCGAGATATGCTGACCTTCAAGGCTCACTGAGAAATCCGATGCT 2573  
Db 1504 TTGTTTCAATTTGATCTGATAGTACCGGCACTCTCCGCTCAACGAAAGTCTGATGTCT 1563  
Qy 2574 ACAGTTATGAAATAGTCTTCTTGAAGTTTAAACCGAAGAAAGCCGTGATGAGAAAT 2633  
Db 1564 ACAGCTACGGCATCTGTTCTGCTGAGCTGTGACCCGCAAGAAAGCAGTGAACAGAT 1623  
Qy 2634 CCAATCTCCACCTCTGATATGTCAAAGACGGGGAACAATGATGATGAAATGGCAG 2693  
Db 1624 GCAATCTCCATCACTTGTATCTATGAAAGCGGCGAGCAAGAGTCTATGAGACGGTGG 1683  
Qy 2694 ATCCAGCATCAATGAGCTGTAAGATCTCGGTGTGTGAAAGAAATTTTCAACTGG 2753  
Db 1684 ACCCGACGTGGAGACACCTGCAAGACCTTGGCCAGAGTGAAGAACTGTTCAAGCTGG 1743  
Qy 2754 CACTCTATGACCAACAAAGACAGCCGAATGATGACCCCAATGACCAAGTATCTGTG 2813  
Db 1744 CGGCTCTCTGACCAAGCGGAGCCCTCGGACCGGCGAGATGACAGAGTGTGCGG 1803  
Qy 2814 TTCTCGGAGTTTATGCTATTCGGAACACACAC 2847  
Db 1804 TCCCTGACTGCTGTGTGAACCCGAGCCGCGCC 1837

## RESULT 13

US-11-218-305-14406  
: Sequence 14406, Application US/11218305  
: Publication No. US2006014195A1  
: GENERAL INFORMATION:  
: APPLICANT: MONSANTO TECHNOLOGY, LLC  
: APPLICANT: Mcleard, Paul L.  
: APPLICANT: Tao, Mengbing  
: APPLICANT: Wu, Kunsheng  
: TITLE OF INVENTION: Polymorphic Markers and Methods of Genotyping  
: FILE REFERENCE: 38-21 (53660)B  
: CURRENT APPLICATION NUMBER: US/11/218,305  
: PRIOR FILING DATE: 2005-09-01  
: PRIOR APPLICATION NUMBER: US 60/606,880  
: NUMBER OF SEQ ID NOS: 25043  
: SOFTWARE: PatentIn version 3.2  
: SEQ ID NO 14406  
: LENGTH: 1714  
: :  
: TYPE: DNA  
: ORGANISM: Zea mays

US-11-218-305-14406

Query Match 22.5%; Score 714.2; DB 9; Length 1714;  
Best Local Similarity 65.8%; Pred. No. 1.7e-203;  
Matches 1120; Conservative 0; Mismatches 543; Indels 40; Gaps 4;

Qy 586 CTGGGACAGAAATTAATCTCAGTGTGATGATCAAGACTTATTTACTGTAATGAGTTCT 645  
Db 13 CTGGGCTCAAAACAAGTAAATGTGTGAAATTTCCGAATCTAATATATGGAATGAGTTCT 72  
Qy 646 TCAATATCTTGGGTTGGGAGAAACAATTAATGTCGTAATTTCTCAAGATTTGTCTCA 705  
Db 73 TCAATATCTTGGGTTGGGAGAG-AAATGTTTGAAGAAAGCTCTCTCCCATATGTGCCA 131  
Qy 706 ACGACAGTGTCTTGTATTTTGAAGTGAAGAAACAAGTTGATGATGATGATGATGATG 765  
Db 132 GTTAATGCTGTGTGTGATTTGATGTGAAGAAACAAATGACTTGAAGGCTCAATACCA 191

QY 766 GACGATAGGAATTCGACCTGCTTCCAGGTTTGGACTGCTTACATCAGTAACTGG 825  
 DB 192 AACATAGGGAACCTGACAGCTTTCAGGCTTGAATTTGCAACATCATCTTACTGG 251  
 QY 826 TGAGATCCCTTTTGACATCGGCTTCTGCAAGTTGCAACATTTATCTTGAAGGCAATCA 885  
 DB 252 AGAAATCCCGTTCAATATGGTTTCTGCAAGTGGTACGTTATCTTTGCAAGGGAACA 311  
 QY 886 ACTCTCTGGGAAGATTTCATCAGATTTGGTCTCATGCAAGCCCTTGACGCTTGAATCT 945  
 DB 312 GTTCTCTGGCTTCTTACCATCAGATTTGGCTTATCGAGCCGCTTCAGGCTGAGATCT 371  
 QY 946 AAGTGGCACTTGTGATGATCTATTTCCCGATTTCTGGAAATCTTACTTACCGGA 1005  
 DB 372 GAGTTTCAAGAGATTCTGGCCCAATACCTCTTATCTGGGCAACTTGACATACCTGA 431  
 QY 1006 GAAATGTATTTGACAGATTAACAAGTACTGTTCAATTCACCTGAGCTTGGAAACAT 1065  
 DB 432 GAAATTTATCTGCAAGCAATAGATTAACTGATGATACCGCCAGAGCTTGGTAAATAT 491  
 QY 1066 GTCAAACTCATTAAGTCTGGAATCAATGATATCATCTCAGGGGTCAATATACCAACA 1125  
 DB 492 GTGACACTCATTAAGTCTGGAATCAATGATATCATCTCAGGGGTCAATATACCAACA 551  
 QY 1126 GCTTGGGAGCTTACTGACTTGTGATCTGAATGTGGCCCAACAATGATCTGGAAGACC 1185  
 DB 552 TCTTGGAAATCTTACAGAAATTTGTTGAATGAACTTGGCAACAACAACCTTATAGAAC 611  
 QY 1186 TATACCTGATCATCTGAGCTCTTGCAACAACTTAAACGCTTAAATGTTACAGGAAACA 1245  
 DB 612 TATCCCTGAGAAATTTAAGTTTCAATGCGCAATCTATAGTTTCAATGCGCAATTA 671  
 QY 1246 GTTTAGTGGCACTTATCCCGAGCATTTCAAAGCTTGAAGAAATGATGACTTAATCT 1305  
 DB 672 CTGGAATGGAACCACTTCCAGCTTCAATTTCAACAGCTGAGAGCTGACTTATGAAATCT 731  
 QY 1306 GTCCAGCAATATTCAGAAAGTCCCAATCCGGTGGAGCTTCTGTAATGCGTAATAGA 1365  
 DB 732 GTATCAAAATCATCTCAGTGAAGCACTTCCAAATGAGGTGCAAGAAATGAGAAATTTAGA 791  
 QY 1366 TACATGATCTTCTTCCAAACAAGATTAATGAAATGATCTTCTTCCCTGGTGGATT 1425  
 DB 792 CACTGTGACTTATCCCTGTAACATGATCATCTGTTCAATTTCCCTCAGCTATGGGAAT 851  
 QY 1426 GAGCATCTTCTCAAGATGAATCTGATGAATCATATACTGTTAGTTCAGGCGA 1485  
 DB 852 AGAGCATCTTCTGAGACTCAACTTAACAAATAATATGTTGGTGGACACATTTCTGCTGA 911  
 QY 1486 CTTTGAATATCTAAGAGATCAATGAATATGATCTTCAATATATGATATCTTGGCCC 1545  
 DB 912 ATTTGGAACTTTAAGAGATCAATGAGATGATTTGTCTTAAACAACCACTCAGTGGCT 971  
 QY 1546 AATTCAGAGAGCTTAAACCAATTAACAGAAATATTTTCTGAGCTGGAATAATATAA 1605  
 DB 972 GATTTCTCAAGAGTGGATGATGCTACAAATTTGATATCTGTAAATTAAGAAACATATA 1031  
 QY 1606 CTTGATCTGTAATGTTGTTCAATTAAGCAACTGCTCAGTCTCACTGATTAATGATATC 1665  
 DB 1032 TATTACTGAGAGATGCTCTTCACTTATTTACTGCTGATCTCAATATCTTAAATGATATC 1091  
 QY 1666 TCATAACAACTCTGATGATATATCCCTAAGAAACATATCTTCAAGATTTTACACAGA 1725  
 DB 1092 ATACAAACATCTTTTATGATGATGATCTTCAAGAAACATCTTCAAGATTTTACACAGA 1151  
 QY 1726 CAGCTTCAATGGAATCTGCTGTTTGGGTAATGTTGCTAACT-----CACC 1773  
 DB 1152 CAGCTTCTTGGGTAATCCCTGAGCTTGTGGCTATATGGCTTCACTCTGCTTCAAGCAACA 1211  
 QY 1774 GTGTCAATGATTTCTGCGAACTGTACAGATGTCATCTTACAGACATAT----- 1824  
 DB 1212 ATATCAAAATGCGAGCAAAATGAAGATCTCTTACGCAAAAGGCTCAATGTGTTGAGC 1271

QY 1825 TCTTGAATAGCTATTTGGGGAAGCTTGTGATCTTCTCATGCTTATATAGCAGTTGCCG 1884  
 DB 1272 TATTGGTTGGTGGCCGTATTTGTTATTTATGCTGCTATCTAGTATATTTGCTG 1331  
 QY 1885 ACCGATATATCTCTCTCTTCTTCTTGAATGATCACTTGAACAAACAGTAACTTATTCAC 1944  
 DB 1332 GCCATATATCTTCCAGTCTCAAGATGCTCTGTAACAAACAGTAACTTATTCAC 1391  
 QY 1945 A-----CCGAGCTCCGTCATCTTCAATATGACATGAGCACTCCAGCT 1986  
 DB 1392 AGCATCAACAAATTCATCTTCAAGCTTGTGATCTTCAATATGACATGAGCACTCCAGCT 1451  
 QY 1987 TTACGAGATATCATGAGATGACAGAGATCTTAAAGTGAATATATATCAATTTGGGCGAG 2046  
 DB 1452 ATATGATGATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1511  
 QY 2047 AGCATCAAGCACTGATATCAATATGTTTGAAGATTTGAACCGGTTGCAATTAAGC 2106  
 DB 1512 AGCCTCAAGTACAGTCTACAGATGCGACCTGAAGAACTGCAAGCAATTCGATTAATAA 1571  
 QY 2107 GCTTACTCTCAACCCCAAGTCAATGAACAGTTTGAACAGACTGAGATGCTAAG 2166  
 DB 1572 GCTGATGCTTCACTTCACTTCAAGCTTGAAGAAATGAGATGATGATGATGATGATG 1631  
 QY 2167 TACATCAAGCAAGAAATCTTGTGAGCTTCAAGCTTATCTCTCTCTCACTTGGGAG 2226  
 DB 1632 AAGCATCAACACCGGAATTTTGAAGCTTCAAGGGTACTCCTGTCAACATCTGGGA 1691  
 QY 2227 TCTTGTGTTCTATGACTATTTGG 2249  
 DB 1692 TCTCTCTCTATGATTAATGAG 1714

RESULT 14  
 US-10-449-902-2426  
 ; Sequence 2426, Application US/10449902  
 ; Publication No. US20060123505A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: National Institute of Agricultural Sciences.  
 ; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
 ; APPLICANT: The Institute of Physical and Chemical Research.  
 ; APPLICANT: Foundation for Advancement of International Science.  
 ; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF  
 ; FILE REFERENCE: MOA-40205X1-US  
 ; CURRENT APPLICATION NUMBER: US/10/449, 902  
 ; CURRENT FILING DATE: 2003-05-29  
 ; PRIOR APPLICATION NUMBER: JP 2002-203269  
 ; PRIOR FILING DATE: 2002-05-30  
 ; PRIOR APPLICATION NUMBER: JP 2002-383870  
 ; PRIOR FILING DATE: 2002-12-11  
 ; NUMBER OF SEQ ID NOS: 56791  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 2426  
 ; LENGTH: 1688  
 ; TYPE: DNA  
 ; ORGANISM: Oryza sativa  
 ; PUBLICATION INFORMATION:  
 ; DATABASE ACCESSION NUMBER: AK060260  
 ; DATABASE ENTRY DATE: 2001-12-06  
 US-10-449-902-2426

Query Match 17.4%; Score 552.4; DB 6; Length 1688;  
 Best Local Similarity 65.4%; P-Value 1.5e-155;  
 Matches 887; Conservative 0; Mismatches 436; Indels 33; Gaps 4;

QY 1698 ACATATATCTTCAAGATTTTCAAGAGAGCTTCAATGGAATCTTGTGCGGTA 1757  
 DB 3 ACATATATTTTCAAGATTTTCAAGAGAGCTTCTTGTGTAATCTGATCTGTGGCT 62  
 QY 1758 GTTGGCTAAATCAAGCTGATGATTTCTGCGAACTGTACAGAGTGTCAATCTTGAAG 1817  
 DB 63 ATGGCTGTGGTCTTGTGCTGATCTCAACAGATGATGAGATGATCTCTGTCTCAAGGT 122

QY	1818	CAGCTATTCTTGGAAATGACCTAATGGGGGACTTGGATCTCTCTCATGGTCTTAAATAGCAG	18777
Db	123	CTGCAAATCTTGGGGATGCTGAGCTGGGCTGTGTAATCTCTGTAGATCTCCAGCTGCTG	182
QY	1878	CTTGGCCGACCGCATTAATCTCTCTCTCTTCTTGTAGATCACTTGACAAACGAG-----	19311
Db	183	CTTGTGGCCACACTGGGGACAAAGTTCCCAAGATGATGTCCTTATGTAACCAAGATATCC	242
QY	1932	-----TAACTTATTCGACACCGAAGCTCGTATCCTTCATATGAACTGGCAC	19791
Db	243	ATGCACATACATCAAGTATGATCTCTCCAAAGCTGTAAATCCTTCATCATGAACAATGGCAT	302
QY	1980	TCCACGTTTACGAGATATCATGAGATGACAGAGATCTAAAGTGAAGTATATCATTG	20391
Db	303	TCTCTGTCTAAGAAATATAATGAGGATGACTGTAATAATTGAGCGAGAAATACATTAATCG	362
QY	2040	GGCAGCGAGCATCAAGCACTGATATCAATGTTTTAAGAAATGTAAACCGGTGGCA	20991
Db	363	GGTATGGGGCATCAAGCACAGTGAACAAATGTGTACTAAGAACTGCAGCCGGTTGCA	422
QY	2100	TTAAGCGGCTTACTCTCAACAACCCACAGTCAATGAAAACGTTTGAACAGAACTCGAGA	21591
Db	423	TAAABAAATTTGATGCTACTACATCCACAGAGCTGAAGAAATGGAAGCTAGCTGAGGA	482
QY	2160	TGCTAATGATCATCAAGCACAGAAATCTTTGAGAGCTTACAAAGCTTATTCCTCTCTCACT	22191
Db	483	CTGTTTGAAGATCAAGACCGGAATCTTGTCAGGCTTCAAGGGGATTTCCCTATACCTGT	542
QY	2220	TGGGGAAGCTTCTGTTCTATGACATTTTGGAAAATGTAGGCTCTGGGATCTTCTCAT-T	22781
Db	543	CTGGAAATCTTCTCTTCTTACGACTATTTGAAAAATGSGACAGTCTGGGATGTTTACATG	602
QY	2279	--GGCCCTACAGAAAGAAAGA-CTCTGATTTGGGACACACGGCTTAAAGTACATATGGTG	23361
Db	603	CAGGCTATCCAAAGAGCAAAACCTAAGATTGGAGGCTAAGGCTCCGATTCGTCTCGGTG	662
QY	2337	CAGCACAAAGTTTATGCTTATCTTACACCATGACTGATGTCBAAGATCATTCACAGAGAC	23961
Db	663	CGGCAACAAGTCTGGCTTATCTTCAATGACTGCACCCACCGATAATTCATAGGGAATG	722
QY	2397	TGAAGTCGTCCAAACTCTCTTGGACAAGAACTTGAAGGCTCGTTGACAAATTTGGAA	24561
Db	723	TGAAGTCGAAGAAATATCCTTCTAGCAAGAGACTATGAAGACATCTTGCCGACTTTGGTA	782
QY	2457	TAGCGAAAGCTTGTGTGTGTCAAAAGTCAACATCTTCAACTTACGTGATGGGACGATAG	25161
Db	783	TTTGCAAAGCTTGTGCACTCTAAAGACACACATCAACTATGTATGGGTACTAATAG	842
QY	2517	GTTACATATGACCCCGAGATAGTCTGCACTTACCGGCTCACTGAGAAATCCGATGTCTACA	25761
Db	843	GCTACATTTGACCCCTGAGATAGCATATCAATCCCGCTCAAGAGAAATCGATGTCTTACA	902
QY	2577	GTTATGGAATAGTCTCTCTGTAGATGTTAAACCGAAGAAAGCGGTATATACAAATCCA	26361
Db	903	GCTATGGAATAGTCTCTCTGTAGATGTTAAACCGAAGAAAGCGGTATATAGTGCCA	962
QY	2637	ATCTCCACATCTGATTAATGTCTAAAGACGGGGAAACAATGAAGTATGAAATGSCAGATC	26961
Db	963	ATCTCCACATCTGATTCCTATCTCAAGACCGCAGACACACGCTATGAGATGTGTCAACC	10221
QY	2697	CAGACATACATCGACGTTGTAAGATCTCGGTGTGTAAGAAAGTTTCCAACTGGCAC	27561
Db	1023	CAGACATACCGGATAGTGTCAAAAGATCTTGGGGAAGTCAAGAAAGGTGTTCCAGTTGGGCG	10821
QY	2757	TCTTATGACACAAAGACAGCCGAATGATCGAACCACAATGACCAAGTGACTGTGTCTC	28161
Db	1083	TCTCTTTGAGACAAAGGAGCGCTTCTGTATCGACCGACATATCAACAGGATCGTGTGTCTC	11421
QY	2817	TCCGCACTTATATGTTATTCGGA-----ACAACCACTGTGCTCGCACTACACAGTCAAG	28671
Db	1143	TGGAATGCTCTGCTCTAACCCCGACCGCCCTCAAAAGCCGGCACTGCAACGGCATTTGGCAC	12021
QY	2868	CGAGCGTGGCTGTGTTGTCGTACGTGATGAGTATGCAAAATCTCAAGACTCCTCAATTCGTG	29271

```

Db      1203 AGTGTCCAGGTTCCGAGCTATGTACAAGAGTACGTAGACCTACGAGCGCGCAGCACCG 1262
Oy      2328 TCAATTG---CTCTTCAGTSAAGTCCTTCGTGATCTCAACTGTCTTCTTCGGTTTGACAAAG 2984
Db      1263 TCTCCTGTGAAAATTCTGTCGAGCGCGTCAGATCGGAGGCTCTTCTTGAAAGTTGGCGAGG 1322
Oy      2985 TTATTTCTCAGAACAGTAGAGTATTTTGGTTGGA 3020
Db      1323 TGAATTCACAGAACACAGAGTAGAGTACTATCTGA 1358

RESULT 15
US-10-519-135-21
; Sequence 21, Application US/10519135
; Publication No. US20060137041A1
GENERAL INFORMATION:
APPLICANT: The Australian National University
TITLE OF INVENTION: METHOD OF PRODUCING PLANTS HAVING ENHANCED TRANSPIRATION EFFICIENCY
FILE REFERENCE: 94948/MRO
CURRENT APPLICATION NUMBER: US/10/519,135
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: AU PS3339
PRIOR FILING DATE: 2002-07-02
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 1273
TYPE: DNA
ORGANISM: partial maize ERECTA
US-10-519-135-21

```

Query Match	16.7%	Score 530.8	DB 6	Length 1273
Best Local Similarity	69.2%	Prod. No. 1.7e-148		
Matches 769	Conservative 0	Mismatches 337	Indels 6	Gaps 3
QY 1742	CCTGCTCTTTGCGGTAGTGGGCTAACTCAACCGTGCATGATTTCTCGTCGAACGTACGA	1801		
DB 1	CTTGAGCTCTGTGGATATTTGGCTTGTTCTTCATCTGTCTTCACTGGCCACCGAGACAA	60		
QY 1802	GTGTCAATCTCTAGAGAGACTAATTTCTTGAATAGCTAATTGGGGGACTTGTGATCTTCTC	1861		
DB 61	CCGCCAATCTCAAAAGGCTGCATATATGTGTGTCTGTGGGTGAGACTTGATATCTCTCTG	120		
QY 1862	ATGCTCTTTAAATAGACGCTTGCCGACCGGATATATCTCTCTCTTTTCTTGAATGATCACTT	1921		
DB 121	ATGATCTTTAGAGCTGTATGTGAGGCGCACACCATCACTCTGTTTTAAAGATGCCACTGTA	180		
QY 1922	GACAAACGAGTAACTTATTTGCAACACCGAAGCTCGTCACTCTTCATATGAACATGGCACTC	1981		
DB 181	AGCAAGCCAGTGAACAATGTCACACCGAAGTGTGATCTTCAATATGACATGGCTCTT	240		
QY 1982	CACGTTTACGAGATATCATGAGATGACAGAGAACTTAACTGAGAGATATTCATTTGGG	2041		
DB 241	CATGCTTTGATGATATATATGAGATGACTGAGAACTTGAAGTGAATAATACATCATTTGA	300		
QY 2042	CACGAGAGATTAAGACTGTTATCAAAATGTGTTTGAAGAAATTTGAAACCGGTGGCATT	2101		
DB 301	TACGGGGGATCAAGTAACTAAGTTTAAATATGTGTTTAAAGAAATTTCAAAACCGTGGCATA	360		
QY 2102	AAGGGGCTTATCTCTCAACATCC-ACAGTCAATGAACAGTTTGAACAGAACTCGAGAT	2160		
DB .361	AAAAAGCTGTATGCCCACTACCTCGCAAGCCTTAAAGAAATTTAAACTGAGCTCGAGAC	420		
QY 2161	GCTAAGTAGCATCAAGACAGAAATCTTGTAGCCT--ACAAGCTTATTCCTCTCTCAC	2218		
DB 421	TGTTGTATGATCAAAACACCGGATCTATAGTAGCCTTGCCAAAGGTATCTGTGTCACT	480		
QY 2219	TTGGGAGATCTTCTGTTCTATGACTAATTTGGAAATGTAGCTCTTGAGATCTTCTTCAT	2278		
DB 481	GTGTGGAACTCTCTTTTATGATTAATATGAGAGTGGCACTTATGGGATGTTTATCAT	540		



QY 2279 ---GGCCCTACGAGAAAAAGCTTTGATTTGGACACAGCGCTTAAGATGATATGTT 2335  
DB 541 GAAGGCTCATCCAGAAAGAACTTGACTGGGTGACTGGCTACGATCGCTTTGTT 600  
QY 2336 GCAAGCAAGAGTTTACCTTATCTACACCATGACTGTATGTCAGAGATCATTCACAGAGAC 2395  
DB 601 GCAGCTCAAGGCTCGCTTACCTTCACCATGACTGACGCCACGAAATTAATTCACCGGAC 660  
QY 2396 GTGAGTCGTCGAACATTTCTCTTGGACAAGACTTTAGAGGCTGTTGACAGATTTTGA 2455  
DB 661 GTAAATTCAAAGATTAATCTCTGACAAAGATTAAGGCCCATCTTACAGACTTCGGC 720  
QY 2456 ATAGCGAAAAAGCTTGTGTGTGTCAAGTCAATATCTCACTTACGTATGGGCACGATA 2515  
DB 721 ATGCTAAGAGCTTATGTGTCTGAGACCTACACGTCACACTACGTATGGGCACTATT 780  
QY 2516 GGTTCATATGACCCCGAGTATGCTCGCATTCACGGCTCACTGAGAAATCCGATGCTAC 2575  
DB 781 GGTTCATATGATCCGAGTACGCCCGCCTCCGCTCAACGAGAAATCTGATGCTAC 840  
QY 2576 AGTTATGAAATAGTCTTCTTGAAGTTTAACCGAAGAAAGCCGTTGATGACGATCC 2635  
DB 841 AGCTACGGCATCGTTCTGTGAGCTGTGACCGGCAAGAGCCAGTGAACAACGAGTGC 900  
QY 2636 AATCTCCACCATCTGATTAATGTCAAGACGGGGAACATGAGTGAATGGAATGGCAGAT 2695  
DB 901 AATCTTCATCACTTGTATCTATGAAAGACGGCGAGCAAGAGTCAATGAGACGTTGAC 960  
QY 2696 CCAGACATCAATCGACGTGTAAAGATCTCGGTGTGTGTAAGAAAGTTTCCAACTGGCA 2755  
DB 961 CCGGACGTGGGAGACACTGCAAGGACCTGGGCGAGGTGAAGAGCTGTTCCAGCTGGCG 1020  
QY 2756 CTCCTATGCAACCAAGACAGCCGAATGATCGAACCCACATGACCAAGGTGACTCGTGT 2815  
DB 1021 CTCCTGTGACCAAGGCGACGCCCTGGACCGGCGCAGATGCAAGAGGTGTCGCGTC 1080  
QY 2816 CTCGGCAGTTTATGCTATCGAACAACGACC 2847  
DB 1081 CTTGACTGCTGTGTGAACCGGAGCCGCGCC 1112

Search completed: September 3, 2006, 18:25:59  
Job time : 393 secs



**THIS PAGE IS BLANK**

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 5, 2006, 17:17:10 ; Search time 3699 Seconds

(without alignments)  
10550.252 Million cell updates/sec

Title: US-10-519-135-1

Perfect score: 3176

Sequence: 1gtttctctctcatgagact.....acttcctataagttcttgc 3176

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.Main:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*  
8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*  
9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*  
10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*  
11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*  
12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*  
13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq:\*  
14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq:\*  
15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq:\*  
16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11E\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3136.2	98.7	3176	US-11-027-304-1	Sequence 1, Appli
2	1486.6	46.8	2750	US-10-425-114-13156	Sequence 1156, A
3	1441.4	45.4	4060	US-10-424-599-28166	Sequence 28166, A
4	1161.8	36.6	3089	US-11-027-304-7	Sequence 7, Appli
5	1112.8	35.0	3100	US-11-027-304-5	Sequence 5, Appli
6	1032.2	32.5	3162	US-10-425-115-182550	Sequence 182550,
7	1015.4	32.0	2533	US-10-425-114-30583	Sequence 30583, A
8	1015.4	32.0	2644	US-10-425-115-77614	Sequence 77614, A
9	995.8	31.4	1872	US-10-425-114-10637	Sequence 10637, A
10	985.6	31.1	3115	US-10-437-963-21341	Sequence 21341, A
11	940.4	29.6	1859	US-10-425-114-7634	Sequence 7634, Ap
12	785.2	24.7	2985	US-10-437-963-67070	Sequence 67070, A
13	758.6	23.9	2523	US-10-425-114-31616	Sequence 31616, A
14	694.8	21.9	3233	US-10-437-963-18958	Sequence 18958, A
15	680	21.4	1798	US-10-425-114-31442	Sequence 31442, A
16	625	19.7	650	US-09-770-149-528	Sequence 528, App
17	560.2	17.6	1496	US-10-424-599-125524	Sequence 125524,

18	543.4	17.1	1456	US-10-425-114-17976	Sequence 17976, A
19	533.8	16.8	4356	US-10-101-464A-888	Sequence 888, App
20	533.8	16.8	4356	US-10-864-252-888	Sequence 888, App
21	515.6	16.2	522	US-09-770-152-994	Sequence 994, App
22	504.4	15.9	1297	US-10-425-115-57919	Sequence 57919, A
23	493	15.5	1848	US-10-425-115-45210	Sequence 45210, A
24	489	15.4	501	US-09-770-961-418	Sequence 418, App
25	480.6	15.1	1384	US-11-096-568A-27210	Sequence 27210, A
26	467.2	14.7	1266	US-10-424-599-14049	Sequence 14049, A
27	429.8	13.5	1582	US-10-424-599-33950	Sequence 33950, A
28	410.4	12.9	1416	US-10-425-114-11772	Sequence 11772, A
29	398.6	12.6	1258	US-10-767-701-12314	Sequence 12314, A
30	371.2	11.7	1079	US-10-425-114-19885	Sequence 19885, A
31	356.2	11.2	1119	US-10-425-115-63542	Sequence 63540, A
32	340.4	10.7	1121	US-10-425-114-32472	Sequence 32472, A
33	339.6	10.7	584	US-10-021-323-9775	Sequence 9775, App
34	276.4	8.7	935	US-10-767-701-106	Sequence 106, Appl
35	275	8.7	6240	US-10-221-596B-22	Sequence 22, Appl
36	271.6	8.6	748	US-10-424-599-142176	Sequence 142176,
37	258	8.1	499	US-10-767-701-21429	Sequence 21429, A
38	248.4	7.8	3375	US-09-938-842A-667	Sequence 667, App
39	248.4	7.8	3375	US-09-938-842A-667	Sequence 667, App
40	241.8	7.6	3468	US-10-437-963-64229	Sequence 64229, A
41	239.2	7.5	2381	US-10-425-115-123127	Sequence 123127,
42	234.8	7.4	911	US-10-424-599-33951	Sequence 33951, A
43	227.2	7.2	722	US-10-424-599-28164	Sequence 28164, A
44	226.2	7.1	579	US-10-424-599-80004	Sequence 80004, A
45	225.4	7.1	3222	US-10-101-464A-839	Sequence 839, App

## ALIGNMENTS

RESULT 1  
US-11-027-304-1  
; Sequence 1, Application US/11027304  
; Publication No. US20050223428A1  
; GENERAL INFORMATION:  
; APPLICANT: Torii, Keiko U.  
; APPLICANT: Shpak, Elena D.  
; TITLE OF INVENTION: METHODS FOR MODULATING PLANT GROWTH  
; FILE REFERENCE: UMOT122663  
; CURRENT APPLICATION NUMBER: US/11/027,304  
; CURRENT FILING DATE: 2004-12-30  
; PRIOR APPLICATION NUMBER: US 60/558,529  
; PRIOR FILING DATE: 2004-04-01  
; NUMBER OF SEQ ID NOS: 88  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 3176  
; TYPE: DNA  
; ORGANISM: Arabidopsis Thaliana  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (51)..(2981)  
US-11-027-304-1

Query Match 98.7%; Score 3136.2; DB 13; Length 3176;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3189; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	27	CTTTAAAGATATCTTAAAGACGCTGTTTAAAGCTGTGTGAGAAATGGCTCTGT	86
DB	1	CTTTAAAGATATCTTAAAGACGCTGTTTAAAGCTGTGTGAGAAATGGCTCTGT	60
QY	87	TTAGAGATATTTGTTCTTCTGTTCTTCTGTTCTGAGCTTAGTACTGTGACTT	146
DB	61	TTAGAGATATTTGTTCTTCTGTTCTTCTGTTCTGAGCTTAGTACTGTGACTT	120
QY	147	CAGAGAGGAGGACGACGTTGCTGAGATTTAAGATTTCAAGATGGAACAATGTTT	206
DB	121	CAGAGAGGAGGACGACGTTGCTGAGATTTAAGATTTCAAGATGGAACAATGTTT	180

207 TTTATGACGTGACAACTTCACTTCTCGATTAATGTGTCTGAGAGGTGTCTGTG 266  
181 TTTATGACTGGACAACTTCACTTCTTCGATTAATGTGTCTGAGAGGTGTCTGTG 240  
267 AAAATGTCACCTTCAATGTGTGTCTTAAATTTGTGCAATTTGAATCTTGATGGAGAA 326  
241 AAAATGTCACCTTCAATGTGTGTCTTAAATTTGTGCAATTTGAATCTTGATGGAGAA 300  
327 TCTGACCTGCGATTTGAGATCTCAAGAGTCTTGTCAATTTGATCTGCGAGGTAAATGCT 386  
301 TCTGACCTGCGATTTGAGATCTCAAGAGTCTTGTCAATTTGATCTGCGAGGTAAATGCT 360  
387 TGTCTGAGCAAAATCCCTGATGAGATGTGTGA CTGTCTTCTTTGCAAAATTTAGACTTAT 446  
361 TGTCTGAGCAAAATCCCTGATGAGATGTGTGA CTGTCTTCTTTGCAAAATTTAGACTTAT 420  
447 CCTTCAATGAAATTAAGTGTGTGACATTAACGTTTGTGATTTGGAAGTTGAACATTTGAGC 506  
421 CCTTCAATGAAATTAAGTGTGTGACATTAACGTTTGTGATTTGGAAGTTGAACATTTGAGC 480  
507 AGCTGATTTCTGAAGAAATTAACCAATTTGATAGGACCGATCCCTTCAACATTTTCAAGATTC 566  
481 AGCTGATTTCTGAAGAAATTAACCAATTTGATAGGACCGATCCCTTCAACATTTTCAAGATTC 540  
567 CAACCTGAAAAATTTCTGGAATTGGCAGACAAATTAACCTGAGTGTGAGATTAACAGACTTA 626  
541 CAACCTGAAAAATTTCTGGAATTGGCAGACAAATTAACCTGAGTGTGAGATTAACAGACTTA 600  
627 TTTTACTGGAATGAAGTTCTTCAATTAATCTTTGGGTTGCGAGAAAAACAATTTAGTCCGTAA 686  
601 TTTTACTGGAATGAAGTTCTTCAATTAATCTTTGGGTTGCGAGAAAAACAATTTAGTCCGTAA 660  
687 TTTTCTCCAGATTTTGTCTCAACTGACCTGCTTTGGTATTTTGAAGTAAGAAAAACAAGTT 746  
661 TTTTCTCCAGATTTTGTCTCAACTGACCTGCTTTGGTATTTTGAAGTAAGAAAAACAAGTT 720  
747 TGACTGTGATGATTAATCTGAGACGATAGAGAAATTTGCACTGCTTCCAGATTTTGGACTTGT 806  
721 TGACTGTGATGATTAATCTGAGACGATAGAGAAATTTGCACTGCTTCCAGATTTTGGACTTGT 780  
807 CCTTCAATTAAGTAACTGTGTGAGATTCCTTTTGAATTCGGCTTCTTCTGCAAGTTGCAAT 866  
781 CCTTCAATTAAGTAACTGTGTGAGATTCCTTTTGAATTCGGCTTCTTCTGCAAGTTGCAAT 840  
867 TATCATTTGCAAGGCAATCAACTCTCTGAGAGATTTCACTAGTATTTGATCTGATGCAAG 926  
841 TATCATTTGCAAGGCAATCAACTCTCTGAGAGATTTCACTAGTATTTGATCTGATGCAAG 900  
927 CCTTGAAGTTTGAATCTAAAGTGGCAATTTGTTGAGTGAATCTTATCTTCCGATTTCTCG 986  
901 CCTTGAAGTTTGAATCTAAAGTGGCAATTTGTTGAGTGAATCTTATCTTCCGATTTCTCG 960  
987 GAAATCTTACTTTTCAACGAGAAATTTGATTTTGGCAATTAACAAGCTGATCTTCAATTC 1046  
961 GAAATCTTACTTTTCAACGAGAAATTTGATTTTGGCAATTAACAAGCTGATCTTCAATTC 1020  
1047 CACCTGAGCTTTGAAAAATGTCAAATCTCATTAACCTGAACTGAACTGAATGATTAATCTCA 1106  
1021 CACCTGAGCTTTGAAAAATGTCAAATCTCATTAACCTGAACTGAACTGAATGATTAATCTCA 1080  
1107 CGGGTCAATATACCAACGAGAGTGGGAAGCTTACTGCACTTGTGTTGATCTGAATGTGCGCA 1166  
1081 CGGGTCAATATACCAACGAGAGTGGGAAGCTTACTGCACTTGTGTTGATCTGAATGTGCGCA 1140  
1167 ACATATGATTTGGAAGGACCTTAACCTGATCTGAGACTCTTGGACAAATTTAAACAGCT 1226  
1141 ACATATGATTTGGAAGGACCTTAACCTGATCTGAGACTCTTGGACAAATTTAAACAGCT 1200  
1227 TAAATGTTCAATGGGAAAGATTTAGTGGCACTATACCCGAGCAATTTCAAAAGCTTAAGAA 1286  
1201 TAAATGTTCAATGGGAAAGATTTAGTGGCACTATACCCGAGCAATTTCAAAAGCTTAAGAA 1260  
1287 GTATGACTTAACCTTAATCTGTCTGAGCAACAAATATCAAAAGTCCCAATCCCGTTGAGCTAT 1346

1261 GTATGACTTAACCTTAATCTGTCCAGAAACAATTAACAAAGTCCCAATCCCGTTGAGCTAT 1320  
1347 CTGATATCGGTAACTTAATGATTAATGATCTTTTCCAAACAACAAGTAAATGAAATCATTC 1406  
1321 CTGATATCGGTAACTTAATGATTAATGATCTTTTCCAAACAACAAGTAAATGAAATCATTC 1380  
1407 CTTCTTCCCTTGGTGAATTTGAGACATCTTCTCAAGATGAACTTGAAGTAAATCATTAAT 1466  
1381 CTTCTTCCCTTGGTGAATTTGAGACATCTTCTCAAGATGAACTTGAAGTAAATCATTAAT 1440  
1467 CTGATGATTTTCAAGCGGACCTTTGGAATTTAAGAACATCATGAAATGATCTTTCAA 1526  
1441 CTGATGATTTTCAAGCGGACCTTTGGAATTTAAGAACATCATGAAATGATCTTTCAA 1500  
1527 ATATGATATCTGTGCGCCAAATTCAGAAAGCTTTAACCAATTAACGAATCAATTAATTTGC 1586  
1501 ATATGATATCTGTGCGCCAAATTCAGAAAGCTTTAACCAATTAACGAATCAATTAATTTGC 1560  
1587 TGAGACTGAAAAATTAATTAACCTGATCTGTAAATGTGTGATTAAGCCAACTGTCTCAGTC 1646  
1561 TGAGACTGAAAAATTAATTAACCTGATCTGTAAATGTGTGATTAAGCCAACTGTCTCAGTC 1620  
1647 TCACTGATTTGAATGATATCTCATTAACAACCTGATGATATCTTAAAGAACATTAAT 1706  
1621 TCACTGATTTGAATGATATCTCATTAACAACCTGATGATATCTTAAAGAACATTAAT 1680  
1707 TCTCAAGATTTTCAACGAGACAGCTTCAATTTGGCAATCTGATCTTTGGGATTTGGCTAA 1766  
1681 TCTCAAGATTTTCAACGAGACAGCTTCAATTTGGCAATCTGATCTTTGGGATTTGGCTAA 1740  
1767 ACTCAACGCTGATCAATGATCTGCTGCAACTGATGATGATCAATCTGATGAGCACTAATTC 1826  
1741 ACTCAACGCTGATCAATGATCTGCTGCAACTGATGATGATCAATCTGATGAGCACTAATTC 1800  
1827 TTGGAATGCTAATTTGGGGGACCTTGTGATCTTCTCATGATCTTAAATGACAGCTTCCGAC 1886  
1801 TTGGAATGCTAATTTGGGGGACCTTGTGATCTTCTCATGATCTTAAATGACAGCTTCCGAC 1860  
1887 CGCATATATCTCTCTCTTTCTTGAATGATCACTGAGCAAAACGATTAATTTGCGAC 1946  
1861 CGCATATATCTCTCTCTTTCTTGAATGATCACTGAGCAAAACGATTAATTTGCGAC 1920  
1947 CGAAGCTGTCATCTTCAATATGAACAATGACACTCCACGTTTACGAGATATCATGAGAA 2006  
1921 CGAAGCTGTCATCTTCAATATGAACAATGACACTCCACGTTTACGAGATATCATGAGAA 1980  
2007 TGACAGAGATCTTAATGAGAGATTAATCTTTGGGCAACGAGCATCAAGCATCTGATTA 2066  
1981 TGACAGAGATCTTAATGAGAGATTAATCTTTGGGCAACGAGCATCAAGCATCTGATTA 2040  
2067 AATGTGTTTGAAGAAATTTGTAACCGGTTGCAATTAAGCGGCTTTACTGCACAAACCCAC 2126  
2041 AATGTGTTTGAAGAAATTTGTAACCGGTTGCAATTAAGCGGCTTTACTGCACAAACCCAC 2100  
2127 AGTCAATGAACAAGTTTGAACAAGAACTCGAGATGCTAATGATCAATCAAGCAAGAAATC 2186  
2101 AGTCAATGAACAAGTTTGAACAAGAACTCGAGATGCTAATGATCAATCAAGCAAGAAATC 2160  
2187 TTGTGAGCTTAACAAGCTTAATTTCCCTGCTCACTTTGGGGAATCTTCTGTTTAAAGATTA 2246  
2161 TTGTGAGCTTAACAAGCTTAATTTCCCTGCTCACTTTGGGGAATCTTCTGTTTAAAGATTA 2220  
2247 TTGAAAAATGCTAGCTCTGAGGATCTTCTTGAATGAGCCCTAAGAGAAAAAGACTCTTGAT 2306  
2221 TTGAAAAATGCTAGCTCTGAGGATCTTCTTGAATGAGCCCTAAGAGAAAAAGACTCTTGAT 2280  
2307 GGAACAACAGGCTTAATGATTAATGATGATGTCAGACACAAGGTTTAAGCTTAATCTACACATG 2366  
2281 GGAACAACAGGCTTAATGATTAATGATGATGTCAGACACAAGGTTTAAGCTTAATCTACACATG 2340  
2367 ACTGATGTCAGAGATCATTTCAAGAGAGCTGAAGTGTCTCAACATTTCTTTGAGCAAG 2426

Db	2341	CTGTAGTCCAAAGGATCAATTACACAGAGAGTGAAGTCGTCCAACATCTCTTGGACAAAG	2400
Qy	2427	ACTTAGAGGCTCTGTTTGACACAGATTTTGGAAATGCCAAAAGCTTTGTGTGTCAAGTCAAC	2486
Db	2401	ACTTAGAGGCTCGTTTGGACAGATTTTGGAAATGCGAAAAGCTTGTGTGTCAAACTCAC	2460
Qy	2487	ATACTCTCAACTTAGCGTGAATGGGACAGATAGGTTTACATAGACCCCGAGTATGCTCGCACTT	2546
Db	2461	ATACTCTCAACTTAGCGTGAATGGGACAGATAGGTTTACATAGACCCCGAGTATGCTCGCACTT	2520
Qy	2547	CACGGCTCACTGAGAAATCCGATGTCACAGTTATGGAATAGTCTTCTTGAATTGTAA	2606
Db	2521	CACGGCTCACTGAGAAATCCGATGTCACAGTTATGGAATAGTCTTCTTGAAGCTTAA	2580
Qy	2607	CCCGAAGAAAAGCCGTTGATGACGAATCCAATCTCCACATCTGTATATGTCAAAACGG	2666
Db	2581	CCCGAAGAAAAGCCGTTGATGACGAATCCAATCTCCACATCTGTATATGTCAAAACCG	2640
Qy	2667	GGAAACAATGAAGTGAATGGAAAATGGAGATCCAGACATCAATCGACGTCTAAAGATCTGG	2726
Db	2641	GGAAACAATGAAGTGAATGGAAAATGGAGATCCAGACATCAATCGAGTCTAAAGATCTGG	2700
Qy	2727	GTTGTGTTGAAGAAAAGTTTTCCTCACTGGCAGCTCTATGACACAAAAGACAGCCGAATGATC	2786
Db	2701	GTTGTGTTGAAGAAAAGTTTTCCTCACTGGCAGCTCTATGACACAAAAGACAGCCGAATGATC	2760
Qy	2787	GACCCACAATGSCAACCCAGGTGACTCGTGTCTTGGGACGTTTATGTCTATCGGAACAACAC	2846
Db	2761	GACCCACAATGSCAACCCAGGTGACTCGTGTCTTGGGACGTTTATGTCTATCGGAACAACAC	2820
Qy	2847	CTGCTGCGACCTGACACGCTCAGGAGACGCTGAGCTTCTGTCTACGTCCATGAGTATGCAA	2906
Db	2821	CTGCTGCGACCTGACACGCTCAGGAGACGCTGAGCTTCTGTCTACGTCCATGAGTATGCAA	2880
Qy	2907	ATCTCAAGACTCCCTCATTTCTGTCAATGTGCTCTTCCATGAGTGGCTTCTGATGCTCAACTGT	2966
Db	2881	ATCTCAAGACTCCCTCATTTCTGTCAATGTGCTCTTCCATGAGTGGCTTCTGATGCTCAACTGT	2940
Qy	2967	TTCTTTCGGTTTGGACAAAGTATATTTCTCAGAAACAGTGAAGTATTTTTCCTTAGAGAGAAA	3026
Db	2941	TTCTTTCGGTTTGGACAAAGTATATTTCTCAGAAACAGTGAAGTATTTTTCCTTAGAGAGAAA	3000
Qy	3027	TCTTTTAAACGGTATCTTTTTCGTTGCGTTAAGCTGTAGAAAATTAATGTCTCATGTAA	3086
Db	3001	TCTTTTAAACGGTATCTTTTTCGTTGCGTTAAGCTGTAGAAAATTAATGTCTCATGTAA	3060
Qy	3087	AGATATTATGACCTGCTTATTTATTTATGACAAAGTGTGTGATGAATATGTCTTCAGAC	3146
Db	3061	AGATATTATGACCTGCTTATTTATTTATGACAAAGTGTGTGATGAATATGTCTTCAGAC	3120
Qy	3147	TGGCACTTAGACTTCTCTATAA	3167
Db	3121	TGGCACTTAGACTTCTCTATAA	3141
RESULT 2			
US-10-425-114-13156			
Sequence 13156, Application US/10425114			
Publication No. US2004003488A1			
GENERAL INFORMATION:			
APPLICANT: Liu, Jindong			
APPLICANT: Zhou, Yihua			
APPLICANT: Kovalic, David K.			
APPLICANT: Screen, Steven E			
APPLICANT: Tabaska, Jack E			
APPLICANT: Cao, Yongwei			
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With			
FILE REFERENCE: 38-21(53313)B			
CURRENT APPLICATION NUMBER: US/10/425,114			
CURRENT FILING DATE: 2003-04-28			
NUMBER OF SEQ ID NOS: 73128			
SEQ ID NO 13156			

```

; LENGTH: 2750
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: JC-GWFL0220115B11_FLI
US-10-425-114-13156

Query Match      45.8%; Score 1486.6; DB 8; Length 2750;
Beet Local Similarity 74.8%; Pred. No. 0;
Matches 1883; Conservative 0; Mismatches 619; Indels 15; Gaps 1;

QY 504 AGCAGCTGATCTTGAGAAATTAACCAATTGATAGGACCGATCCCTTCAACATTTCACAGA 563
Db 1 AGAATCTGATTTTGAAGAACCAACCAATTGATAGGACCAATTCCTTCAACTTGTCTCAGA 60
QY 564 TTCCAAACCTGAAAAATTTCTGACTTGGCACAGAAATAAACTCATGTTGAGATACCAAGAC 623
Db 61 TTCTCGATTTGAAGATTTCTAGACTGGCTCAAAATATCTTAGCGGAGAAATACCAAGGC 120
QY 624 TTATTTACTGGAATGAAGACTTCTCAGATCTTTGGGTTCGAGAAACAATTAGTCGTA 683
Db 121 TTATATATTTGGAAAGCAAGTTTGGCAAAATCATAGGCTTGAGGGGCAAAATTTGGTGT 180
QY 684 ACATTTCTCCAGATTGTGTCAACTGACTGCTCTTGGTATTTTGAAGTAAGAAACA 743
Db 181 CACTATACCAAGACATGTGCGAGTTAACTGGCTGTGTGATTTTGAATGTGAACAATTA 240
QY 744 GTTTGACTGTGATGATACCTGAGACGATAGAAATTTGCACTGCCCTCCAGGTTTGGACT 803
Db 241 GCCGGAAGGAAGATTTCCAGAGAACATAGGCAATTTGATCTGCTTCCAGGTTTGGATT 300
QY 804 TGTCTTAACAATCAGCTTAAGTGTGAGATCCCTTTTGAATCTGCGCTTCTGCAAGTTGCA 863
Db 301 TATCTTAACAACAATTAAGTGTGAGATTAACCATTAATTTGAAATCTTGGCAATAGCA 360
QY 864 CATTATGATGCAAGGAATCAACTCTCTGGGAAGATTCATCGATATGTGTCATGCG 923
Db 361 CTTTGTCTTGGCAAGGCAATTAACCTCTGTGACATTAATTCACCGGTATGGTCTCATGC 420
QY 924 AAGCCTTGGAGCTTATAGATCTAAGTGGCAACTGTGTGAGTGAATCTAATTCCTCCGATTC 983
Db 421 AAGCACTTGTGCTGTGACTTGAAGCTTGAAGTGCACATTTGTAAGTGAATGATCCCTCTATCT 480
QY 984 TCGGAAATCTTACTTTCACCGAGAAATTTGATTTTGAACAGTAAACAGCTGACTGTGTTCAA 1043
Db 481 TGGGAAATTTGACTTTCACAGAAAAATTTGATCTTGCAATGGAACAAACCTGACTGGCTTCA 540
QY 1044 TTCCACTGAGCTTTGGAAACATGTCAAACTCCATTTACCTGGAACTGAATGATATATCATC 1103
Db 541 TCCCCCAAGAGCTTGGAAATTAATGTCAAAAGCTTCACTATTTGGAACTGAATGATATACCAT 600
QY 1104 TCACGGGTCAATATACCAACAGAGCTTGGGAAGCTTATCTGACTTGTGTGATCTGAATGTGG 1163
Db 601 TAAATGCAATATATCCGCCGAGCTTGGAAAGCTTAAAGATCTGTGATCTTAATATGTGG 660
QY 1164 CCAACAAATGATCTGGAAGAACCTATACTGATCACTGAGCTCTTGGCAAAATTTAAACA 1223
Db 661 CAACCAACAAATCTTGAAGGGGCAATTTCTAGTAACTTAGTCAATGTAAAAATCTCAACA 720
QY 1224 GCTTAAATGTTTCATGGGAACAAGTTTATGTGGCACTAATCCCGAGCAATTTCAAAAGCTAG 1283
Db 721 GCCCAATGTGCAATGGGCAACAAAGTTGAATGATCAATTTCCCTTCTTTGCAAGGTTTGG 780
QY 1284 AAAGTATGACTTACCTTAATCTGTCCAGCAACAATATCAAAAGTCAATCCCGGTTGAGC 1343
Db 781 AAGACATGACCTCTTTGAATCTTTCTTCCAAACAATCTTCAAGGCGCAATTTCAATAGAAC 840
QY 1344 TATCTCGTATCGTAACTTGAATCAATTGATCTTTTCCAAACAACAAGATAATGAAATCA 1403
Db 841 TGTGCGGGAATTTGGCAATTTGGAATCAATTTGATATTTTCAACAATAATCACTAGTTGGTTCA 900
QY 1404 TTCTCTTTCTTCCCTTGGTGTGATTTGGAGCATCTTCTCAAGATGAACCTTGAATGAATCATTA 1463

```

Db 901 TCCCTCTTCCCTTGGTGAAGCTTGGAAACATCTTCTGAAGTTGAATCTAAGCAGAAACAATT 960  
Qy 1464 TAACTGGTGAAGTTCAGAGCGACCTTTGGAAATCTAAGAGCATCATGGAAATAGATCTTT 1523  
Db 961 TAAACGAAATTAATTCACAGAAATTTGGAAATCTTAAGAGTTATAGAAATGATCTTT 1020  
Qy 1524 CAATTAATGAATATCTGGCCCAATTCAGAAAGCTTAAACCAATTAACAGAACTAAATTT 1583  
Db 1021 CAATTAATCACTCTGCGCTTGAATTCCTGATGAACCTTAAGTCAAGTCCAAACATGATAT 1080  
Qy 1584 TGCAGAGCTGGAAATTAATTAAGTGAATGTTGTTGTTCAATTAAGCCTGCTCA 1643  
Db 1081 CTTTGAAGCTTGAATTAACAAATTAAGTGAATGTTGTTCACTTTCAAATTTGCAATTA 1140  
Qy 1644 GTCTCACTGATTAATGAATGATCTCAATAACAAGTGAATGATATCCCTTAAGAAACATA 1703  
Db 1141 GTCTCTCTTAATTAATGTTGTTCAATAACAATTAATTTGTTATTTCCCAAGAGTAAACA 1200  
Qy 1704 ACTTCTCAAGATTTTACAGACAGCTTCAATGGCAATCTGCTCTTTCGGTGAAGTGGC 1763  
Db 1201 ACTTACAGAGTTTCCCTGACAGATTTCAATGGAAACCTGGTCTTGTGTTAATTTGGC 1260  
Qy 1764 TAACTCACTGATTAATGAATGATCTGGAAGTGAATGATGATCAATCTTAAGACAGTA 1823  
Db 1261 TGAATTTGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320  
Qy 1824 TTTCTTGAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1883  
Db 1321 TTTCTTGAATTAATCTTGGTCCCTTGGATTTCTTCTTAATGATGATGATGATGATGATG 1380  
Qy 1884 GACCGCATTAATCT 1943  
Db 1381 GACCAATATGATCCCT 1440  
Qy 1944 CACCGAAGCTGATCT 2003  
Db 1441 CCCCAGAGCTAATGATTTCTTAATTAATGAATGAGCACTAATGATGAATGAATGAATGA 1500  
Qy 2004 GAATGACAGAAATCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2063  
Db 1501 GGAATGATGAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1560  
Qy 2064 ACAATGATGTTGAAGATGTTGAACCGGTGCGATTAAGCGGCTTACTCTCAACACC 2123  
Db 1561 ATAATGATGTTCTTAAGATTTGCAAGCGGTGCTATCAAGAGATCAATCTCAATATC 1620  
Qy 2124 CACAGTCAATGAACAGTTTGAACAGAACTGAGATGCTTAATGATGATGATGATGATG 2183  
Db 1621 CCAATGATTAATGAATTTGAACCTGAACCTGAGCGTTGGAGCACTCAAGCAACCGGA 1680  
Qy 2184 ATCTTGTAGAGCTCAAGCTTATTCCTCTCTCACTTGGGAGTCTTCTGTCTATGACT 2243  
Db 1681 ATCTGTCAGTCTCAAGGTTATTCCTTGTCTCCATATGGGCACTCTCTGTTTATGACT 1740  
Qy 2244 ATTTGGAATATGATGCTCTGGGATCTTCTTCAATGGCCCTTAAGAGAAAGACTCTTG 2303  
Db 1741 ACAATGAAATGAGAGCTATGAGATCTTCTTCAATGAGCTCAACAGAGAAAGAGCTTG 1800  
Qy 2304 ATTTGGAACACAGGCTTAAGATGATGATGATGATGATGATGATGATGATGATGATG 2363  
Db 1801 ACTGGAGAGCTGCTTAATTAATTAAGCTTGGAGAGCACTTGGAGCTTATCTTAACCC 1860  
Qy 2364 ATGATCTAGTCAAGGATCAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2423  
Db 1861 ATGATCTGCTGCTTAAGATCACTCAAGAGATGATGATGATGATGATGATGATGATG 1920  
Qy 2424 AAGATTAAGAGCTGCTTGAAGATTTTGAATTAAGAGAAAGCTTGTGTGTCAAGT 2483  
Db 1921 CAGATTTGAGCCCTCACTCTCAATTTTGTATTTGGCCAAAGTCTGCCCCCAAGT 1980  
Qy 2484 CACATACCTTAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2543  
Db 1981 CCAATACCTTCACTTAATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040

Qy 2544 CTTACAGGCTCACTGAGAAATCCGATGCTTACAGTTATGAAATAGTCTTGAAGTGT 2603  
Db 2041 CTTACAGCTCACTGAGAAATGCTGATGCTTACAGTTATGAAATAGTCTTGAAGTGT 2100  
Qy 2604 TAAACGAGAGAAAGCGTTGATGATGATGATGATGATGATGATGATGATGATGATG 2663  
Db 2101 TAACTGAGAGAAAGCGTTGATGATGATGATGATGATGATGATGATGATGATGATG 2160  
Qy 2664 CCGGAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2723  
Db 2161 CAGCAACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2220  
Qy 2724 TCGGTGATGAGAAAGTTTCCAACTGAGCTCTTATGATGATGATGATGATGATGATG 2783  
Db 2221 TAGAGCTGTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 2280  
Qy 2784 ATGAGCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2835  
Db 2281 ATAGGCGAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2340  
Qy 2836 -----GSAACAACCACTGCTGCGACATGACATGATGATGATGATGATGATG 2888  
Db 2341 CACCAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2400  
Qy 2889 ACGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2948  
Db 2401 ACGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2460  
Qy 2949 CTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3005  
Db 2461 CTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2517

RESULT 3  
US-10-424-599-28166  
; Sequence 28166, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21 (53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 28166  
; LENGTH: 4060  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(4060)  
; OTHER INFORMATION: unsure at all n locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_125435C.1  
US-10-424-599-28166

Query Match 45.4%; Score 1441.4; DB 8; Length 4060;  
Best Local Similarity 69.0%; Pred. No. 0;  
Matches 2049; Conservative 0; Mismatches 886; Indels 36; Gaps 4;

Qy 68 GTGAGAAATGAGCTGCTGTTTGAAGATATGTTCTTGGGTTTCTCTTCTGAGC 127  
Db 505 GTTGCAGCTAATGAGCATTTGATTTGAGTCTTATTTGCTTGAATTTGTTGAG- 563  
Qy 128 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 187  
Db 564 --TGTCAATTTGTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 621

OY	188	AAAGTGTGAACAATGTTCTTTATGACGTGAGCAACCTTCAACCTTCTCGAATTATGTGC	247
Db	622	AGGATGTGATTAATGTTCTCTATATGGACTGATATCAACATCATGATTAATGTGCC	681
OY	248	TGAGAGGTGTGTCTTGTGAANAATGTCACTCAATGTGTGTCTTAAATTTGTCAAT	307
Db	682	TGAGAGGGATATGACATGTGATATGTCACTTCAATGTTGTTGCCTCAATCTTCAAGG	741
OY	308	TTGAATCTTGATGAGANAATCTCACTGTCTATTTGAGATTTCTAAGAGT-----	355
Db	742	TTGAATCTTGATGTGGAATTTCACTGCATATAGGANAATGTGACAGTTTGGCTGGAAG	801
OY	356	-----CTCTTGCAATGATCTGCCAGATATGCTGTCTGCACAAAATCCCTGATGAAT	411
Db	802	AAAGCTGTGACAAATGAATCCAACTCCGACCATCTTAATTTGTGTCCAGGCAAGCAACAT	861
OY	412	TGTGTACTGTTCTTCTTGCAGAAACTTATGACTTATCTTCAATGAATTAAGGTGATAT	471
Db	862	GCTGTGATGTGAACAGTGTATCCGACATTTACTGCCAAGGCAAGACCTATGACTGTC	921
OY	472	ACCGTTTTGCATTTTCGAATGTGAAGCAACTGACAGCTGATTTTGAAGATTTACCAAT	531
Db	922	TAAGTGTATTTACAGCTTGCTTTATTTATGACAAAAGAGATTTTGAAGATCGGCCAAT	981
OY	532	GATAGGACCGCATCCCTTCAACACTTTCACAGATTTCCAACTGAAAATTTTGGACTTGGC	591
Db	982	GATTGGCCAAATGACCAACCGTTTGTCTCCAATTTCTGATTTGGAAGATTTAGACTTGGC	1041
OY	592	ACAGAAATTAACACTAGTGTGTGAGATACCAAGACTTTATTAAGTGAATGAAGTTCTTCAGTA	651
Db	1042	TCAAAATTAATCTTACGGAGAAATACCAAGTCTTATATCCAAGACGAAGTTTTCAGATA	1101
OY	652	TCTTGGGTGGAGAGAAAACAATT--AGTCGGTAACTATTTCCAGATTTGTGTCAACTG	709
Db	1102	TCTGTAGCTGAACCTCAACACTTTGCATTTAGTAAACAGCCCTCAATTTGTGCTTCAAA	1161
OY	710	ACTGTCCTTGTGATTTTGAAGCTTAAGAAAACAAGTTGACTGTGATATACCTGACAGC	769
Db	1162	CTGGCACTCTCTCTCTGTTTGGAGAGCAATCTCTCAAAACAGTGAAGTAGAGAGG	1221
OY	770	ATAGAAATTTGCACTGCGCTCCAGGTTTGTGACTGTGCTCAATCAGCTPAACGTGTAG	829
Db	1222	ATTTTGAATTTGAATAATCATTTCTCAATCTTGGATTATCTTCAACAAACTPAACGTAGAG	1281
OY	830	ATCCCTTTTGACATGCGCTTCTCGAAGTTGCAACATTATCATTTGCAAGGCAATCAATC	889
Db	1282	ATACCATTCATATTTGATCTTGTGAATGAGCACTTTGTCTTTCAGAGGCAATTAATCTC	1341
OY	890	TCTGGGAAGATTCACACAGATGATTTGTCTCATGAAGCCCTTTCAGCTTTAGATCTAAGT	949
Db	1342	TCTGGACATATTTCCACCGGTGATCGGTCTCATGCAAGCACTTGCTGCTAGACTTGAAC	1401
OY	950	GGCAACTTGTGAGTGAATCTATTTCTCTCCGATTTCCGAAAAATCTTACTTTTCAACGAGAA	1001
Db	1402	TGTAAACATGTTAAGGATTCGATTCCTCTTAATCTTGGGCAATTTAATCACTTCAACAATAAA	1461
OY	1010	TTGTATTTTGACAAGTAAAGCTGACTGGTTCAAATTTCCACCTGACCTTGGAAAACATGTCA	1065
Db	1462	TTGTACTTGCAATGAGAAACAAGCTGACTGGCTTCAATCCCCAGAGCTTGGAAATATGTCA	1522
OY	1070	AAACTCCATTACTTGGAACTCAATGATATCATCTCAGGGCTCATATACACAGAGCTT	1122
Db	1582	GGAAAGCTTACTGATCTGTTTGAATTAATGTGTGAAAACAACAACTCTCAAGGGGCAATTT	1641
OY	1190	CCGTGATCATGTGAGCTCTTGCACAATCTTAAACACTTAAATGTTCAAGGAAACAAGTTT	1245
Db	1642	CCGTGATATCTTGACTCATGTAAAAATCTCAACAGCTCAATGTGTGATGTGCAACAAAGTTG	1701
OY	1250	AGTGGCACTATACCCCGAGCAATTTTCAAAAGCTGAAAGTATGACTTAACTTAATCTGTGC	1305

Db	1702	AATGGATCAATTC	CCCCCTTCTTTGCAGAGTTTGGAGGAGTGAAGTCACTCTTTGAATCTTTCT	1761
Qy	1310	AGCAACAATATCAAAAGGTCCAATCCGGTTGAGCTATCTCGTATCGGTAACTTAGATACA	1369	
Db	1762	TCCAAACATCTTCGAGGCGCGCAATTCCAATAGAACTGTCCGGGATTGGCAATTTGGATACA	1821	
Qy	1370	TTGGATCTTTCCAAACAACAAGATTAATGAATACATTCCTTCTTCCCTTGGGATTTGGAG	1429	
Db	1822	TTGGATATTTCCAAACAATACTTAAGTTGGTTCCATCCCTTCTTCCCTTGGGACTTGGAA	1881	
Qy	1430	CATCTTCTCAGAGATGAATCTTGAGTAAGAAATCATCTTAATCTGGTGTATTCAGCGGACTTT	1489	
Db	1882	CATTTTCTGAAGTTGAATCTTAAGACAAACAAATTTAAACAGAAATATTTCCAGCAAAATTT	1941	
Qy	1490	GGAATCTAAGAAAGCATCATGAAATAGATCTTTCAAATAATGATATCTCTGGCCAAAT	1549	
Db	1942	GGAATCTTAAGAGTGTATAGAAATTTGATCTTTCAATATATCAACTCTGGCTTGATT	2001	
Qy	1550	CCAGAGAAGCTTAAACAATTAACAGACATAATTTTCTGAGACTGGAATAATATAACCTG	1609	
Db	2002	CTGTATCAACTTAAGTACGCTTCCAAACATGATATCTTTGAGACTTGAATAATACAAATTTG	2061	
Qy	1610	ACTGGTAAATGTGGTTGATTAAGCCCAACTGTCTCAGTCTCACTGATTAATGATATCAT	1669	
Db	2062	ACTGGCAATGGGCATCACTTCAAAATGCAATTAATGTCTCTCTCTACTTAATGTGTCTAT	2121	
Qy	1670	AACAACCTCGTAGGTGATATCCCTTAAGAACATAATCTTCAAGATTTTCAACAGAGC	1729	
Db	2122	AACAACATATTTGGTGTATATCCAAACAGATTAACAATTTACAGAGTTTCCCGTCAGACGT	2181	
Qy	1730	TTCAATGGCAATCTCGGTCTTTTGGCGGTAGTTGGCTAACTCAACCTGTCAATATCTTGT	1789	
Db	2182	TTCAATGGAAACCTCGGTCTTTTGGGTAAATGGCTGAATTTGGCCGTCTCATATGGCTCGC	2241	
Qy	1790	CGAATCTAAGAGGTCAATCTCTAAGAGCAACTATCTTGGAAATAGCTATTTGGGGGACTT	1849	
Db	2242	CTTTCAGAGGAGTTACATTAATCTTAAGGCTGCACTTTTGGAAATTAATCTTTGGGCCCTT	2301	
Qy	1850	GTCATCTCTTCATATGCTCTTAATATAGACAGCTTGGCCGACCGCATATCTCTCTCTTTTCTT	1909	
Db	2302	GTGATTTCTTCTTAATGTATATGTCTCCGAGAAAGACAGACAGAAAGGGGTCCCTCTCTTTTCT	2361	
Qy	1910	GATGATCACTTGAACAACAGATTAATTTCTCCCCCCAAAGCTAAGATTTCTTCATATG	1969	
Db	2362	GATGATCACTTGAACAACAGATTAATTTCTCCCCCCAAAGCTAAGATTTCTTCATATG	2421	
Qy	1970	AACATGGCACTCCACGCTTTACGAGATATCATGAAATGACACAGAAATCTTAATGAGAG	2029	
Db	2422	AATATGGCACTCACTGTGTATGAAGATATCATGAGATGACTGAAACCTGACAGGAGAG	2481	
Qy	2030	TATATCTTTGGGGACGAGAGATCAAGACACTGTATACAAATGTGTTTGAAGAAATTTGAAA	2089	
Db	2482	TATATTAATTTGAGATTAAGAGCAATCAAGTACAGTTTATTAATGTGTTCTTAAGAAATTCAG	2541	
Qy	2090	CCGGTTCGATTAAGCCGCTTTACTCTCAACAACCCACAGTCAATGAAACAATTTGAAA	2149	
Db	2542	CCGGTTCGATTAAGAGAGATCTATTTCTCACTATCCCAATGTATTAAGAATTTGAAACT	2601	
Qy	2150	GAACTCGAATGCTTAAGTAGATACAGACAGAAATCTTTGAGCCTACAAAGCTTATTTCC	2209	
Db	2602	GAACTTGAAGCGTTTGCACAGATCAACACCGGATCTGGTCACTTCCAAAGTTATATTC	2661	
Qy	2210	CTCTCTCACTTGGGGAGTCTTGTTCTATGACATTAATTTGAAATGTGTAGCCTCTGGGAT	2269	
Db	2662	TTGTCTCCCAATATGGGCACTCTCTGTTTTATGACTACATGAAATGTGCAAGTCTATGGGAT	2721	
Qy	2270	CTTCTTCATGAGCCCTACGAAGAAAAGACTCTTGATTTGGACACACGCGCTTAAAGTATGA	2329	
Db	2722	CTTCTTCATGAGCCTACGAAGAAAAGACTTGAAGCTGGAGCTGCTTAAAAATATGACA	2781	
Qy	2330	TATGTGACAGACAAGTTTATGCTTATCTACCATGACTGTATGTCCAAAGATTAATTCAC	2389	

Db	2782	TTTGGAGACGACCAAGGGCTTGTTATCTACACCATGATGTGTCTTAGAATCATCCAC	2841
Oy	2330	AGAGACGTGAAGTGCCTCCACATTTCTTTGGACAAAGACTTBAGSGCTCGTTTGACAGAT	2449
Db	2842	AGAGATGTGGAATCATCTTACATCTTATTTGATGTGCAGACTTTGAGCCCTCATCTCATGAT	2901
Oy	2450	TTTGGAAATAGCGAAAAGCTGTGTGTGTCTCAAGTACATCTTCAACTTAAGTATGGGC	2509
Db	2902	TTTGGCATTTGCCAATAAGTCTCTGCCCCCTCAAGTCCCATCTTCTCATTAATATGGGC	2961
Oy	2510	ACGATAGGTTCATATGACCCCGAGTATGCTGSCATTTCACGGCTCATGTAGAAATCCGAT	2568
Db	2962	ACAATTTGGCTATATGAGCCCTGAGATATCTTGAACTTACGCTCTCATGAGAAAGTCTGAT	3021
Oy	2570	GTCTACAGTTATGGAATAGTGCCTTTTGAAGTTGTAAACCGAAGGAAGCCGTTGATGAC	2629
Db	3022	GTGTACAGTTACGGAATGTTGTTTACTTGAATGTTGTCTAATCTGAGAGAAAGCTGTTGACAT	3081
Oy	2630	GAATTCCAATCTCCACCATCTGTATTAATGTCAAGACGGGGAAACAATGAATGATGAATG	2689
Db	3082	GAATTCCAACCTCCACCATCTGTATTTTGTCCAAAGCAGCAACCAATGCAGTATGGAACA	3141
Oy	2690	GCAGATCCAGACATACACATTCGACGTTGTAAAGATCTCGGTGTGTGTGAAGAAAGTTTCCAC	2749
Db	3142	GTTGATTCGAGACATTAATCTGCGCATGACAGGACCTTAGAGCTGTAAAGAGTTTATCAG	3201
Oy	2750	CTGGCAGCTCTATGACACCAAGACAGCCGATGATTCGACCCCAATGCAACAGGTGACT	2809
Db	3202	CTTGCTCTATTATGACCAAGAGGACGACGAGTGTATGAGCGACATGACAGAGTGACA	3261
Oy	2810	CGTGTTCCTGGCAGTTTATCTATC-----GGAAACACACCTGCTGCG	2854
Db	3262	CGTGACTCTGGAAGCTGTGTGTCTCAAAACCCCAACCAAGCAACTGCTGCACCTACCA	3321
Oy	2855	ACTGACACGTGACGACCGCTGGCTGTGTGCTGCTACGTGATGATGATGACAAATCTCAAG	2914
Db	3322	CCTGTTCAAAATTCATCTGCGCAAGGTGCCATGCTACGTGATGATGATGACAAACCTCAAG	3381
Oy	2915	ACTCTCTATTCTGTCAATTTGCTCTTTCATGAGTCTTCTGATGCTCAACTGTTTCTTGG	2974
Db	3382	ACTCCACACTTGTGTAACTGCCCCCTCAATGAGCACTCAGATGCTCAACTCTTCTCTCAAG	3441
Oy	2975	TTTGGACAAAGTTATTTCTCAGAACAGTAGT	3005
Db	3442	TTTGGAGAAATATCTCTCAAAACAGTAGT	3472
RESULT 4			
US-11-027-304-7			
Sequence 7, Application US/11027304			
Publication No. US20050223428A1			
GENERAL INFORMATION:			
APPLICANT: Torii, Keiko U.			
APPLICANT: Shupak, Elena D.			
TITLE OF INVENTION: METHODS FOR MODULATING PLANT GROWTH			
FILE REFERENCE: UW01212663			
CURRENT APPLICATION NUMBER: US/11/027,304			
CURRENT FILING DATE: 2004-12-30			
PRIOR APPLICATION NUMBER: US 60/558,529			
PRIOR FILING DATE: 2004-04-01			
NUMBER OF SEQ ID NOS: 88			
SOFTWARE: PatentIn version 3.2			
SEQ ID NO 7			
LENGTH: 3089			
TYPE: DNA			
ORGANISM: Arabidopsis Thaliana			
FEATURE:			
NAME/KEY: CDS			
LOCATION: (186)..(3089)			
US-11-027-304-7			

	Matches	1760:	Conservative	0:	Mismatches	927:	Indels	12:	Gaps	3:
QY	150	AGAGAGGACCAACGTTGCTGGAGATTAAAGATCAATTCAAAGATGTGAACAATGTTCTTT	209							
Db	274	ACGAAGGAAAAAGCGTTGATGGCGATTAAAGCGTTCAATTCAGCAAGCTGGCGAATATGCTTC	333							
QY	210	ATGACTGGAACAATTCACTTCCTCCGATTATTTGTCGTGGAGAGGTGTCTGTGAAA	269							
Db	334	TTGATTTGGAGCGATGTTTATTAACCAACGCTTTTGTCTTGGAGAGGTGTCTTCTGTGATA	393							
QY	270	ATGTCACCTTCAAATGTTGTTGCTCTCTTAATTTGTGCAATTTGAAATCTTGATGAGAAAAATCT	329							
Db	354	ACGTTAGCCTCAATGTTGTCTCTTTAATCTGTCAAACTGAAATCTTGATGAGAGATAT	453							
QY	330	CACCTGCTATTGGAGATCTCAAGAGTCTCTTGTCATATGATCTGGAGGTATGCGTTCT	389							
Db	454	CATCGCCCTTGGAGATTGTGATCGCAATCAATAGACTTCCAAAGAAATTAATTTGG	513							
QY	350	CTGGAACAATCCCTGATGAGATTGGTGACTGTCTTCTTTGCAAACTTAACCTTAATCCT	449							
Db	514	GTGGCAAAATTCAGATGAGATTGGAAACTGTGTTTCTCTTGCTTAATGTGATTTCTCCA	573							
QY	450	TCAATGAATTTAAGTGTGACATACCGTTTGTGATTTGCAATTTGAAGCACTTGAGCAGC	509							
Db	574	CCAAATTTGTGTTGGAGACATACCGTTTCAATCTCAAACTCAACAGCTGGAGTTTC	633							
QY	510	TGATTTGAGAGAAATPAAACCAATTGATAGGACCGATCCCTTCAACATTTCAACAGATTCCAA	569							
Db	634	TGAACCTTAAGAAATATATATACAGCTCACTGGTCCAAATACAGCAACCTTAACTCAGATTCCAA	693							
QY	570	ACCTGAAATTTCTGGAATCTTGGCAACAGAAATTAATCAAGTGTGAAATPACCAAGACTTATTT	629							
Db	694	ACCTTAAACCCCTTGACCTCCGAAAGAAACGCTTACGTGTGAATPACCAAGTTACTCT	753							
QY	630	ACTGGAATGAAGTTCTTTCAGTATCTTGGGTTGACGAGAAACAATTTGTCGATAACATTT	689							
Db	754	ACTGGAATGAAGTTTATACAGTATCTCGGTTTACGTGGAAATATGTTAACTGGGCAATTTGT	813							
QY	690	CTCCAGATTTTGTCAACTGACTGCTCTTTGGTATTTTGAAGTAAGAAACAACGTTTGA	749							
Db	814	CTCCGATATATGTGTACGCTGACGGGTGTGTGTACTTTGATGTGAGAGGCAACAACCTTA	873							
QY	750	CTGGTAGTATACCTGAGACGATAGAGAAATTGCACTGCCCTTCAGATTTTGGACTTGTCT	809							
Db	874	CTGGAACTATCCCAAGAGACATTGGCAATTGGCAACAGCTTGAATCTTGGATGTATCTT	933							
QY	810	ACAATTCACCTAACTGCTGAGATCCCTTTTGAATCCGCGCTTCGCAAGTTGCAACATTA	869							
Db	934	ATTAATCAATTAACCGAGATTATACCTTAACAATATTTGTTCTTCCAAAGTACCTACTGT	993							
QY	870	CATTGCAAGGCATCAACTCTCTGGGAGATTTCCATCAGTATGTTGCTCATGCAAGCC	929							
Db	994	CACTTCAAGGAAACAAGTTGACTGGCAAGAAATTCGGAAGTATTTGGTCTGATGCAAGGCTC	1053							
QY	930	TTGCACTTTAAGTCTAAAGTGCACTTTGTGAGTGAATCTATTCTCCATTTCTCGGA	989							
Db	1054	TTGCTGTATTGATTTGATGACATGAAATTAACCTGGGCTCAATTCACCAATATCTTGGGA	1113							
QY	990	ATCTTAATTTTAAACCGAGAAATTGATTTTGGCACTTAACAAGCTGACCTGTTCAATTCAC	1049							
Db	1114	ATCTGTCAATTTACCTGAGAAACTGTATCTCCATGCGCAACAGCTCACTGGACAAATCCAC	1173							
QY	1050	CTGAGCTTGAAGACATGTCAAACTCAATTAACCTGGAACCAATGATTAATCATCTCAAG	1109							
Db	1174	CCGAGCTTAGGCAATATGTACAGACTCAGACTATTGGCAACTTAATGATATAGTAATTAAGG	1233							
QY	1110	GTCATATACCAACGAGCTTGGGAAGCTTACTGACTTGTGATCTGAATGTGCCAACA	1169							
Db	1234	GAAAGATCCCACTGAGCTTGGGAAGCTGGAACAATTTGTTGAACTGAATCTTGCAGAAC	1293							
QY	1170	ATGATCTGGAAGGACATTAATCTGATCATCTGAGACTCTTGCACAAAATCTAAACAGCTTAA	1229							
Db	1294	ACAATCTTTGAGGGCTGATTTCCATCTAAATTAATGTTCTGTGCTGCTTGAATCAATTTCA	1353							





QY	251	AGAGGTGTCGTCCTTGAAAAATGTCACCTCTCAATGTTGTGCTCTTAATTGTCAGATTGG	310
Db	383	CGAGGTGTTTTCTGCGAACAGCGTTAGCTACTCCGTTGCTCTCTCGAAATTTGTCCAGCTCG	442
QY	311	AATCTGTAATGGAGAAATCTCACTCGCTATTTGGAGTCTCAGAGCTCTTGTGCAATTGAT	370
Db	443	AATCTTGGAGGGGAAATATCTTCACACTATGGAGCTTAGGAAATTTGCAATCAATAGAC	502
QY	371	CTGCGAGGTAAATCGCTTGCTTGGACAAATCCCTGATGAGATTGGTGACTGTTCTTTTGG	430
Db	503	TTTGCAGGTAATTAACTAAGCAGGTCAAAATTCAGATGAGATTGGAAACTGTGCTCTCTT	562
QY	431	CAAAAATTAGACTTATCCTTTCAATGAATTAAGTGTGCATACCGTTTGGATTGGAAG	490
Db	563	GTTTATCTGGATTGTGCCGAAATCTGTTAATATGGAGCATACCTTTCTCATCTCTAA	622
QY	491	TTGAAGCAACTTGGACACTGATTTCTGAAAGTAATCCAAATTGATATGAGCCGATCCCTTCA	550
Db	623	CTCAAGCAGCTTGAACCTGTGAATTTGAAGAACATACGCTCACAGGCTCTGATCCAGCA	682
QY	551	ACACTTTACAGATTCCCAAACTCGAAAAATTTGCGACTTGGACAGAAATAACTCAATGTT	610
Db	683	ACCTTAACCCAGATTCCAAACTTTAAGAGCTTGATCTTGTGGCAATCATCTAACGGGT	742
QY	611	GAGATACCAAGACTTATTACTGSAATGAAGTTCTTCAGTATCTTGGGTTCGAGAAAC	670
Db	743	GAGATATCGAGATTGCTTTACTGGAATGAAGTTTGGCAGTATCTTGGATTACGAGGAAAT	802
QY	671	AACCTAATGCGGTAACATTTCTCCAGATTGTGTCAACTGATCTTTGGTATTTTGAC	730
Db	803	ATGTTGACTGGAAAGCTTATCTTCTGATATGTGTACGCTTAACCGGTTGTGGTACTTTGAT	862
QY	731	GTAAGAAACAAACAGTTTGAAGTGTAGTATTAAGCTGAGACGATAGGAAATTTGACCTGCTC	790
Db	863	GTAGAGGAAATTAATCTAATCTGGAACCATCCCGAGAGACATGGAAATTTGACAAAGTTT	922
QY	791	CAGGTTTGGACTGTCTCTAACAATCAGCTAACTGTGATGATCCCTTTGACATCGGCTTC	850
Db	923	CAAAATCCCTGGACATATCTTAAATCAGATTAACAGAGAGATTCCTTCAATATGCGCTTC	982
QY	851	CTGCAAGTTGCAACATTAATCAATGGAAGCAATCACTCTGGGAGATTCCTACATCGT	910
Db	983	CTCCAGTTGCTACTCTGTCACTTCMAAGAAACAGATGAGGGTATGAATTCAGAAATT	1042
QY	911	ATTGCTCATGCAAGCCCTTGCAAGTCTTAATCTAAGTGGCAACTTGTGATGATGATCT	970
Db	1043	ATGSGTCTAATGCAAGGCTCTTGCTGTTTGGATTTGAGTGCAATGAGCTTGTGTGCTCT	1102
QY	971	ATTCTCCGATTCCTCGAAATCTTACTTCAACCGAGAAATTTGATTTGGACAGTAAACG	1030
Db	1103	ATCCACCGAATCTTGGCAATCTCTCATTTTACCGGAAGTTGATCTTCATATGGCAATATG	1162
QY	1031	CTGAATGTTCAATTCACACTGAGTTGGAAACATGTCAAACTCCATTAAGTGAATCTC	1090
Db	1163	CTCACTGGCTCAATCCCTCTGAGGTTGGAAATATGTACGTCTCAGCTATTGCAACTA	1222
QY	1091	AATGATTAATCAATCTCAGGGTCAATTAACACAGAGCTTGGGAACTTACTGACTTGT	1150
Db	1223	AACGACATTAATAGTGGGAACTTTCACCTGAGCTTGGAAAGCTGGAGCAATTTGTT	1282
QY	1151	GATCTGAATGTGGCCACAATGATCTGGAAGGACCTATACCTGATCATCTGAGCTTTGC	1210
Db	1283	GAACTGAATCTTGGCCACAGCCGTTTATGTAAGGCCCATACCATCAATATGATCTATGT	1342
QY	1211	ACAAATCTAAACAGCTTAAATGTTCAATGGGAACAAGTTTATGGCACTATACCCCGAGCA	1270
Db	1343	GCAGCTTGAATCAATTAATGTTTCATGGGAACTCTTGAATGATCTATATCCACTGGCG	1402
QY	1271	TTTCAAAAGCTAGAAAGTATGACTTAATCTGTCCAGCAACAATATCAAGGTCTCA	1330
Db	1403	TTTCCCAATCTCCGGAAGCTGACTTATCTGAAATCTTTGTGTGMAACAATTTCCAGGAAAA	1462
QY	1331	ATCCCGGTTGAGCTATCTGTATCGGTATCTTAAGTATCATTTGATCTTTCCACAACAAG	1390

Dp	1463	ATACCGATTGAGCTTGGACATATATATCAATCTTGACAACTAGATCTGTCTGGCAATAC	1522
Qy	1391	ATAAATGAAATCATCTCCTCTCCCTGGTGTATTTGGAGCATCTTCTCAAGATGACTTG	1450
Dp	1523	TTCTCAGGCTCTATACCATTTAAGCTGGGCACTTTBAACACCTTCTCATTTAAATCTT	1582
Qy	1451	AGTGAATATCATATPACTGTGTAGTTCACGGCAGCTTTGGAAATCTAAGAGCATCATG	1510
Dp	1583	AGCGAAACCACTTTAGAGGACAATTAACCTGCAGAGTTGGGAACCTTCGAGCATTCAG	1642
Qy	1511	GAATATAGTCTTTCAATTAATGATATCTCGGCCCATTCAGAAAGCTTAACCAATTA	1570
Dp	1643	ATGATATGATATCAATTCATCTGCTCTCCGAGTTATTCACCTGAACCTTGGCCAAATG	1702
Qy	1571	CAGAAATATTTTGTGAGAGCTGGAAATATATTAACCTGACTGGTAAATGTT---GGTTCA	1627
Dp	1703	CAGAAATTTAACTCTTTATATTTGAACACACAGACTTCATGGGAAATTCACGATCAG	1762
Qy	1628	TTAGCAACTGTCTCAGTCTCAGTATATGATATATCTCATTAACAACCTGTAGTAT	1687
Dp	1763	CTTAGCAACTGCTTCACTCTGTCAATCTGAATGTCTCTTCAACAATCTCTCCGGGATA	1822
Qy	1688	ATCCTTAAGAACATTAACCTTCAAGATTTTACACAGACGCTTCAATTGGCAATCCGTGT	1747
Dp	1823	GTCCACCAATGAAGAAATCTTCTCAGCTTTGTCTCAGCAGCTTTGTGTGAATTCATAT	1882
Qy	1748	CTTTGCGGTATTTGGCTAACTCAACCGTGTCAATTTCTCGTCGACCTGTACGAGTGTCA	1807
Dp	1883	CTTTGTGGAACCTGGGTGTGATCTATTTGTGTGTCTTTACCGAATCTCGA-----GTA	1936
Qy	1808	ATCTCTAGAGACGCTATTTCTTGGAAATGCTATTTGGGGGACTTGTATCTCTTCATGCTC	1867
Dp	1937	TTCTTCAGAGGTGCTTGTATCTGCAATGTCTTGGCGTCACTCTCTCATATGTATATTT	1996
Qy	1868	TTAATAGAGCTTGGCCGACCGCATTAATCTCTCTCTTCTGTATGATATCACTTGACAA	1927
Dp	1937	TTCTCTGAGATTAACAATCAATCAGACAGAAAGATTTCAAGGCTC-----CTCA	2050
Qy	1928	CCAGTAATCTTATTTGGACACCGAAGCTCGTCACTCTTCAATATGAACATGGCACTCCAGTT	1987
Dp	2051	AAACAGCTGAAGGTTTAAACCAAGCTAGTATTTCTCAATGACATAGGCAATTCATATCA	2110
Qy	1988	TACGAGATATCATGAGATGACAGAGAAATCTAAGTAGAAGTATATCTATTTGGGACGGA	2047
Dp	2111	TTTATGATATCATGAGAGTACGTAGAGATCTTAACGAAAGTTTATATTTGATATGTGT	2170
Qy	2048	GCATTCAGACTGTATACAAATGTGTCTTTGGAAGATTTGTAAACGGGTTCGATTAACGG	2107
Dp	2171	GCTCTTACACAGGTATACAAATGTGCATTAAGAAAGTTCCGACCTATTTGCTCATTAACGA	2230
Qy	2108	CTTTACTCTCAACCAACCAAGCTCATGTAAGAACAGTTTGAACAGAACTCGAGATCTAAT	2167
Dp	2231	CTCTTCATCTAGTATCCGACATTAACCTTGGGGAATTTGAGACAGAACTTGAAGCATTTGG	2230
Qy	2168	AGCATCAAGCACAGAAATCTTGTGAGCCTCAAGACTTATTCCTCTCTCACTTGGGAGT	2227
Dp	2291	AGCATTTAGGCACAGAAACATAGTAGCTCAGCTTGATGATATGCTGTCTCTACTGCGAAC	2350
Qy	2228	CTTCTGTCTATGACTATTTGGAAATGTATAGCTCTTGGGATCTTCTTCATAGGCCCTACG	2287
Dp	2351	CTTCTTTCTATGACTACATGGAATGTAGTACCTTTGGGACCTTCTTCATGGGGTCAATTG	2410
Qy	2288	AAGAAATAGACTCTTGATTTGGGACACACGCGCTTAAGATAGCATATTTGGTGCACAAAGT	2347
Dp	2411	AAGAAATGAAAGCTTGTGTGGGAGCAAGTTGAAGATAGCGGTTGGAGCTGCACAAAGA	2470
Qy	2348	TTAGCTTATCTACACCATGACTGTATGTCAGAGATCATTCACAGAGACGTAAAGTGTCTC	2407
Dp	2471	CTAGGCTATCTTCAACCAAGATTGATCTCTGCAATCTCACCGTGACATCAATCATATCG	2530
Qy	2408	AACATCTCTTGGACAAAGACTTGAAGGCTGTTGACAGATTTTGGAAATGCGAAAGC	2467

Db 2531 AACATCTCTTGATGAAATTCGAAGCACACTTATCTGATTTGGGATTGTGAAGC 2590  
Qy 2468 TTGGTGTGTCAAGAGTCAACTTCACTTACGTGATGGGACGATAGGTTACATAGC 2527  
Db 2591 ATACCACTGACAAACCCAGCTCGACTGATGATTTGGGAACAATGGTTATATAGC 2650  
Qy 2528 CCCGAGATATCTCGCACTTTCAGCGGCTCACTGAGAAATCCGATGTCTACAGTTATGAATA 2587  
Db 2651 CCAGAGATATCTGCTGATCTTACGATATCAATGAGAAATCCGATATATACAGCTTCGATTT 2710  
Qy 2588 GTCTCTTGTAGTTGTTAAACCCGAAGAAACCGTGTATGATCGAATCAATCTCCACCAT 2647  
Db 2711 GTTCTTCTTGAAGCTTCTCAGCTGGGAGAAAGCAGTGTATTAACGAACTTAACCTGCACTAA 2770  
Qy 2648 CTGATATATGTCAAAGACGGGAAACAATGAATGTAATGGAATGCAATGCCAGATCACA 2707  
Db 2771 CTGATATATGTCAAAGCTGATGATTAATCTGTATGAGAACAGTGTATCCAGAGTTACT 2830  
Qy 2708 TCGACGTGTAAAGATCTCGGTGTGTGTAAGAAAGTTTCCAACTGGCACTCTATGCAAC 2767  
Db 2831 GTGACTGTATGACTTGGACATATCAAGAAAGCAATTTCAAGCTGCTCTTATGACACA 2890  
Qy 2768 AAAAGACAGCCGATGATGCAACCCCAATGCAACCAAGTGAATGCTGTCTCGCAAGTTT 2827  
Db 2891 AAGCGAAACCTTTAGAGAGAACCAATGCTTGAAGTCTTAGGGTTCTGCTCTCTT 2950  
Qy 2828 ATGCTATCGGAACACACACC 2847  
Db 2951 GTCCCACTCTCTGCAAGTAGC 2970

## RESULT 6

US-10-425-115-182550  
; Sequence 182550, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ. ID NOS: 369326  
; SEQ ID NO 182550  
; LENGTH: 3162  
; TYPE: DNA  
; ORGANISM: Zea mays  
; OTHER INFORMATION: Clone ID: MRT4577\_98067C.1  
US-10-425-115-182550

Query Match 32.5%; Score 1032.2; DB 9; Length 3162;

Best Local Similarity 63.5%; Pred. No. 5.3e-286; Matches 1644; Conservative 0; Mismatches 933; Indels 12; Gaps 4;

Qy 305 GATTGAATCTTGATGAGAAATCTCACTGCTATGAGATCTCAAGAGTCTTGTCTCA 364  
Db 14 GATCTAAACCTCGGAGGAGATCTCGCGCTATAGGAGCTCAAGAGCTCAAGTTG 73  
Qy 365 ATTGAATCTGAGAGTATGCTCTGTGACAAATCCCTATGAGATGATGCTGTTCT 424  
Db 74 GTGGAATCTCAAGCTGAACAGCTCAAGGCCAAATCCCAATGATGATGGGATGGTCT 133  
Qy 425 TCTTTCGAAAACCTTAGACTTATCTTCAATGAATTAAGTGTGATACACGTTTTCATT 484  
Db 134 TCTTAAATATTTGATTTGTGGGCAACTTGTGATGAGACATCCCTTCTTCATC 193  
Qy 485 TCGAAGTTGAAGCACTTGACAGCTGATTTCTGAGAAATTAACCAATGATAGACCGATC 544  
Db 194 TCTAAGCTCAAGCACTTGAGACCTGATTTTGAAGAAACAACCACTCACCGGACCATC 253

Qy 545 CTTTCAACACTTTCACAGATTCGAAACCTGAAATTTCTGGACTTGGCAGAGAAATTAACCTC 604  
Db 254 CCTTCACACTGTGACAGATTTCCAAATCTCABAACCTTGATCTGGCGGAGAACAACTT 313  
Qy 605 AGTGTGAGATTAACCAACTTATTTAATGAAATGAAGTTCTTGAGTATCTTGGGTTGCGA 664  
Db 314 ACCGGGAGATTCGCCAGGCTCATCTGATGAAATGAAATGAAATTAACCAATTAACCTGAGG 373  
Qy 665 GGAACAACCTTAATGCTGTAACATTTCTCCAGATTTGTGTAACCTGATCTTTGGTAT 724  
Db 374 GGTAACTCACTGAATGAAATTTGTCACTGACATGTGCAACTGACTGCGCTGTGTAC 433  
Qy 725 TTTGAGTAAAGAAACAAGTTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 784  
Db 434 TTTGACATTAAGGGGAAACAATCTCAAGAAACAATTCAGAGGCAATAGGAACTGACT 493  
Qy 785 GCCTTCAGGTTTGTGACCTTGTCTCAATCACTCAATCTGATGATGATGATGATGATGATGATGAT 844  
Db 494 AGCTTGAAGATTTGTGATTTTATATCAACCAATCTGAGAAATTAACCAATTAACCAATTA 553  
Qy 845 GGCCTTCGCAAGTTGCAATTAATATGATGCAAGCAATCACTCTGAGAAAGATTCCA 904  
Db 554 GGTAACTTCAGATGACCACTGATCACTTCAACGAAATGATGATGATGATGATGATGATGATGAT 613  
Qy 905 TCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 964  
Db 614 GAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 673  
Qy 965 GATCTATTTCTTCGATTTCTCGGAAATCTTAATCTTCAACGAGAAATTTGATGATGATGAT 1024  
Db 674 GGGCTTATTTCTCTTATTAATCTTGAACCACTGATGATGATGATGATGATGATGATGATGATGAT 723  
Qy 1025 AACAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1084  
Db 734 AACAACTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 793  
Qy 1085 GAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1144  
Db 794 CAGCTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 853  
Qy 1145 TTGTTGAT 1204  
Db 854 TTATTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 913  
Qy 1205 TCTTGAACAAATTAACAGCTTAAATGTTATGATGATGATGATGATGATGATGATGATGATGAT 1264  
Db 914 TCTTGAAGTCACTGAAACAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 973  
Qy 1265 CGAGCAATTCAAAGCTGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1324  
Db 974 GTGTTTCCAGAGCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1033  
Qy 1325 GGTCAATCCCGGTAGCTATCTGATCGTAACTGATGATGATGATGATGATGATGATGATGATGATGAT 1384  
Db 1034 GGGCAATTCCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1093  
Qy 1385 AACAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1444  
Db 1094 AATGAATTCCTCGGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1153  
Qy 1445 AACTGAT 1504  
Db 1154 AATTTGAT 1213  
Qy 1505 ATCATGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1564  
Db 1214 GTCCAGAT 1273  
Qy 1565 CAATTAAGAAATTAATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1621  
Db 1274 CAGCTCAAAAACCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1333

QY 1622 GGTTCATTAGCACTGCTCAGTCTCACTGATATGATATCTCAATCAACCTGTA 1681  
DB 1334 GCTCAGCTGGGTAACTGTTAGTACCTTAACCTGATCAACAACTTCTCT 1393  
QY 1682 GGTGATATCTCTTAAGAAATATCTTCAAGATTTTCAACAGACTTATTTGGCAAT 1741  
DB 1394 GGGGACATCTCCGCTATCGAAATCTTCTCAAAAGTTCCCAATGAGAGCTTCTATGGGAT 1453  
QY 1742 CTTGATCTTTCGCTAGTGGCTAACTCAACGATGATGATTCGTCGACATGTAAGA 1801  
DB 1454 CTGATGCTTCATGATGTAATGCAAGACTCCAGCTGTGACATTTCTCATGAAACAA--A 1510  
QY 1802 GTGTCAATCTCTAGAGAGCTATTTCTTGAATGCTATTTGGGAGACTTGTGATCTTCTC 1861  
DB 1511 GTTAGCATCTCTCGGAGCGGCTTGCTGCTGATGATCTTAGGCTTCTGATATCTCTCTGC 1570  
QY 1862 ATGTCCTTAATAGAGCTTGGCCACCGCATATCTCTCTCTTCTTGTGATGATCACTT 1921  
DB 1571 ATGCTGCTGGGATATACAAAGACCAACGACCAAGC--TACCTGAGAAAGCATCC 1627  
QY 1922 GACAAACAGTAATCTTATTCAGACCGAGCTGCTCATCTTCTTATGAAACATGGCACTC 1981  
DB 1628 GACAGGCACT--GCAAGGCGCCAAAGCTGTTGTTCTTCAATGATGATGCGCTG 1684  
QY 1982 CAGCTTACGAGATATCATGAGATGACAGAAATCTAAAGTGAAGATATATCATTTGGG 2041  
DB 1685 CACACGTACGAGGATCATGATGAGCTGACGAGAACTGAGCGAAGATCATCATCGGA 1744  
QY 2042 CACGAGATATCAAGACTGTTATCAAAATGTTTGAAGATTTAAACCGGTTGCAAT 2101  
DB 1745 TACGCGCGCTGACACCGTGTATCAGGTGTACCTCAAGACCGGACCGCATGCGCTC 1804  
QY 2102 AAGGCGCTTACTCTCAACCCACAGTCAATGAAACGTTTGAACGAACTGAGATG 2161  
DB 1805 AAGGCGCTCTACAGCCATGATACCAACAGCTCCGAGATTCGAGAGGAGCTGAGACG 1864  
QY 2162 CTAAATGATCAAGACAGAAATCTTGTAGCTTACAGCTTATCTCTCTCACTTG 2221  
DB 1865 ATCGGAGCATCCGCGACAGGAACTCTGACCTTCCAGCGCTTCTGCTCTCCCTCAC 1924  
QY 2222 GGAAGTTTCTGTTTATGACTATTTGAAATGTTAGCTTGGATCTTCTTCAATGCG 2281  
DB 1925 GGGAACTGCTGTTTACGACTATGATGAGAACGCTCTGTTGGATCTTCTTCAATGCG 1984  
QY 2282 CTTACGAGAAAGAAAGCTTGTATTTGGACACAGCTTAAAGATATGATGACAGCA 2341  
DB 1985 CCGTCGAGAAAGGAGAGCTGAGCTGGGACACAGAGCTGAGATGCGAGTGGGCGCGC 2044  
QY 2342 CAAGTTTACCTTATCTACACCATGACTGTATGTCMAAGATCATTCACAGAGCTGAG 2401  
DB 2045 CAGGCGCTGCGTACCTCCACAGCATGCAACCGCGCATCTGTGACCGGGAAGCTCAAG 2104  
QY 2402 TCGTCAACATCTCTTGTGACAAAGACTTGAAGCTGCTTGAAGATTTTGAATAGCG 2461  
DB 2105 TCTCCCAACATCTCTGTGACGAGAGCTTGAAGGAGCTGCTGCTGCTGCTGCTGCTG 2164  
QY 2462 AAAAGCTTGTGTGTCAAAAGCTCATATCTTCAACTTACGATGAGGACGATGATGCTTAC 2521  
DB 2165 AAGTGCCTGCGCGCGCGCAAGTCCAGCTCCACCTACGCTGCTGCGGACCATGGGATAC 2224  
QY 2522 ATGAGACCCGAGATATGCTCGACTTCAAGGCTCATGAGAAATCGATGCTTACATTTAT 2581  
DB 2225 ATGAGACCCGAGATATGCTCGACTTCAAGGCTCATGAGAAATCGATGCTTACATTTAT 2284  
QY 2582 GGAATGCTCTTCTGATGTTTAAACCGAAGAAACCGTGTATGACGAATCCAACTCTC 2641  
DB 2285 GGGCTGCTCTGCTGAGCTGCTACAGGAGGAGAAAGCGTGTACAGATCCAACTTG 2344  
QY 2642 CACCATCTGATTAATGTCAAAGACGAGGAAACATGATGATGAAATGCGAGATCCAGAC 2701  
DB 2345 CACCAAGTGTATCTCTGAGAGCGGACGAGACACGATGATGAGAGCGCTGAGACCGGAG 2404  
QY 2702 ATCATCATGACGTGTAAAGATCTCGTGTGTGTAAGAAAGTTTTCATCTGCGACTCTTA 2761

DB 2405 GTGTGCTGAGAGTGCAGACGACATGAACTGTGTGCGGAGGCTTCCAGCTGCGCTGCTG 2464  
QY 2762 TGACACCAAGAGACCGGATGATGATCCACCAATGACACAGGATCTGCTGTTCTGCGC 2821  
DB 2465 TGACACCAAGGCGCACCGCGGACCGGCGACCATGATGACAGGCTGCGAGGCTGCTGCTC 2524  
QY 2822 AGTTTATGCTATTCGAAACCAACCTGCTGCGACTGACAGCTGACGAGCTGCTGAT 2881  
DB 2525 TCCCTCTCTGCGCGCGCGCGGCAAGCTCTCCGCTGTCAGAGCGGCGGCTTGGGCGCGC 2584  
QY 2882 TCGTCTAC 2890  
DB 2585 GCGGCGCAGC 2593

RESULT 7  
US-10-425-114-30583  
Sequence 30583, Application US/10425114  
Publication No. US20040034888A1  
GENERAL INFORMATION:  
APPLICANT: Liu, Jindong  
APPLICANT: Zhou, Yihua  
APPLICANT: Kovalic, David K.  
APPLICANT: Screen, Steven E.  
APPLICANT: Tabaska, Jack E.  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
FILE REFERENCE: 38-21(5313)B  
CURRENT APPLICATION NUMBER: US/10/425,114  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 73128  
SEQ ID NO 30583  
LENGTH: 2533  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: UC-ZMFLB73041B04\_FLI  
US-10-425-114-30583

Query Match 32.0%; Score 1015.4; DB 8; Length 2533;  
Best Local Similarity 68.7%; Pred. No. 3.2e-281;  
Matches 1413; Conservative 0; Mismatches 641; Indels 3; Gaps 1;

QY 794 GTTTTGACTGTCTTCAATCAAGCTAAGTGTGAGATCTCTTTGATCATGCGCTCTG 853  
DB 48 GTTAGGATTTGTTTCAACCGCTTACTGAGACCAATCCCATTCACATTTGTTCTTA 107  
QY 854 CAAGTTGCAATTTATCATTTGCAAGGCAATCACTCTGCGGAAAGATTCCATCATGATTT 913  
DB 108 CAAGTGTCTACATCTTCTTGAAGGGAACAAGTTCACTGGCCCAATCTCTCATGATTT 167  
QY 914 GGTCTATGCAAGCCCTTGAAGTCTTATGATCTAAGTGTGCAACTTTGTAAGTATGAT 973  
DB 168 GGCCTTATGAGGCTCTGCTGCTCTTGAATCTAAGTATCAACCAATTTATCTGTTCTATA 227  
QY 974 CTTCCGATCTCGGAAATCTTACTTTCACCGAGAAATGATTTGCAAGTAAACAGCTG 1033  
DB 228 CATCTTACTTGAAGCACTTGAACATACATGAGAGCTGTACATGCAAGGCAAGGTTA 287  
QY 1034 ACTGTTCAATTCACCTGAGCTTGAAGACATGATCAAAATCTCATTTACCTGAACTCAAT 1093  
DB 288 ACTGATGATGATCAACAGAGCTAGGAAATATGCAACATCTTATTAAGTAACTGAAT 347  
QY 1094 GATTAATATTCACGCGTCTATATACACAGAGCTTGGAGAGCTTACTGACTTTGAT 1153  
DB 348 GATTAATCACTTCTGCTGCTCAATTTCCACAGAGCTTGAAGGCTTAAACAGGCTTGTGAC 407  
QY 1154 CTGAATGTGCGCAACATGATGTAAGAGCTATACCTGATCATCTGAGCTTGTGACA 1213  
DB 408 CTGAACCTTGCATTAACCACTTGAAGAGCAATTCCTGACAACTTAAGTTATGTTG 467

1214 AATCTAAACAGCTTAATGTTATGGAACAAGTTAGTGGCACTATACCCCGACATTT 1273  
1274 CAAAAGCTAGAAAGTATGACTTAACTTAACTGTCGACAAATATCAAAAGTCCATC 1333  
528 CGAAACCTTGAAAGCATGACCTTAACTTTAACTTTCACTCAATTTCACTAAGTGGCTAT 587  
1334 CCGGTGAGCTATCTCGTATCGGTAAGTATGATATCATTTGATCTTCCAAACAAGATA 1393  
588 CCAATGAGCTATCAAGAGCAACAAATTTGACACGTTGACCTTATCTTAACTGATG 647  
1394 AATGGAATCTTCCTCTCTCTGATTTGAGGACATCTTCAAGATGAATCTTGA 1453  
648 ACGGTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 707  
1454 AGAATCATATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1513  
708 AAGAAATGATCTAGTGGATTCATCCCTGCGAGTTGGTAAATTTGAGAAATGTCATGAG 767  
1514 ATGATCTTCAATATATGATATCTCTGCGCAATTCGAAAGCTTAACAAATTAAG 1573  
768 ATGATTTATCTTAATATCTTGTGATGATCTCAAGAACTTGAATGCTGAA 827  
1574 AATCATATTTGCTGAGACTGAAATATATATACCTGATGATGATGATGATGATGATGAT 1633  
828 AACTGATGTTGCTTAAACCTGAAACAAATTAATCTGCGATGCTCTCTCTGATG 887  
1634 AACTGTCAGTCTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1693  
888 AACTGCTTCACTCAATATCTTAAATGTCATTAATTTGATGATGATGATGATGATGATGAT 947  
1694 AAGAAATATATCTTCAATTTTCAACGACGATTCATTTGCAATCTCTGCTTTC 1753  
948 ACTGAACAACTTCAACGATTTTCAATGATGATGATGATGATGATGATGATGATGATGAT 1007  
1754 GGTAGTGGCTAAACTCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1813  
1008 GATATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1067  
1814 AGAGCACTATTTCTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1873  
1068 AAGGCTGCTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1127  
1874 GCACTTGGCAGACCGATATCT 1933  
1128 GCTGATGAGGACCACTCACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1187  
1934 ACTTATTCGACACCGAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1993  
1188 AGCAATGCTCACTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1247  
1994 GATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2053  
1248 GATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1307  
2054 AGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2113  
1308 AGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1367  
2114 TCTCAAAACCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2173  
1368 GCCCACTACCTCAAGCTTAAAGATTTGAAATGATGATGATGATGATGATGATGATGATGAT 1427  
2174 AAGCAGAAATCTTGTGACCTTCAAGCTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2233  
1428 AAGCAGAAATCTTGTGACCTTCAAGCTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1487  
2234 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2290  
1488 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1547  
2291 AAAAAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2350

1548 AAGACAACTTACCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 1607  
2351 GCTTATCTACCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2410  
1608 GCTTATCTACCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1667  
2411 ATTCTGTTGACAAAGCTTGAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2470  
1668 ATACTCTGACAAAGCTTGAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1727  
2471 TGTGTTCAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 2530  
1728 TGTGTTCAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 1787  
2531 GAT 2590  
1788 GAT 1847  
2591 CTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2650  
1848 CTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1907  
2651 ATATGTTCAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 2710  
1908 ATCTATGCAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 1967  
2711 ACCTGTTAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 2770  
1968 ACCTGTTAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 2027  
2771 AGACAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 2830  
2028 CGGACGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 2087  
2831 CTATCGAAACCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2847  
2088 AACCGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 2104

RESULT 8  
US-10-425-115-77614  
; Sequence 77614, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 77614  
; LENGTH: 2644  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_17080C.1  
US-10-425-115-77614

Query Match 32.0%; Score 1015.4; DB 9; Length 2644;  
Best Local Similarity 68.7%; Pred. No. 3.3e-281;  
Matches 1413; Conservative 0; Mismatches 641; Indels 3; Gaps 1;

794 GTTGGATGCTTGTCTCAATCACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 853  
48 GGTAGGATTTGCTTCAACCGCTTACTGACCAATCCATTCACATGATGATGATGATGATGATGAT 107  
854 CAAGTTGCAACATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 913

Db 108 CAATGGCTACCTATCTTGGCAAGGAGCAAGTTCAGTGGCCCAATTCCTTCAGTAAT 167  
 Qy 914 GGTCTCATGGAAGCCCTTGGAGTCTTGAATCTAATGGCAACTTGTGAGTGAATCTAAT 973  
 Db 168 GGGCTTATGAGAGGTCTCGCTGCTCTAGATCTGAGTACCAACCAATTAATCTGGGCTATA 227  
 Qy 974 CCTCCGATTCGGAATCTTAACTTTCACCGAGAAATTTGTAATTTGACAGATCAACAGCTG 1033  
 Db 228 CCAATCTACTAGGCAACTTGACATACCTGAGAAAGCTGACATGCAAGGCAACAGTTA 287  
 Qy 1034 ACTGTTCAATTCACCTGAGCTTGGAAACATGTCAAACTCCATTAACCTGGAACTCAAT 1093  
 Db 288 ACTGATCGATACCAAGAGCTGAGAAATATGTCAACACTTCACTTACAGAACTGAAT 347  
 Qy 1094 GATTAATATCTCAAGGGTCAATATACCAAGAGCTTGGAAAGCTTACGATGTTGAT 1153  
 Db 348 GATTAATCACTTATGAGGTCAATTCACCAAGAGCTTGGAAAGGCTTGTGTTGAC 407  
 Qy 1154 CTGAATGTGCGCAACAATGATCTGGAAGAGCTTATACCTGATCACTGAGCTTTGACA 1213  
 Db 408 CTGAACCTTGGCAATACCACTTGAAGAGCAATTCCTGCAACCTTAAGTCAATGTGTG 467  
 Qy 1214 AATCTAAACAGCTTAAATGTTCAATGGAACAAGTTTATGAGCACTATACCCGAGCAAT 1273  
 Db 468 AATCTCAATAGCTTCAATGCTTATGGAACAAGTTTAAATGGAAACATTCCTCGTTCCTG 527  
 Qy 1274 CAAGAAGTAAAGATGAGCTTACCTTAATCTGCGCAACAATATCAAAAGGCTCAATC 1333  
 Db 528 CGGAACCTTGAAGCAATGACCTTATTTAACTTTCAATCAAAATTTCAATAGGCTCTAAT 587  
 Qy 1334 CCGGTTAGAGCTATCTCGATCGATCTAGATCAATGATCTTTCCTCAACCAACAGATA 1393  
 Db 588 CCAATGAGCTATCAAGATCAACAAATTTGGACAGCTTGGACCTTATCTGTAACATGATG 647  
 Qy 1394 AATGGAATCAATCTTCTTCCCTTGTGATTTGAGACATCTTCAAGATGAATGATGAT 1453  
 Db 648 ACGGATCAATTCATCATCATGAGCAACCTAGAGCATCTATGAGGCTTAACTTATGAG 707  
 Qy 1454 AGAAATATATTAATCTGATGATTCAGAGGAGCTTGGAAATCTAAGAGATCATGGA 1513  
 Db 708 AAGATATATCTAGTGAATTCATCTCTGCGAGTTTGGAAATGATGATGATGAG 767  
 Qy 1514 ATAGATCTTTCAAATAATGATATCTGAGCCCAATTCAGAGAGCTTAAACCAATTAACG 1573  
 Db 768 ATTGATTTATCTAATATCAATCTGTGTGATTCCTCAAGAACTTGGAAATGCTGCA 827  
 Qy 1574 AACATTAATTTTCTGCAAGCTGGAATAATTAACCTGATGTAATGTTGCTTCAATTAAGCC 1633  
 Db 828 AACCTGATGTGCTAAACCTGGAACAACAATAATTAACCTGCGATGTCTCTCTGATG 887  
 Qy 1634 AACTGTCTCAGTCTCAGTGTATGATGATCTCATTAACAACCTGTAAGGATATACCT 1693  
 Db 888 AACTGCTTCAAGCTCAATATCTTAAATGTGTCAATACAAATTAATTTGGCTGTGTCTCT 947  
 Qy 1694 AAGAACATAATTAATCTCAAGATTTTCAACAAGCTTCAATTTGGCAATCTCTGTCTTTC 1753  
 Db 948 ACGACAAACAATCTCACACGGTTTTCATGACAGCTTTTAAAGTAATCCGAGCTCTGT 1007  
 Qy 1754 GGTAGTTGGCTAAACCTGATGATGATTTCTGTGAACTGTACAGATGTCAATCTCT 1813  
 Db 1008 GGTATATTGGCTTGTGTTTCTATGTCTTCACTGCGCAACCGAACCAACCGCCCAATCTCA 1067  
 Qy 1814 AGAGCACTTATTTTGGAAATAGCTATTTGGGGAGCTTGTGATCTTCTCATGAGTCTTAATA 1873  
 Db 1068 AAGGCTGCTCAATTAATTTGTTGCTGTGTGGTGGAGCTTGTATCTCTCTGATGATTTAGTA 1127  
 Qy 1874 GCAGCTTGGCAGCGCAATAATCTCTCTCTTCTTCTTGTGATGATCACTTGAACAACAGTA 1933  
 Db 1128 GCTGTATGAGGGCAGACCACTCCAGCTTTTAAAGATGCACTGTAAAGAACAGCAGTG 1187  
 Qy 1934 ACTTATTCGACACGGAAGCTGTATCTTCAATGAACATGAGCACTCCAGCTTTAGAG 1993  
 Db 1188 AGCAATGTCTCACCAAGCTGTGTATCTTCAATGAACATGAGCTTCTTCAATGTCTTGTAT 1247

Qy 1994 GATATCATGAGATGACAGAGATCTAAGTGAAGATATCATTTGGGCGAGGAGCATCA 2053  
 Db 1248 GATATTAATGAGATGACTGAGAACTTGAATGAGAAATATCACTTTGATACGGGGCATCA 1307  
 Qy 2054 AGCACTGTATTAACAATGTGTGTTTGAAGAAATTTGAAACCGGTTGCAATTAACGGCTTAC 2113  
 Db 1308 AGTACAGTTTATTAATATGTGTTTAAAGAAATTTGCAACAGATGCAATTAAGAAAGCTGAT 1367  
 Qy 2114 TCTCAACAACCCAGATCAATGAAACAGTTTGAACAGAACTGAGATGCTAATTAATGATC 2173  
 Db 1368 GCCACATACCTCAGAGCCCTTAAGAAATTTGAAACAGAGCTGAGACTGTGTGATGATC 1427  
 Qy 2174 AAGCAAGAAATCTTGAAGCTTACAGGCTTATTCCTCTGATCTGAGTGGAGATCTTCTG 2233  
 Db 1428 AAACACCGGAATTAATGATGAGCTTCAAGGATCTGCTGACACTGTGGGAACCTCTC 1487  
 Qy 2234 TCTATGACTAATTTGAAAAATGATGAGCTTGTGGATCTTCTGAT--GAGCTTACGAG 2290  
 Db 1488 TTTTATGATTAATATGAGAGTGGAGCTTATGGAGTTTATCATGAAAGGCTCATCAAG 1547  
 Qy 2291 AAAAGACTTGTATTTGGGACACAGGCTTAAATAGATGATATGATGACAGCAAGTTTA 2350  
 Db 1548 AAGAACAACTTGAATGAGGATGAGCTGCTTACGAGATGCTTGTGTGAGCTCAAGGCTC 1607  
 Qy 2351 GCTTATCTACACCATGACTAGTATCCAGGATCATTCACAGAGAGCTGAAGTGTCTCAAC 2410  
 Db 1608 GCTTACCTTACCATGATGATGACAGCCAGCAATTAATTCACGGGACCTTAATTAAGAAAT 1667  
 Qy 2411 ATTCTCTGCAACAAGCTTATGAGGCTCGTTGACAGATTTTGAATAGCAAAAGCTTG 2470  
 Db 1668 ATACTCTCGACAAATTAATGAGGCCATCTTACAGACTTCGGCATTCGCTTAAGACTTA 1727  
 Qy 2471 TGTGTGCAAAAGTCAATCTTCACTTACGTATGAGGACAGTATGATTAATAGAGCCCC 2530  
 Db 1728 TGTGTCTGAAAGCTCACAGTCAACCTTACGTATGAGGACATATGATTAATTAATCCC 1787  
 Qy 2531 GAGTATGCTGCACTTACAGGCTCACTGAGAAATCCGATGCTTACAGTTATGGAATAGTC 2590  
 Db 1788 GAGTACGCCCGGACCTCTCCGCTCAACAGAAATCTGATGTCAACAGCTACGCAATCGTT 1847  
 Qy 2591 CTCTTGAATGTTTAAACCGGAAGAAACCGTGTATGATGAGATCAATCTCCACATCTG 2650  
 Db 1848 CTCTGAGAGCTGTGACCGGCAAGAAAGCCAGTGAACAACAGATGCAATCTCCATCTG 1907  
 Qy 2651 ATAAATGCAAGAGCGGGGAACAATGATGATGGAATAGGCAATCCAGATCAATCATG 2710  
 Db 1908 ATCTTATCGAAGAGCGGAGCAACGAGTATGGAAGCGTGAACCCGAGCTGGAGAC 1967  
 Qy 2711 ACGTGTAAAGATCTCGGTGTGGAAGAAATTTTCCAACTGGCACTCTATGACACCAA 2770  
 Db 1968 ACCTGCAAGAGACTGGGCGAGTGAAGAAAGCTTTCCAGCTGGCGCTCTCTGACCAAG 2027  
 Qy 2771 AGACAGCCGAATGATGAGCCCAATGACACAGTGAATCTGTGTCTCGCAGTTTATG 2830  
 Db 2028 CCGCAGAGCTTGGACCGGCGAGAGATGACAGAGTGTGTGCTTGTGACTGCTGTG 2087  
 Qy 2831 CTATCGGAACAACACC 2847  
 Db 2088 AACCCGAGCGCGGCC 2104

## RESULT 9

US-10-425-114-10637  
 ? Sequence 10637, Application US/10425114  
 ? Publication No. US20040034888A1  
 ? GENERAL INFORMATION:  
 ? APPLICANT: Liu, Jingdong  
 ? APPLICANT: Zhou, Yihua  
 ? APPLICANT: Kovalic, David K.  
 ? APPLICANT: Screen, Steven E.  
 ? APPLICANT: Tabaska, Jack E.  
 ? APPLICANT: Cao, Yongwei



1 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
2 OF INVENTION: Plants and Uses Thereof for Plant Improvement  
3 FILE REFERENCE: 38-21 (5313)B  
4 CURRENT APPLICATION NUMBER: US/10/425,114  
5 CURRENT FILING DATE: 2003-04-28  
6 NUMBER OF SEQ ID NOS: 73128  
7 SEQ ID NO 10637  
8 LENGTH: 1872  
9 TYPE: DNA  
10 ORGANISM: Glycine max  
11 FEATURE:  
12 OTHER INFORMATION: Clone ID: 700954473\_FLI  
13 US-10-425-114-10637

Query Match 31.4%; Score 995.8; DB 8; Length 1872;  
Best Local Similarity 73.9%; Pred. No. 1,2e-275;  
Matches 1283; Conservative 0; Mismatches 437; Indels 15; Gaps 1;

1286 AGTATGACTTACCTTAATCTGTCGACGACATATCAAGTCCGATCCGCTTGAGCTA 1345  
2 AGCATGACCTCTTGATCTTCTTCCACAACTTCAGGCGCAATTCATTAAGACTG 61  
1346 TCTGTATCGGTAACTTATGATGATCTTCCAAACAAGATTAATGATCAT 1405  
62 TCGCGGATGGCAATTTGATGATGATGATTTCAAAACAATTAAGTTGGTTCATC 121  
1406 CCTTCTTCCCTTGATGATTTGAGCATCTTCTCAAGATGAACTTGATGATAT 1465  
122 CCTTCTTCCCTTGATGATTTGAGCATCTTCTCAAGATGAACTTGATGATAT 181  
1466 ACTGTGTAGTTCGAGGCGACTTTGGAATCTAAGAAAGCATCAGGAAATAGATCTTCA 1525  
182 ACGAGATTAATTCACAGAAATTTGGAATCTTGAAGTGTATGAAATGATCTTTCA 241  
1526 AATATGATATCTCTGCGCCCAATTCAGAAAGCTTAACCAATTAAGAACTATTTTG 1585  
242 AATATGATATCTCTGCGCCCAATTCAGAAAGCTTAACCAATTAAGAACTATTTTG 301  
1586 CTGAGACTGGAATTAATTAATCTGATGATGATGATGATGATGATGATGATGATGAT 1645  
302 TTGAGACTGGAATTAATTAATCTGATGATGATGATGATGATGATGATGATGATGAT 361  
1646 CTGAGACTGGAATTAATTAATCTGATGATGATGATGATGATGATGATGATGATGAT 1705  
362 CTGAGACTGGAATTAATTAATCTGATGATGATGATGATGATGATGATGATGATGAT 421  
1706 TTCTCAAGATTTTACACAGACCTTCAATTTGCAATCTGATGATGATGATGATGAT 1765  
422 TTACAGAGTTTCCCTGACAGTTTCAATTTGCAATCTGATGATGATGATGATGATGAT 481  
1766 AACTCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1825  
482 AATTTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 541  
1826 CTGGAATAGCTATTTGGGGGACTTGGATCTTCTGATGATGATGATGATGATGATGATGAT 1885  
542 CTGGAATAGCTATTTGGGGGACTTGGATCTTCTGATGATGATGATGATGATGATGATGAT 601  
1886 CCGCATATATCTCTCTCTTCTTCTGATGATGATGATGATGATGATGATGATGATGAT 1945  
602 CCGCATATATCTCTCTCTTCTTCTGATGATGATGATGATGATGATGATGATGATGAT 661  
1946 CCGAGAGCTGATCTCTCTCTTCTTCTGATGATGATGATGATGATGATGATGATGATGAT 2005  
662 CCGAGAGCTGATCTCTCTCTTCTTCTGATGATGATGATGATGATGATGATGATGATGAT 721  
2006 ATGACAGAGATTAAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2065  
722 ATGACAGAGATTAAGTGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 781  
2066 AATGTGTGTTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2125  
782 AATGTGTGTTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 841

2126 CAGTCATGAAAGAGTTTGAAGACAGAACTGAGATGCTAAGTACCAAGACAGAAAT 2185  
842 CAATGATTAAGAAATTTGAAGCTGAACTGAACTGAACTGAACTGAACTGAACTGAACT 901  
2186 CTGTGAGCTTACAGATTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2245  
902 CTGTGAGCTTACAGATTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 961  
2246 TTGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2305  
962 ATGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1021  
2306 TGGGACAGACGAGTTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2365  
1022 TGGGACAGACGAGTTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1081  
2366 GACTGTAGTTCAGATTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2425  
1082 GATTGCTGTCTGATTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1141  
2426 GACTGTAGTTCAGATTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2485  
1142 GACTGTAGTTCAGATTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1201  
2486 GACTGTAGTTCAGATTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2545  
1202 GACTGTAGTTCAGATTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1261  
2546 TCAAGGCTCAGTGAAGATTCAGATGATGATGATGATGATGATGATGATGATGATGAT 2605  
1262 TCAAGGCTCAGTGAAGATTCAGATGATGATGATGATGATGATGATGATGATGATGAT 1321  
2606 ACCGAG 2665  
1322 ACTGAG 1381  
2666 GGGAG 2725  
1382 GAG 1441  
2726 GGTGTGTGAAG 2785  
1442 GAG 1501  
2786 GAG 2835  
1502 AGGCGAG 1561  
2836 -----GAG 2890  
1562 CCGAG 1621  
2891 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2950  
1622 GTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1681  
2951 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3005  
1682 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1736

RESULT 10  
US-10-437-963-21341/C  
Sequence 21341, Application US/10437963  
Publication No. US20040123343A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
APPLICANT: Wu, Wei  
APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad  
APPLICANT: Li, Ping  
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53221)B  
CURRENT APPLICATION NUMBER: US/10/437,963  
CURRENT FILING DATE: 2003-05-14  
NUMBER OF SEQ ID NOS: 204966  
SEQ ID NO 21341  
LENGTH: 3115  
TYPE: DNA  
ORGANISM: Oryza sativa  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT4530\_26620C.1  
US-10-437-963-21341

Query Match 31.1%; Score 986.6; DB 8; Length 3115;  
Best Local Similarity 64.9%; Pred. No. 7.7e-273;  
Matches 1630; Conservative 0; Mismatches 724; Indels 159; Gaps 5;

510 TGATTCGAGAAATTAACCAATTGATAGACCGATCCCTCAACATTTCACAGATTCCAA 569  
2760 TGATATTGAAGAACACCAACTGATCGAGTATCCATCAAGCTCTCACAGCTCCCAA 2701  
570 ACCTGAAAATTCGACTTGGCAGAGATAAATCAAGTGTGAGATACCAAGATTATT 629  
2700 ATTGAAGATTTTGGACTTGGCAGAGATAAATCAAGTGTGAGATACCAAGATTATT 2641  
630 ACTGGAATGAAGTTCTTCAGTATCTTGGGTTGGCAGAGAACTTATGTTGTTAATT 689  
2640 ATTGGAACGAGTTCTTCATTAATCTTGGGATTAACGGGTAATTAATTTGAAGGACAGACT 2581  
690 CTCGAGATTTGTGTCACACTGCTGCTTGGATTTTGAAGTAAGAAACAAGTTTGA 749  
2580 CCCGAGTATATGCGACTGATGCTGCTTGGATTTTGAAGTAAGAAACAAGTTTGA 2547  
750 CTGCTAGTATATCTGAGACGATAGAAATTCGACTGCTTCCAGTTTGGACTTGTCT 809  
2546 -----CTTGGATTTGTCTT 2533  
810 ACAATCAGCTTACCTGTGAGATCCCTTTTGAATCGGCTTCTGCAAGTTGCAACTTAT 869  
2532 ACAATAAATCTTCTGATCAATTCCTTTCAACATTTGTTCTTCAAGTTGCTCAACTAT 2473  
870 CATTCGAAGCAATCAACTCTCTGGAAGATTCCATGATGATGATGCTCAATGCAAGCC 929  
2472 CTTTGCAGAGGACATGTTTATCTGCTCTTCAATGATGATGATGCTCAATGCAAGCTC 2413  
930 TTGCACTCTTATGATCTAAGTGGCAACTTTGATGATGATCTTCTCCGATTTCTGGA 989  
2412 TCCTGTATGATGATCTGATGATCAACCAATTTGTCTGCTCTTATTCATGATGATGCA 2353  
990 ATCTTACTTTCACCGAAGAAATTTGATTTGCAAGTAAACAGCTGATCTGATTTCAAT 1049  
2352 ATTTAATATCACTGAGAAAGCTGTATATGCAAGGCAATAGTTAAAGGCTCAATACAC 2293  
1050 CTGAGCTTGAAGAAATGATCAAAATCTCCATTAAGCTGAACTCAATGATCAATCTCAG 1109  
2292 CTGAGCTTGAAGAAATGATCAAAATCTCCATTAAGCTGAACTCAATGATCAATCTCAG 2233  
1110 GTCATATACCAACGAGCTTGGAGCTTACTGACTTGTGATGATGATGATGATGATG 1169  
2232 GGTTCATCTCTCCGAGATTCGGAAGCTTAAACAGGGTATTTGATTTAAACCTTGAACA 2173  
1170 ATGATCTGGAAGGCTTATACCTGATGATCTGATGATCTTGGCAAAATCTAAACGCTTAA 1229  
2172 ACAACTTTGAAGGCTTATACCTGATGATCTGATGATCTTGGCAAAATCTAAACGCTTAA 2113  
1230 ATGTTCAATGGAAGCAATTTAGTGAATATACCCGAGCAATTTCAAAAGCTAAGTA 1289  
2112 ATGTTCAATGGAAGCAATTTAGTGAATATACCCGAGCAATTTCAAAAGCTAAGTA 2053  
1290 TGACTTACTTAACTGTCTCCAGCAACATATCAAAAGCTCAATCCCGGTTGAGCTATCTC 1349

2052 TGACTTATTTGAATTTGTCTATCAAAATTTCTAAGTGTCTATCTATGAGCTATCGA 1993  
1350 GTATTCGTATCTAATATATATGATGATCTTCCAAACAAGATAATGAAATATCTCT 1409  
1992 GAATCAACAATTTGGACCTTT----- 1970  
1410 CTTCCTTGTGATTTGGACATCTTCTCAAGATGAATGAACTGATGAAATATATATCTG 1469  
1969 -----AACTTGACCAACAATGCTGATG 1945  
1470 GTGTAGTTCCAGCGCACTTTGGAATCTAAGAACATCATGAAATGATCTTCAATA 1529  
1944 GATTCATCTCTCGAAGAAATTTGGCACTTGGAGGATATCAAGGAGATGATATGTCACA 1885  
1530 ATGATATCTCTGGCCCAATTTCCAGAAAGGCTTAACCAATATACGAAATATTTGCTGA 1589  
1884 ATCATCTTGGCGGTTGATTTCTCAAGAACTCGGAATCTGCAAAATCTGATTTGTTAA 1825  
1590 GACTGAAAATTAATTAACCTGACTGTATGTTGTTTCAATGACCACTGTCTCAGTCTCA 1649  
1824 ATCTCAAAAACAACATTAATCTGGGATGTCCTTCACTGATGAATCTGCTCAGCTCA 1765  
1650 CTGTATTGAATGATATCATTAACAACCTGATGATATCTTAAAGAACATTAATCTCT 1709  
1764 ATATCTTAAATGATCTATTAATTAATTTGGCTGTGTTGATCTGATGATTAACAATCTCT 1705  
1710 CAAGATTTTACACAGACAGCTTCAATTTGGCAATCTGCTGTTGGAGTTGCTAACT 1769  
1704 CAGGTTTTCCTGACAGCTTTTGGGATATCAAGACCTTTGATATTTGCTGTTGTT 1645  
1770 CACGTTGTCATGATTTCTGTCGAATCTGATGATCAATCTGATGATGATGATGATG 1829  
1644 CTTCGTCGCTGATGATGTCATGATGATGATGATGATGATGATGATGATGATGATG 1585  
1830 GAATGATATTTGGGAGCTTGTATCTTCTCATGATGATGATGATGATGATGATGATG 1889  
1584 GAATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1525  
1890 ATATCT 1949  
1524 ATATGTCACCTGTTTCAAAAGATGTCCTGTTAGCAACAGATGATGATGATGATGATG 1465  
1950 AGCTGTCATCT 2009  
1464 AGCTGTCATCT 1405  
2010 CAGGAATCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2069  
1404 CTGAAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1345  
2070 GTGTTTGAAGATTTGAACCGGTTGCGATTTAAGCGGCTTCTCTCAACACCCACAGT 2129  
1344 GTGTTTGAAGAACCGCAACAGTGGCAGTAAAGAAAGCTATATGCCCCACTATCCACAGA 1285  
2130 CAATGAAAAGATTTGAACAGAACTGAGATGCTAATGATGATGATGATGATGATGATG 2189  
1284 GCTTCAAGGAATTTGAACAGTGGCAGTAAAGAAAGCTATATGCCCCACTATCCACAGA 1225  
2190 TGAGCTTCAAGCTTATTTCT 2249  
1224 TCAGCTTCAAGATATTTCT 1165  
2250 AAATGCTAGCTCTGAGATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2306  
1164 AAATGAGACCTCTGAGATGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1105  
2307 GGAACACAGCTTAAAGATATGATGATGATGATGATGATGATGATGATGATGATGATG 2366  
1104 GGGAACTGCTTACGAATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1045  
2367 ACTGTAGTCCAAAGATATTTCAAGAGCTGAAGTGTCTCAACATTTCTTGGACAAAG 2426

Db 1044 ACTGTACCCACGATATAACAGGAGATGTGAATCAAAAATATACCTCTTGATAAG 985  
Qy 2427 ACTTAGAGGCTCGTTGACAGATTTTGAAATAGCGAAAAGCTGTGTGTCGAAGTCAC 2486  
Db 984 ATTATGAGGACATCTTACAGACTTTGGCACTTGGCAATGCTTAAGAGTTGTGTTCACAAAAATC 925  
Qy 2487 ATACTCACTTACATGATGGGCAAGATAGTTATAGACCCCGAGTATGCTGGCACTT 2546  
Db 924 ACAGTCCACCTATGTATGGAACTATGGCTATATGACCTGAGATAGCTGCACCT 865  
Qy 2547 CACGCTCACTGAGAAATCCGATGTCTACATTAAGAAATAGTCTTCTTGAAGTTTAA 2606  
Db 864 CCGCTCATGAAATGATGTCTATAGCTATAGTGCATTTGTTCTGTGAGCTGTGA 805  
Qy 2607 CCGGAGAAAGCCGTGTGATGACGAATCCATCTCCACCATGTATATGTCAAAGCG 2666  
Db 804 CCGGAAAAAGCCGTGTGACGAACAGAGTGCATCTCCATCACTTGATCTTGTCAAAAGCG 745  
Qy 2667 GGAACAATGAAGTATGAAATGGCAGATCCAGATCCACATCGACGTTGAAGATCTCG 2726  
Db 744 CTATCAATGCTGTCTATGAGACACTGCACCGACATTTGACAGACTTGCAGAGATCTTG 685  
Qy 2727 GTGTGTGAAGAAAGTTTTCACATCTGCACCTCTATGCAACCAAAAGACGCGAATGATC 2786  
Db 684 GTGAGTCAAGAAAGTGTTCAGCTGGCGCTCTTTGACCAAGACAAACCATCGATC 625  
Qy 2787 GACCCACAATGACACAGGTGACTGTGTCTCGGCAAGTTTATGCTATCGGAACAACAC 2846  
Db 624 GGCAGCAATGACAGAGTGTGTGCGCTCTCGAGCTCTAGTTCTGCCGACCGCGAC 565  
Qy 2847 CTGTGTG-----GACTGACAGCTCAGGAGCGTGGGTGCTGCTAGCTGATG 2897  
Db 564 CGAAGTCGCACAGCACTGCGCAGTGCAGCGCGCTGCTGCCAGCTACATCAACG 505  
Qy 2898 AGTATGCAAAATCTCAAGACTCTTCATTTCTGCAATTCCTC---TTCCATGAGTCTTCTG 2954  
Db 504 AGTATGCACTTATAGAGGACCAAGCGTGTCTCTCGGCAACTCGTGTGATCTTCCG 445  
Qy 2955 ATGCTCACTGTTTCTTCTCGTTTGGACAAGTTATTTTTCAGAACGATGATG 3007  
Db 444 ATCTGTAGCTGTTTCTCAAGTTTGGCAGAGTCAATTTCTCAGAACACAGATGAG 392

RESULT 11  
US-10-425-114-7634  
; Sequence 7634, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(5313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; NUMBER OF SEQ ID NOS: 2003-04-28  
; SEQ ID NO 7634  
; LENGTH: 1859  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700676958\_FLI  
US-10-425-114-7634

Query Match 29.6%; Score 940.4; DB 8; Length 1859;  
Best Local Similarity 74.4%; Pred. No. 1.2e-259;  
Matches 1206; Conservative 0; Mismatches 401; Indels 15; Gaps 1;  
Qy 1399 AATGATTCCTTCTCCCTGTGTGATTTGGACATCTTCTCAAGATGAAGTGAAGTGAAGAA 1458

Db 4 AAGATTCCTTCTTCCCTTGATGACTTGGAAACATCTTCTGAATTTGATGATGACGAGAA 63  
Qy 1459 TCATATATAGTGTAGTTCAGGCGACTTTGAAATCTTAGAAGATCATGGAATAGA 1518  
Db 64 CAATTTAAACAGAAATATTCACAGACAAATTTGAAATCTTAGAAGTGTATGGAATAGA 123  
Qy 1519 TCTTTCAATATGATATCTGTGGCCCAATTCAGAAAGCTTAACCAATTAGAGACAT 1578  
Db 124 TCTTTCAATATATCACTCTGTGGCTTGATTCCTGATGAACCTTAGTACCTTCAAAACAT 183  
Qy 1579 AATTTGCTAGACTGGAATATATTAACCTGACTGTAATGTGTTCATTAGCAACTG 1638  
Db 184 GATATCCTTAGACTTGAATTAACAAATTTGATGCGAGATGTGGACATCACTTCAAAATG 243  
Qy 1639 TCTGAGTCTGATTTGATTAATGTATCTATTAACAACCTGTAGTGTATTCCTTAAGA 1698  
Db 244 CATTAGTCTCTCTATTAATGTATCTAATAACAACTATTGTGTGTATCCCAACGAG 303  
Qy 1699 CAATTAATCTCAAGATTTTACACAGACCTCATTTGGCAATCTGTGCTTGGCGTAG 1758  
Db 304 TAACACTTACAGAGTTTCCCTGACAGTTTCATTTGAAACCTGTGTTCTTGTGTAA 363  
Qy 1759 TTGGCTAACTCACCGGTGATGATTTCTGTCGAACCTGTAGAGTGTCAATCTTAGAGC 1818  
Db 364 TTGGCTGAATTTGCCGTGTATGTGTGTCGCCCTTGAGACGAGTTAATATCTAAGGC 423  
Qy 1819 AGCTATTTCTTGAATAGCTATTTGGGAGCTTGTGATCTTCTCATGTCTTAATAGACG 1878  
Db 424 TGCCATCTTGAATTAATCTTGTGTGCTTGTGATTTCTTATGTGTATGTGTGCGAGC 483  
Qy 1879 TTGCCAGCCGATATCTCTCTTCTTGTATGATCATCTGACAAACCAATTAATTA 1938  
Db 484 TTGCCAGCAATATGCTCTCTCTTCTGTATGATCATTTGACAAACCAATTAATTT 543  
Qy 1939 TTGCACACGAGCTGTCTCTCTTCTATATGAACATGACCTCAGCTTACAGAGATAT 1998  
Db 544 CTCGCCCAAGCTAGTATTTCTCATATGAATATGCACTACATGTGTATGAAGTAT 603  
Qy 1999 CATGAGATGACAGAGATTTAAGTGAAGTATATCTATTGAGCAGAGACATCAACAC 2058  
Db 604 CATGAGGATGACTGAATAACCTGAGTGAAGTATATTTGATATGAGACATCAAGTAC 663  
Qy 2059 TGTATCAATGTGTTTGAAGATTTGAACCGGTGCGATTAAGCGGCTTAATCTCA 2118  
Db 664 AGTTTAAATGTGTTCTTAAGAAATGCAAGCGGTGCTATCAAGAGATCTATTTCTCA 723  
Qy 2119 CAACCCACAGTCAATGAAACAGTTTGAACAGAACTCGAGATCTAATGATCAACGA 2178  
Db 724 CTATCCCATGTATTAAGAAATTTGAACGTAACCTTGAGACGTTGGCAGCATCAAGCA 783  
Qy 2179 CAGAAATCTTGTAGACCTACAGACTTATCTCTCTCACTTGGGAGTCTTCTGTTCTA 2238  
Db 784 CCGGAATCTGTGACGCTCCAGAGTTATCTTCTGCTCCCAATAGGGGATCTCTGTGTTA 843  
Qy 2239 TGACTATTTGGAAGATGTAGCTCTGAGATCTTCTTCATAGGCGCTACGAAGAAAGAC 2298  
Db 844 TGACTATGAGAAATGTAGCTCTAGAGATCTTCTTCATAGGACCTACGAAGAAAGAAA 903  
Qy 2299 TCTTGATTTGGACACAGGCTTAAGATAGCATATGTGACGACCAAGGTTTACCTTATCT 2358  
Db 904 GCTTGAGTGGAGCTGTGTTAAATATAGCACTTGGAGCAGCAAGAGGCTTGTCTATCT 963  
Qy 2359 AACACATGACTGTATGTCGAAGATCATTTCAAGAGACGTGAAGTGTCTCAACATTTCTT 2418  
Db 964 AACACATGATGTGTCCTAGAAATCATCCAGAGATGTGAATCATCTTAACATTTCTAT 1023  
Qy 2419 GGAACAAGACTTAGAGCTGTGTGAAGATTTTGAATAGCAAAAGCTGTGTGTCT 2478  
Db 1024 GGAATGACACTTGAAGCTATCTACTGATTTTGGATTTGCCAAAGTCTTGCCCCCTC 1083  
Qy 2479 AAGTCACTACTTCAACTTACGTGATGGCAGATAGTTACATAGACCCCGAGATATGC 2538

Db 1084 AAAGTCCCATCTTCTTACTTACATATATGCGCAATTGGCTATATAGACCTGAGTATGC 1143  
Qy 2539 TCGCACTTCAAGGCTCACTGAGAAATCGATGTCTACAGTTATGGAATGATGCTTCTTGA 2598  
Db 1144 TAGAACTTCAAGCTCTGAGAACTGATGTGTACAGTTTACGATTTGTTTACTTGA 1203  
Qy 2599 GTTGTTAACCGGAGAAAGCCGTTGATGACGAATCCATCTCCACATCTGATATATGC 2658  
Db 1204 GTTGTAACTGGAAGAAAGCTGTGACAAATGATCCAACTCCACATCTGATTTGTGTC 1263  
Qy 2659 AAAGACGGGGAAACAATGATGATGAAATGCGAGATCCAGACTCATCTGACAGCTGTA 2718  
Db 1264 CAAGGACGCAACCAATGATGAGAAACGTTGATCCAGACATTCCTGCGACATGCAA 1323  
Qy 2719 AGATCTGCGTGTGATGAGAAAGTTTTCCAACTGCGACTCTATGACCAAAAGACAGCC 2778  
Db 1324 GGACTTGAAGAGCTTAAAAAGTTTATCAGCTTGTCTTATATGCAAAAGAGGAGCC 1383  
Qy 2779 GAATGATCGAACCAATGCAACGAGTGACTGCTGTTCTGCGCAGTTTATGCTATGC 2835  
Db 1384 AGCTGATAGGCGCAATGCAAGAGTGAACGTTACTCGGAAGCCCTTGCTGCTGCAAA 1443  
Qy 2836 -----GGAACAACCACTGCTGCGACTGACATGACGTCAGCGCTGCTGCTTC 2883  
Db 1444 CACCCCAACCAAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1503  
Qy 2884 GTGCTACGCTGATGATGATGCAAAATCTCAAGACTCTCATTTCTGCAATTTGCTTCCAT 2943  
Db 1504 ATGCTACGCTGATGATGATGCAAAATCTCAAGACTCTCATTTGCTGCAATTTGCTTCCAT 1563  
Qy 2944 GAGTCTTCTGATGCTCAACTGTTTCTGCTTTCGCAAACTTATTTCTGCAAGACGTGA 3003  
Db 1564 GAGCACTCAAGATCTCAACTCTTCTCAAGTTTGAGAAATATCTCTCAAAACAGTGA 1623  
Qy 3004 GT 3005  
Db 1624 GT 1625

## RESULT 12

US-10-437-963-67070/C  
; Sequence 67070, Application US/10437963  
; Publication No. US2004012343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437, 963  
; NUMBER OF SEQ. ID NOS: 204966  
; SEQ. ID NO 67070  
; LENGTH: 2985  
; TYPE: DNA  
; ORGANISM: *Oryza sativa*  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_67963C.1  
US-10-437-963-67070

Query Match 24.7%; Score 785.2; DB 8; Length 2985;  
Best Local Similarity 60.0%; Pred. No. 1.1e-214;  
Matches 1571; Conservative 0; Mismatches 853; Indels 194; Gaps 8;

Qy 438 TAGACTTATCTTCAATGATTAAGTGTGACATACCGTTTTCATTTCCAGTTGAGAC 497  
Db 2771 TCGACTTGAAGTGAATGAATCTTCTGGGCGATCCCTGATGAGATTGGCGATTCACGT 2712

Qy 498 AACTGAGCAGTGAATCTGAGAAATTAACCAATGATAGAGCCGATCCCTTCAACATTT 557  
Db 2711 CGCTTAAACTCTGATCTTGAAGAACACACGCTGTGGGAGATGATCCGCTGCACACTCT 2652  
Qy 558 CACAGATTCACAACTGAAAAATTTCTGAGCTTGGCACAAATTAATCTGATGTTGAGATAC 617  
Db 2651 CTCAGCTAACCAAAATTTGAAATTTTGAATTCGACTCAAAAACAGCTAAATGTTGAGATTC 2592  
Qy 618 CAGACTTATTTCTGGAATGAAAGTTCTTCAATCTGAGTCTGGGCTTGGCGAGAAACACTAG 677  
Db 2591 CGAGTTAATCTTCTGGAATGAAAGTTCTTCAATCTGAGTCTGGGCTTGGCGAGAAACACTAG 2533  
Qy 678 TCGGTAACTATTTCTGAGATTTGTCATGCTGCTGCTTGTGTATTTTGAAGTAAAGAA 737  
Db 2532 -----GGGCAATATGTTGGGGAATTCGGA 2508  
Qy 738 ACAACAGTTGACTGATGATATCTGACAGATAGAAATTCGACTGCTTCCAGTTT 797  
Db 2507 GCAATATATTTAGAAAGAGCCCTCTCTGAGATGTGCCAGTTGACTGCTGCTGCTGCTGCT 2448  
Qy 798 TGGACTTGTCTCAATCACTAAGTGAATCCCTTGTGATGATGCTGCTGCTGCTGCTGCTGCT 857  
Db 2447 TGGATCTGTCTTCAACCGGCTCAAGGAGAAATCCCATTCACATTTGCTTCTTCAAG 2388  
Qy 858 TTGCAACATTTGATGCAAGGCAATCACTCTGCGAAGATTTGATGATGATTTGCT 917  
Db 2387 TGGCTATATTTGCTTTCGAAAGGAAATTTCTGCGCCCTATTTCAATGATTTGCGC 2328  
Qy 918 TCATGCAAGCCCTTGCAGTTTATGATGATGCAATTTGATGATGATGATGATGATGATGATG 977  
Db 2327 TTATGCAAGGCGCTGCGAGTCTGATGATGATGATGATGATGATGATGATGATGATGATG 2268  
Qy 978 CGATTCGGAATTTTACTTTCACCGAGAAATTTGATTTGACAGATTAACCACTGACTG 1037  
Db 2267 CAATTTCTGCAATTTAATCACTGAGAAATCTGATCTGCAAGGCAATGAGCTAATG 2208  
Qy 1038 GTTCAATTTCCAGCTGAGCTTGGAAACATGTCMAAATCTCAATTCGTAATGATGAT 1097  
Db 2207 GATCAATACCAACCGAGCTTGTATATGTCACATCTATATC ----- 2164  
Qy 1098 ATCATCTACGGGTCAATATACCAACGAGCTTGGAAAGCTTACTGACTTGTGATCTGA 1157  
Db 2163 -----TTGA 2160  
Qy 1158 ATGAGCAACAAATGATCTGAGAGACCTTATCTGATCATCTGAGCTTTCGACAAATC 1217  
Db 2159 ACCTGCAACAAACAACTTGAAGACCAATCCCTGATATATATAGCTCATGATGATC 2100  
Qy 1218 TAAACAGCTTAAATGTTCAATGAGAACAAAGTTTATGAGCACTATACCCGACATTTCAA 1277  
Db 2099 TCATTTAGCTTGAATCTATCATCAAACTATCTTATGAGGCAATTCATTTGAGCTAGCA 2040  
Qy 1278 AGCTAAGAAATGATGATCTTAACTGATCTGACGACAAATATCAAAAGCTCAATCCGG 1337  
Db 2039 AAATGAAAACTTGGACACATTTGACTTATCTGTAACAGATGTTGCTGTGCAATTCCT 1980  
Qy 1338 TTGAGCTATCTGATCGTATCGTATCTGATGATGATGATGATGATGATGATGATGATGATG 1397  
Db 1979 CGGCAATTTGGAGACTTATGAGATCTTTTGAAGCTAATTTTATGCAATTAATTTTGGT 1920  
Qy 1398 GAATCATTTCTTCTTCCCTTGTGATTTGAGATCTTTCAGATGAACTTGAATGAGAA 1457  
Db 1919 GATATACCTCTGCTGATTTGAAATCTTGAAGATGATGATGATGATGATGATGATGATGAT 1865  
Qy 1458 ATCATATATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1517  
Db 1864 -----CCTCTGTTTATGTTAGT 1851  
Qy 1518 ATCTTCAATTAATGATATCTGCGCAATTCAGAGAGCTTAAACAAATTAACAGAA 1577  
Db 1850 ATTGTCTATATCACTTGTGTTGATTTGATTTCCAAAGAGTTGGCAGCTCCAAAC 1791



QY 1121 CAGAGCTTGGGAAGCTTACTGACTTGTGATGTAATGAGCAACATGATCTGAA 1180  
DB 242 GCTGAGCTTGGCAAACTCAGAGAGTATTGATGATGATGCAACAACTCTGAG 301  
QY 1181 GGAAGCTTATCTGATCTGAGCTCTTGGCAAACTGAAACAGCTTAAATGTTACGG 1240  
DB 302 GGGCATATCCCTGGAAACATCAGCTCTTGGCAGTGCACATGAACTGATGAGC 361  
QY 1241 AACAAAGTTGAGGCACTATGACCCCGAGCATTTCAAAAGTAGAAGATGATTAACCTT 1300  
DB 362 AATGAGACTGATGAGCTATGCTGCTGCTGCTTCCAGAAAGCTGAGAGTTGACATACCTA 421  
QY 1301 AATCTGTCAGCAACATATCAAAAGGTCATCCCGGTGAGTATCTCGTATCGGTAC 1360  
DB 422 AACCTTCTTCAAAAGCTTCAAAAGCCAGATCCCTGAGCTTGGTCAATAGTCAAC 481  
QY 1361 TTGATATCATTTGATCTTTTCCAAACAAGATTAATGGAATCATCTCTTCCCTTGGT 1420  
DB 482 TTGACACACTGATCTCTTCTTCAATGAATTCCTCGGGCCAGTTCCTCTCACTATTTGGT 541  
QY 1421 GATTGAGCATCTTCTCAAGATGAACTTGAGTAGAATCATATTAACCTGAGTGTCA 1480  
DB 542 GATTCGAGCATCTTCTTGAATTAATTTGATGAAACATCTCACTGATCTGTGCT 601  
QY 1481 GCGCATTTGGAAATCTAAGAAAGCATGAGAAATGATCTTTCAAAATGATATCTCT 1540  
DB 602 GCTGAATTTGGAACTTGAGAAAGTGTCCAGATGATGATGATGATGATGATGATGATGAT 661  
QY 1541 GGGCAATTTCCAGAAAGCTTAACCAATTAAGAAACATTAATTTTGGTGAAGCTGAAAT 1600  
DB 662 GGGTACCTCTCTGAGAAAGCTTGAACAGTCAAAACCTGATGATGATGATGATGATGATGAT 721  
QY 1601 AATTAACCTGAGTGTGTAATGT---TGGTTTATTAGCCAACTGCTCACTGATATG 1657  
DB 722 AACGTTTGGTGGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 781  
QY 1658 AATGATCTCAATCAACCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1717  
DB 782 AACTGTCATCAACCACTCTCTGAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 841  
QY 1718 TCACCAACAGCTTCAATTTGGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1777  
DB 842 CCAATGAGAGCTTCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 901  
QY 1778 CATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1837  
DB 902 GGACATTTCTGATGAAAC---CAAAGTTAGCATCTCTGAGAGGCGGCTTGCCTGAT---G 955  
QY 1838 ATGGGGGAGCTTGTGATCTTCTGATGCTTAAATGACAGCTTGCAGACGATATCTT 1897  
DB 956 ATCTTAGGCTTCGATATGCTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1015  
QY 1898 CTTCTTTTCTTGTGATGATCTTGGCAACCAATTAATTTGACACCGAAGCTGCTC 1957  
DB 1016 CCAAGCTTACCTGAAAGCACTCCGACAAAGCACT---GCAAGGCGCAACCAAGCTGCTG 1072  
QY 1958 ATCTTATATGAAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2017  
DB 1073 GTTCTTATGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1132  
QY 2018 CTAAATGAGAAATGATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2077  
DB 1133 CTGAGCGAAGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1192  
QY 2078 AAGAAATGTAACCGGCTTGCATTAAGCGGCTTAACTCTCAACCCAGCTCAATGAA 2137  
DB 1193 AAGAGCGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1252  
QY 2138 CAGTTTGAACAGAACTGAGATCTAAGTCAAGCAAGCAAGAACTTTGTGAGCTTA 2197  
DB 1253 GAGTTGAGAGCGAGCTGAGAGAGATCGGCAAGATCCGGCAAGAACTTGTGAGCTTC 1312  
QY 2198 CAAAGCTTATCTCTCTCACTTGGGAGCTTCTGTTTATGATGATTTGAAATGCT 2257

DB 1313 CAGGCTTCTCGCTCTCTCCCTCAAGGGAACCTGTTCTACACTATCAGGAAACGGC 1372  
QY 2258 AGCTCTGGGATCTTCTTCAATGAGCCCAAGAAAGAAAGCTTGAATTTGGAACAACGG 2317  
DB 1373 TCCCTGTGGATCTTCTTCAATGAGCCCGCTGAGAAAGGTGAAGCTGGAGACAGAG 1432  
QY 2318 CTTAAGATGACATATGATGAGCAACAAGTTTATGATATCTACACATGATGATGATGATGATGAT 2377  
DB 1433 CTGAGATGAGCAAGGAGCGCGGAGGAGGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1492  
QY 2378 AGGATCTTCAAGAGAGCTGAAAGTGTCTCAACATTTCTTTGACAAAGCTTGAAGCT 2437  
DB 1493 CGATCTGACCGGAGCTGAAAGTCTCTCAACATCTGCTGAGAGCGCACTTTCAGAGCG 1552  
QY 2438 GGTTCAGATTTTGGATAGGAAAGCTTGTGTGTCAAGTCACTATCTTCACT 2497  
DB 1553 CACTGTCCGACTTCGATGCGCAAGT 1612  
QY 2498 TACGTATGAGGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2557  
DB 1613 TACGTATGAGGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1672  
QY 2558 GAGAAATCCGATGCTTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2617  
DB 1673 GAGAAATCCGATGCTTCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1732  
QY 2618 GCGGTGATGAGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2677  
DB 1733 GCGGTGATGAGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1792  
QY 2678 GTGATGAGGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2737  
DB 1793 GTGATGAGGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1852  
QY 2738 AAAGTTTCCAACTGAGCTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2797  
DB 1853 AAAGCTTCCAACTGAGCTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1912  
QY 2798 CACGAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2857  
DB 1913 CACGAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2912  
QY 2858 GACACGTCAAGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2917  
DB 1973 AAGCGGCGGCGGCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2972

RESULT 14  
US-10-437-963-18958  
Sequence 18958, Application US/10437963  
Publication No. US2004012343A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
APPLICANT: Wu, Wei  
APPLICANT: Bouharov, Andrey A.  
APPLICANT: Barabuk, Brad  
APPLICANT: Li, Ping  
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
FILE REFERENCE: 38-21(53221)B  
CURRENT APPLICATION NUMBER: US/10/437,963  
CURRENT FILING DATE: 2003-05-14  
NUMBER OF SEQ ID NOS: 204966  
SEQ ID NO 18958  
LENGTH: 3233  
TYPE: DNA  
ORGANISM: Oryza sativa  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT4530\_24466C.1







Thu Sep 7 09:31:07 2006

us-10-519-135-1.rnpbm

Page 21

QY 2794 AATGCACGAGTGACTCGTGTCTTCGGCAGTTTATGCTATCGGAACAACACC 2847  
 |||||  
 Db 1373 GATGCACGAGGTGTGCGCGCTCTTGACTGCTGTGTAACCCGGAGCCGCGCC 1426  
 |||||

```
Search completed: September 5, 2006, 18:50:27
Job time : 3718 secs
```

**THIS PAGE IS BLANK**



```

417 GAGGAGAAATTTCCCGAGTATGGAAATCGAAGAAAGCTTAGAGTCAATGACCTTAAAG 476
QY 378 GTATATGCTTGTCTGGAGCAAAATCCCTGATGAGATTTGGTACTTCTTTTGGAAAAC 437
Db 477 GAAATGCTCTCTGAGGCCAAATTCGCGAGATTTGAGATTTGCTCTGCAATGAAAATCT 536
QY 438 TAGACTTATCTTCAATGAATTAAGTGTGACATACCGTTTTCGATTTTCGAAGTTGAAGC 497
Db 537 TAGATGCTCTTTTAAATTAATTAATGAGAGACATCTTCTTTTCAATATCGAAGTTGAAAC 596
QY 498 AACTTGAGCAGCTGATTTCTGAAGATAACCAATTTGATAGACCGATCCCTTCAACACTTT 557
Db 597 AACTGAGAACAACTGATTTGAGAGATAACCAATTTGAGGCGCTATATCTTCAACAGTTGT 656
QY 558 CACAGATTTCCAAACCTGAAAATTTCTGACCTTTGGACAGATTAACCTGAGTGTGATAC 617
Db 657 CTGAGATTTCCAAACCTGAAAATTTGATATTTGACAAATCAATTAAGTGGGAGATTC 716
QY 618 CAAGACTTATTTACTGGAATGAAGTTCTTCAGTATCTTGGGTTGCGAGAAACAACCTTAG 677
Db 717 CCAGGCTTATCTATTTGGAATGAAGTTTTCGAAATTTTGGGGCTGCGCAACACTTCTTAG 776
QY 678 TCGGTAAACATTTCTCGAGATTTGTGCAACTGACTGTGCTTTGGTATTTTGAACGTAAAG 737
Db 777 TTGGGACTCTTTCCCTGATATGATGTCAATTTGACAGATTTGTGGTTCTTTGATGTGCGAG 836
QY 738 ACAACAGTTTGAAGTGTGATTAAGTGTGACAGATTAAGAAATTTGACATGCGCTTCCAGTTT 797
Db 837 GCAACAACTTTGTACAGGAGCAATTCCTGAGAAATATTTGCAACTGTAAAGCTATGCAAGTTT 896
QY 798 TGAAGTGTCTTCAATCACTAGCTAACTGATGATCCCTTTTGAACATGCGGCTTCCCTGAG 857
Db 897 TGAAGTGTCTTCAATCACTAGCTAACTGATGATCCCTTTTGAACATGCGGCTTCCCTGAG 956
QY 858 TTGCAACATTAATCAATTCGAAAGCAATCACTCTCTGGAAAGATTCATCAAGTATTTGCTC 917
Db 957 TGCGTACTCTGTGCTTCAAGAAACAAGCTGACCGGAAAGATTCATCAAGTATTTGCTC 1016
QY 918 TCATGCAAGCCCTTGGACGCTTATGATCTAATGAGCACTTGTGAGTGTCTATTTCTC 977
Db 1017 TCATGCAAGCCCTTGGACGCTTATGATCTAATGAGTATTAATCTTCAAGCAATTTCTT 1076
QY 978 CGATTTCTCGGAAATCTTACTTTTCCGAGAAATTTGATTTGACAGTAAACAGCTGACTG 1037
Db 1077 CGATTTCTCGGAAATCTTACTTTTCCGAGAAATTTGATTTGACAGTAAACAGCTGACTG 1136
QY 1038 GTTCAATTTCACTGAGCTTGGAAACATGTCAAAATCTCATTTACCTGGAACCTCAATGATA 1097
Db 1137 GATCTATTTCCGCAAGATTTGGGGAACATGACAAAGCTGGGATACCTGACAGTAATGACA 1196
QY 1098 ATGATCTCAGGGGCTATATCCACAGAGCTTGGGAAGCTTACTGACTTGTGATGATGTA 1157
Db 1197 ATGATCTCAGGGGCTATATCCACAGCTGAGGGAATTTGGAAACAGCTTGTGAAATGT 1256
QY 1158 ATGT 1161
Db 1257 AAGT 1260

RESULT 2
US-10-101-464A-839
; Sequence 839, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020C2
; CURRENT APPLICATION NUMBER: US/10/101.464A
; CURRENT FILING DATE: 2002-03-18
```

```

; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: PileSeq for Windows Version 4.0
; SEQ ID NO: 839
; LENGTH: 3222
; TYPE: DNA
; ORGANISM: Pinus radiata
US-10-101-464A-839

Query Match 7.1%; Score 225.4; DB 3; Length 3222;
Best Local Similarity 45.7%; Pred. No. 1.2e-61;
Matches 1015; Conservative 0; Mismatches 1186; Indels 18; Gaps 6;

QY 426 CTTTGCAAACTTAGACTTATTCCTTCAATGAATTAAGTGTGACATACCGTTTGCATTT 485
Db 444 CTCGAAATATCTGAGCTGTCTAACAATGATTTCTGGAGAGTTCCCGTTTCGGTTG 503
QY 486 CGAATTTGAACAATTTGAGCAGCTGATTTCTGAAGATAACAATGATGAGAC--CGA 542
Db 504 GGAATTTGAACAATTTGAGCTGTCTGAGCTGGGATTAATATGTTCAATCGGGAACGA 563
QY 543 TCCCTTCAACATTTCAAGATTTCAAACTGAAATTTCTGCACTTGGACACAGATAAAC 602
Db 564 TTCAGAGGAGCTCATGCGACTGACAGACCTGAGTGGCTGTATCAACAATTTGCAACT 623
QY 603 TCAGTGTGATGATCAACAAGACTTATTTAGTGAATGAAGTTTCTCAAGTATCTTGGGTTGC 662
Db 624 TTTATGAGTCAATTTCCAGCTTCTCTGAGCAATCTTTCGAGCTGGAAACCTGAGCTCT 683
QY 663 GAGGAAACAACCTTAAGTGTGATTAATTTCTCAGATTTGTGTCAACTGACTGTCTTTGCT 722
Db 684 CGATGAATGACTTGAAGTGTGATTAATTTCTCAGAGAGATTTCTCAGAGCTGGAATTTGA 743
QY 723 ATTTTGAAGTGAACAACAAGTTGATGATGATGATGATGATGATGATGATGATGATGATG 782
Db 744 AGCTGAGCTTTTTCAGCAATTTATGTCGGGAGAGATTTCTCAGAGCTGGAATTTGA 803
QY 783 CTGCTTCCAGGTTTGGACTTGTCTTCAATCAATGATGATGATGATGATGATGATGATGATG 842
Db 804 CATCATTTGAAGATTTTGAATGCTTCCAGAAATTTCTGTGTGGAGAAATTTCCGAGACT 863
QY 843 TCGGCTTCTGCAAGTTGCAACAT--TATCATTTGCAAGGCAATCACTCTGGGAGA 899
Db 864 TTGGGAAGCTGGAAGGTTTCAATTTTATTAATTAATTAATTAATTAATTAATTAATTAAT 923
QY 900 TTGCTATGATGATTTGCTGTATGCAAGCCCTTGCAGCTTTAGATCTTAAGTGAACCTTGT 959
Db 924 TACCAGAAAGATTTGAGATTAAGATTAATTCGGTATTTTCTATGTATCAAAATTAATTC 983
QY 960 TGAATGATCTATTTCTCCGATTTCTCGAATCTTACTTTTACCGAGAAATTTGATTTGC 1019
Db 984 TCACAGGCCCCCTGCCCCCAAGCTGGATCTGTGTGTAATTTCAATATGATGATGCT 1043
QY 1080 AACTGGAAGCTGATGATTAATCATCTCAAGGCTCATATACCAAGAGCTTGGGAAGCTTA 1139
Db 1104 ATATTTCTTGTCTTGAATTAAGAAATTTACAGGCCAAATCTTGAATGCTTAAGGAACCTGA 1163
QY 1140 CTGACTGTTTGAATGGAATGAGGCCAAATGATGCTGGAAGACCTATACCTGATCATC 1199
Db 1164 AGAGTATGCTGCGGTTTCTGTATGATGAATTAAGCTGACAGGGAAGATTTCCAGGGGAA 1223
QY 1200 TGAAGCTTTGCAACAATCTTAACAGCTTAATATGTTTCAATGGAACAAGTTTATGTCAC 1259
```



Db 1224 TTGGGAGTCCCAATGTTTCATCTGGATCTCAGCTTCAACTCTTTGAAGGGGAGA 1283  
Qy 1260 TACCCGAGATTTCAAAAGTGAAGTATGACTTACTTATCTGTCCAGCAACATA 1319  
Db 1284 TCCCTCTGCAATTTGGAAATGCGAGAAATTTGTGTGCTATATCTGCAGAGAAATGGT 1343  
Qy 1320 TCAAAAGTCCAAATCCCGTTGAGCTATCTGTATCCGTAATTAAGATATGATCTTT 1379  
Db 1344 TCTCTGAAATCTGCTGCAGAAATTTGGGCAAGCTTGCAGTTGATTAATAATGATGTTA 1403  
Qy 1380 CCAACAAAGATTAATGGAATCAATCTCTTCTTCCCTGGATTTGAGACATCTTCTCA 1439  
Db 1404 GCGGTAAAGATTAATGAGAGCTGTATCTTCCGAGATTTGGAAATTAAGCTTGTGATA 1463  
Qy 1440 AGATGAATCTGATAGAAATCATATTAATCTGTAGTTCAGGCGACTTTGGAAATCTTA 1499  
Db 1464 GTCTGTCTTTGAGGAAATATCTTTTCAGGACCCATACAGCTCAGATTTGACACTGTA 1523  
Qy 1500 GAAGCATCATGAAATGATCTTTCAAAATATGATATCTGTGGCCCAATTCAGAAAGAGC 1559  
Db 1524 AGTTTCTGTCTTCATTAATCTTGCATATTAATGCTCAGGAGCCCATTTCTGGCAGCC 1583  
Qy 1560 TTACCAATTAACAACATTAATTTTGTGAGACTGAGAAATAATTAACCTGACTGTATG 1619  
Db 1584 TTGGTTTATGAGAGTCTTAATTTCTGTGATCTTTCCCAATATGCTTTCTGGAGAAA 1643  
Qy 1620 TTGGTTTATGAGCAATCTGTCTGATCTCACTGTATTAATGATCTCATTAACACTCG 1679  
Db 1644 TACCAACACCTTGGCCGCTGAGCTCAGTCTGTGAGATTTCTAGGAAATCTTTAA 1703  
Qy 1680 TAGGTATATCCCTAGAAACATTAATCTCAAGATTTTACAGACAGCTTCAATGGCA 1739  
Db 1704 CAGGACAGGCGCAATTTGACTCA--TCAGCCAGACCAACAGCA--AGCTTTTCTGAAA 1760  
Qy 1740 ATCTGATCTTTCCGAGTATGCTAACTCACCGTGTCAATCTCTGCTGCAACTGTAC 1799  
Db 1761 ACCCTGGCTCTGTGTGCAAGGCTGGAATCTTTGCAAGCTGTATTAACATCAAGAG 1820  
Qy 1800 GAGTGTCAATCTTGAAGACGCTATTTTGGAAATGATTAATGAGGAGACTTGTGATCTTC 1859  
Db 1821 ATCTTATCAAGAGAGTGTATTAATCTGGGATGTTTGTAGTGGAACTGTATTAATCT 1880  
Qy 1860 TCAATGCTTAAATAGACGCTTGGCCGACCCGATATCTCTCTCTTTCTTGATGATCAC 1919  
Db 1881 TGAATCTCGGCAATGCTCATGAGAGATGACGTTGATTCAGAGGATTCACAAAT 1934  
Qy 1920 TTGACAAACAGTAACTTATTTGACACCGAAGCTCGTCAATCTTCAATGAAATGGCAC 1979  
Db 1935 AGGTCAACAAACGAACTTTTGGAGATGAAATCTTCCACAAAGCTGAATTTGATGAGC 1994  
Qy 1980 TCCAGCTTAAAGAGATATCATGAAATGACAGAAATTAAGTGAAGATATATCATTTG 2039  
Db 1995 ATGAATTTCTGGAATCATGAGAGAGACATTAATGATGATGAGCTGTGATCAG 2054  
Qy 2040 GGAACGAGATTAAGACATGTATACAAATGTGTTTGAAGATTTGAAACCGGTTGCA 2099  
Db 2055 TGTATCGAATTAATTAAGTAATGAGAGATGTGTGTGTAATAAACTCTGACCTGCA 2114  
Qy 2100 TTAAAGGGCTTTACTCTCAACACCAAGTCAATGAAACAGTTTGAACAGAACTGAGA 2159  
Db 2115 AAAATGGCCACCTATGGCGAGCAGGGCTGTATTAACAGGAATTTGAAGCGAAAGTTGAA 2174  
Qy 2160 TGTAAATGATCAAGACAGAAATCTTGTGAGCTTCAAGCTTATTCCTCTCTCACT 2219  
Db 2175 CACTGGAAAGCATTCGGCAAGAAATATGTCAAACTCTACTCTATTTCTCAAAATGGGG 2234  
Qy 2220 TGGGAGTCTTCTGTATGATATTTGAAAAATGTTACCTCTGGGATCTTCTTCAATG 2279  
Db 2235 ATTCAATATGCTGTGTAGAGATGACATGCCAATGAAATTTGTGGAAATCCCTGACG 2294  
Qy 2280 GGCCTGAGAAAGAACTCTGATTTGGACACAGGCTTAAGATGATATGATGTCAG 2339

Db 2295 TAGGCAATAGGGAGGAGCTGTGATTTGGCCCATCTGTTACAAATATGCTGTGGTGTG 2354  
Qy 2340 CACAAGTTTAAAGTTATCTACACCATGATGTATGCCAAGATCATTTACAGAGACGTGA 2399  
Db 2355 CCAACGACTGGCTTATCTTCATCAGATGACGTCACCAACCGATATCATTCACAGAGATGCA 2414  
Qy 2400 AGTGTCAACATCTCTTGGACAAAGACTTAAAGCTGTGTTGACAGATTTGAAATAG 2459  
Db 2415 AGTCAACAATATCTTGTGATGACGAAATCAGGCTGTGTTGAGATTTTGGTTTG 2474  
Qy 2460 CGAAAGCTTGTGTGTGT---CAAAGTCAATCTTCAATTAACGTATGAGGACCATAG 2516  
Db 2475 CTAAAGATTTCTCAAGCTGCTCCAGAGGTGATTTCTTCAATTAATCTGCAACCATG 2534  
Qy 2517 GTTACATAGACCCGAGTATGCTGACCTTACGGGCTCACTGAGAAATCCGATGTACA 2576  
Db 2535 GCTATATGCTTCAAGATACGTTATTCATCAGGGTACCGAGAAAGATGACATCTTACA 2594  
Qy 2577 GTTATGAAATATGCTCTTCTTGAATGTATTAACCCGAGAAAGCCGTTGATGACGAATCC 2635  
Db 2595 GCTTGGTGTGTGTTTACTGAGCTCATTTACAGGAGGCGCCAGTGGAGAGAAATTC 2653

RESULT 3  
US-10-101-464A-880  
; Sequence 880, Application US/10101464A  
; Patent No. 6768041  
; GENERAL INFORMATION:  
; APPLICANT: Strabala, Timothy  
; APPLICANT: Nieuwenhuizen, Nicolaas  
; APPLICANT: Higgins, Colleen M.  
; TITLE OF INVENTION: Compositions Isolated from Plant Cells  
; TITLE OF INVENTION: and their use in the Modification of Plant Cell Signaling  
; FILE REFERENCE: 11000.10202  
; CURRENT APPLICATION NUMBER: US/10/101,464A  
; CURRENT FILING DATE: 2002-03-18  
; PRIOR APPLICATION NUMBER: 09/704,302  
; PRIOR FILING DATE: 2000-11-01  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR APPLICATION NUMBER: 60/162,866  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: PCT/US00/00724  
; PRIOR FILING DATE: 2000-01-11  
; NUMBER OF SEQ ID NOS: 989  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 880  
; LENGTH: 4017  
; TYPE: DNA  
; ORGANISM: Pinus radiata  
US-10-101-464A-880

Query Match 7.1%; Score 224.8; DB 3; Length 4017;  
Best Local Similarity 45.7%; Pred. No. 2,2e-61;  
Matches 1081; Conservative 0; Mismatches 1252; Indels 35; Gaps 7;

Qy 294 TTAATTTGACAGTTGAATCTTGTATGAGAAATCTCACTGCTATTTGAGATCTCAAGA 353  
Db 718 TGAATTTATCGCAATCTTTTGTGGGAACTTCCGACTTATTTAGAGCTCGCAG 777  
Qy 354 GTCTCTTTCATTAATGATCTGCGAGTATGCTGTGTGGAACAAATCCCGATGAGATTG 413  
Db 778 AGCTGGAATATCTGATATCTGAGTAAATTTCTGTGTTGATTTCTGCGAGCATTTG 837  
Qy 414 GTGACTGTCTTCTTGGCAAACTTATGACTTATCTTCAATGAATTAAGTGTGACATAC 473  
Db 838 GGAAGTCCGAAGCTTCAAGTACTGACCTGTGCGAATCTGTAAAGACATATCC 897  
Qy 474 CGTTTTCATTTGAAAGTGAACAACTTGAAGAGCTGATTTCTGAAAGATTAACCAAT 531  
Db 898 CAACATTTCTGGGAAATCTCAGCAATCTGAGCAATTAATTTGCTGGGATCAATCCCTTG 957  
Qy 532 -GATAGAGCGAATCCCTTCAACACTTCAAGATTCCAAACCTGAAATTTCTGGAATGG 590

Db 958 CCCCCGCTGATTCCTCCAGAGCTGGGGAAGTACAGAAAGTTACAGAACTATAGGCTA 1017  
Qy 591 CACAGAAATAACTCAGTGTGAGATACCAAGACTTATTTACTGGAATGAAGTTCTTCACT 650  
Db 1018 CTTCTGTATATTTTGTGGGCTATTCGGGATTTCTATTTGGCAATCTGCTCTTTGACGA 1077  
Qy 651 ATCTTGGGTTGCGAGAAACACTTACTGCTGTAACATTTCTCCAGATTGTGTCACTGA 710  
Db 1078 ATCTGATCTTTCTGAAATCAGCTCTGGGAATTTATCCAGAGCCATCAAAAGTTAA 1137  
Qy 711 CTGCTCTTGTGATTTTGAAGTAAAGAAACAAGTTGACTGCTGATGATACCTGAGCA 770  
Db 1138 ATCAAAATGATACAGATTAGACTCTATCATACAACTTACAGGAGGATTTCTGAGAACT 1197  
Qy 771 TAGAAATGACATCGCCTTCAGGTTTGGACTGTGCTCAAAATCAGCTAATCTGAGTGA 830  
Db 1198 GGGCTAATCTTGTCTTCTCTAGACATTTTGTGTCTCAAAATATGCTTTACGGGACCA 1257  
Qy 831 TCCCTTTTGACATCGGCTTCTGCAAGTTGCAACATTATCATTTGCAAGGCAATCACTCT 890  
Db 1258 TACTGAGCAGTTGGGCAAGTTGGCACTTTCGTCTTGAACTGTGTGAGAAATATTTGG 1317  
Qy 891 CTGGGAAGATTCCATCAGTATGTGTCTCATGCAAGCCCTTGGCAGTCTTATGATTTAAGT 950  
Db 1318 TAGGACACATTCGGAGGCTATTTGGGTAATCTCCAACTGTGTGAGCTCAAGCTGTTTA 1377  
Qy 951 GCAACTGTGAGTGAATCTATTCTCCGATTCGGAATCTTACTTTACCGAGAAAT 1010  
Db 1378 CGAATTAACCTTGAATGTAGCTTGCTCTGAAATTTGGGGAAATTTCCGGCTACAAAGC 1437  
Qy 1011 TGTATTTGACAGTAAACAGTGACTGCTTCAATTCACCTGAGCTTGGAAACATGTCAA 1070  
Db 1438 TAGATATTTGACAGAAATTCGACTGAGTGTACTCTTCGCGGAACTTTGCAAGTATGGGA 1497  
Qy 1071 AACTCCATTACCTGAGACTCAATGATATATCATCTCAAGGCTCATATACACAGAGCTTG 1130  
Db 1498 AGCTGCAACTTTGAAATATTTTAAACAACATTCACCTGGGCAAGTCTCTTTGCAATACG 1557  
Qy 1131 GGAAGCTTACTGACTTGTGTGATCTGAATGTGGCCAACTGATCTGGAAGGACTATAC 1190  
Db 1558 GTGCATGTTTGAAGCTTTCAAAAGGTTGAAATTAAGCCCAATGAGCTATGAGACAAATGC 1617  
Qy 1191 CTGATCATCTGAGCTCTTGGACAATCTTAAACAGCTTAAATGTTTATGAGGAAACAAGTTTA 1250  
Db 1618 CTAGTTTCATTTCTGGGGTCTCCCTCAGCTTATTAATCTGAACTGATTAACAACAAGTTGG 1677  
Qy 1251 GTGGCACTAATCCCGGACATTTCAAAAAGCTAGAAAATGATGACTTACCTTAATCTGTCCA 1310  
Db 1678 AAGGCTCGATTTCTTGAATTAAGAAATGCAAGAACTATCAGCGCTATGATATCCG 1737  
Qy 1311 GCAACAAATATCAAGGTCGAATCCCGGTGAGCTATCGATGCGTACTGATGATCAT 1370  
Db 1738 GTAAACGTTTCTCCGGACCTTACTCTTGAATAGGAGCTTGTGGCTAATCTTTCTGTAA 1797  
Qy 1371 TGGATCTTTTCAACAACAGATTAATGAAATCAATTCCTTCTTCCCTTGTGATTTGGAGC 1430  
Db 1798 TTGATGGTACCAACATCAATTCACAGGTCTCTTCCAGCAACTTTGGTTCGTGTAACA 1857  
Qy 1431 ATCTTCTCAAGATGAATGATGATGAATATCATTAATCTGTGTAGTTCCAGGAGCACTTGG 1490  
Db 1858 AATTTAGATTAAGTTGATCTTCCAGAAATCAAGTTCTCCGGTACGCTTCTACATGACATAC 1917  
Qy 1491 GAATCTTAAGAACATCATGGAATAAGATCTTTCAATTAATGATATCTTGGCCCAATTC 1550  
Db 1918 TGTCAATGAAATGAGCTTACAGACTTAATCTGTCAAAATTAACAAGTTTCCGGGCCATATTC 1977  
Qy 1551 CAGAAAGCTTAAACAATTAACAAGAACTAAATTTGCTGAGACTGGAATAATTAATCACTGA 1610  
Db 1978 CTAAAGAGCTTAAAGGAGAGCTCCAGTTCTGACATATCTGGATCTTTCTGTAAAGCTTGA 2037  
Qy 1611 CTGTATATGTTGGTCAATTAGCCAACTGTCTCACTCATCTGATTTGAATGATATCTATA 1670

Db 2038 CAGAGAAATCCCTCCTGAAATTTGGGCAATTTGAAGCTTAACAGTTTCAATCTTTGGATA 2097  
Qy 1671 ACAACCTGTAAGGTGATATCCCTAAGAAACAATACTTCTCAAGATTTTCCAGACAGCT 1730  
Db 2098 ATCAGCTAATCTGGCATTTGTTCTTCTGCTTTCAGTCTC---AGTTTTTACAGTCAAGTT 2154  
Qy 1731 TCAATGGCAATCTTGTCTTTTGGGATGTTGGCTAACTCACCGGTGATGATATCTGTCTC 1790  
Db 2155 TAAATGGCAATCTTGGCTTTTGGCAGCAATGATGCTTTAAAGGGTTTAAAGTCTGTCTCT- 2213  
Qy 1791 GAACTGTACAGATGTCAATCTCTAGAGCAGCTATTTCTGGAATAGCTATTTGGGGACTTG 1850  
Db 2214 GACATGAGAAATAGCGGAGAAAAGTGTACAGTTGGGCAATGAGCTGCCAGACAGCTG 2273  
Qy 1851 TGAATCTTCTCATAGTCTTATATAGCAGCTTGCCGACGCAATTAATCTCTCTTTTCTTG 1910  
Db 2274 TTTGCTTTGGCTGGGCTCATTTTGTGTATAGACTGCGCTGTTTATTAACAATACCT 2333  
Qy 1911 ATGATATCACTTGAACAACAGTAACTTATTCGACACCGAAGCTGTATCTTCAATGA 1970  
Db 2334 GAATTAACAATAAGCTAAAGTTAAAGATTGTGGCAAGCAATTAAGTCTCCCTGATGCTG 2393  
Qy 1971 ACATGGCACTCCAGCTTTACAGAGATATCATGAG-AAATGACAGAAATCTAATGAGAG 2029  
Db 2394 ACCACGTTTCAACGATTTGGGTTTCAAGAAATATGAATTTCTGATTTGCATTAAGACAGAA 2453  
Qy 2030 TATATCATTTGGGACGAGCATCAACACACTGTATTAACAATGTGTTTGAAGAATTTGTA 2089  
Db 2454 AATGTATTTGGAAGTGTGTGATCAGAAAAGTATACAAGCCACACTCGGGAATGGAGAA 2513  
Qy 2090 CCGGTTGCAATTAAGGGCT-----TTACTCTACAACCAACAGTCA 2131  
Db 2514 ACTGTGGCCATCAAGAGGCTGTGAAACAATGAAATGCTGMAAGCTCTATCATCTCGCAAT 2573  
Qy 2132 ATGAACAGTTTGAACAGAACTCGAGATGCTAATGATGATCAAGACAGAAATCTTGTG 2191  
Db 2574 GATTAATGATTAACAGGACAGAAATTTGAACCTTTGGAAATTTATGAGCAATTAACAATAGT 2633  
Qy 2192 AGCTTACAAGCTTATTCCTCTCTCACTTGGGAGTCTTGTCTTATGACTATTTTGA 2251  
Db 2634 AACTCTGTGTGTGTCTGTGATGACATGACATTCATCTTTTGGTATACAGATCAATGCC 2693  
Qy 2694 AATGGCAGTTTGGGGATCTCTTCAATGGCC---CCAAAGCTGTGACCTTAATTTGGCT 2750  
Db 2312 ACAAGGCTTAAGTATGATATGTTGAGACACAGAGTTTATGCTTATCAACCATGACTGT 2371  
Qy 2751 ACAAGTTACAAATTTGACATTTGAGAGAGCTCAGGGTTTGGCTTATTTGCAATCAATGATGT 2810  
Qy 2372 AGTCCAAGATCATATCAAGAGAGCTGAAGTGTCTCCAACTTCTTGGACAAGACTTA 2431  
Db 2811 GTACCTTCATATCATCATGCGAGATGTAAGTCAACAATATTTGTGTATAGTGTCAATTT 2870  
Qy 2432 GAGGCTGTGTTGACAGATTTTGAATGAGCAAAAGCTT-----GTGTGTCAAAAGTCA 2485  
Db 2871 GGTGCTGTGTGTGCTATTTTGGACTTGGCCAAAGGCTCTTCAAGAGCTATGAGAAAGGAATC 2930  
Qy 2486 CATATCTTCAACTTAAGATGAGGACAGATAGGTTACATTAAGTACCCGAGATATGCTGCAGCT 2545  
Db 2931 GATTTTATGTCTGCAATTTGCTGATCTTAATGTTATATAGCTCAAAATATGATATCACT 2990  
Qy 2546 TCAAGGCTCAGTAGAATCCAGTGTCTACAGTTATGAAATAGTCTTCTTGAAGTTGTA 2605  
Db 2991 CTGAAGTGAATGAAGAAAGTACATCTACAGTTTGGATGTGTCTTACAGGCTAAGT 3050  
Qy 2606 ACCGAAAGAAAGCCGTTGATGACGAAT 2633  
Db 3051 ACGGCAAGCAGCCGGTAAATTCAGGAAT 3078

RESULT 4  
US-10-101-464A-833

; Sequence 833, Application US/10101464A  
; Patent No. 6768041  
; GENERAL INFORMATION:  
; APPLICANT: Strabala, Timothy  
; APPLICANT: Nieuwenhuizen, Nicolaas  
; APPLICANT: Higgins, Colleen M.  
; TITLE OF INVENTION: Compositions Isolated from Plant Cells  
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling  
; FILE REFERENCE: 11000.102062  
; CURRENT APPLICATION NUMBER: US/10/101,464A  
; CURRENT FILING DATE: 2002-03-18  
; PRIOR APPLICATION NUMBER: 09/704,302  
; PRIOR FILING DATE: 2000-11-01  
; PRIOR APPLICATION NUMBER: 09/228,986  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR APPLICATION NUMBER: 60/162,866  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR APPLICATION NUMBER: PCT/US00/00724  
; PRIOR FILING DATE: 2000-01-11  
; NUMBER OF SEQ ID NOS: 989  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 833  
; LENGTH: 4056  
; TYPE: DNA  
; ORGANISM: Pinus radiata  
US-10-101-464A-833

Query Match 7.1%; Score 224.8; DB 3; Length 4056;  
Best Local Similarity 45.7%; Pred. No. 2,2e-61;  
Matches 1081; Conservative 0; Mismatches 1252; Indels 35; Gaps 7;

QY 294 TTAATTTGTCAGATTGATCTTGATGAGAAATCTACCTGCTATGAGATCTGAGA 353  
DB 587 TGAATTTATGCGAATCTTTTGTGGGAACTTCCGACTTATTTTCAGAGCTGAG 646  
QY 354 GTCTCTGTCATGATGATGTCGAGATGCTGTCGTCGACAAATCCCTGATGAGATTG 413  
DB 647 AGCTGGAATCTTGATCTCTCGAGTAACAATTTCTGTGATTCCTGCGAGGACTTG 706  
QY 414 GTGACTGTTCTTTTTCGAAAATCTTACATTTATCTTCAATGAAATTAAGTGAGATAC 473  
DB 707 GGAATCTGCCAAGCTTCAAGTACTGAACCTGTGTCGAACTGTGCAAGACATATCC 766  
QY 474 CGTTTCGATTTGAGATTGAGAACTTGAGACGCTGATTCGAAATGAACAAT-- 531  
DB 767 CAACATTTCTGGAAATCTAGCAATCTGAGCAATTAATGCTGGCAATACATCCCTTG 826  
QY 532 -GATAGAACCGATCCCTTCAACATTTACAGATTCGAACTGAAAATCTGGAATTTG 590  
DB 827 CCCCCGTGTGATTTCTCCAGAGCTGGGGAAGCTAGCAAAAGTTACAGAACTATAGGCTA 886  
QY 591 CACAGATAAATCACTAGTGTGAGATACCAAGACTTAATTTAATGAAATGAATCTTCAGT 650  
DB 887 CTCTTGTAAATTTTGGGGGTGCTATTCGGATTCTAATGGCAATCTGCTCTTTGACGA 946  
QY 651 ATCTTGCTTGGGAGAGAAACAATTAAGTGGTAACTTTCTCAAGTTTGTCTCACTGA 710  
DB 947 ATCTGATCTTTCTTGAATCAGCTCTCGGGAATTAATTCAGAGGCCATCAAAAGTTAA 1006  
QY 711 CTGCTCTTGGTATTTTTCAGTAAGAAACAAGTTTGAATGATGATAGTATACAGACGA 770  
DB 1007 ATCAATATAGACAGATTGAGCTCTATCATTAACAATTAACAGAAAGATTCCTGAGAACT 1066  
QY 771 TAGGAATTCGACTGCTCTTCAAGTTTTCAGATTTGCTGTAATCAATCACTGAGTGA 830  
DB 1067 GGGCTATCTTGTCTCTCAGACATTTTGTATGATCTCAACAAATATGCTTTAAAGGAGCA 1126  
QY 831 TCCCTTTTGCATCGGCTTCTGCAAGTTGCAACATTAATCAATGCAAGGAATCAACTCT 890  
DB 1127 TACCTGACAGTTGGCAGAGTTGCACTTTCTGCTTGAACCTGTTTGAAGATTAATTTGG 1186  
QY 891 CTGGAGATTCATCATGATGATGCTCTCAATGCAAGCCCTTGCAATCTTGAATCTAAGT 950

DB 1187 TAGGACCAATTCGAGAGCTATTTGGATTTCTCAACTCTGTCGAGCTCAAGCTTTTA 1246  
QY 951 GCAACTTTGAGTGATCATTTCTCGATTTCTGGAAATCTTACTTTCACCGAGAAAT 1010  
DB 1247 CGAATTAATCTGAATGTAGCTTCCCTTCAAAATTTGGGAAATTTTCGGCTTCAAAAGC 1306  
QY 1011 TGAATTTGACAGTAAACAAGCTGAGTCTTCAATTCACCTGAGCTTGGAAACATGTCA 1070  
DB 1307 TAGATTTGAGAGAAATTCAGACTAGGTATCTTCCGCGGATCTTTGCAATATGAGGA 1366  
QY 1071 AACTCAATTAACCTGGAATCAATGATATCAATCTCAAGGCTCATATACCAAGACTTG 1130  
DB 1367 AGCTGCAAACTTTGAATATCTTTAAACAACAATCTCACTGGGCGATTTGCTTCAATACG 1426  
QY 1131 GGAAGCTTACTGACTTTGATCTGAATGTGGCCAAACAATGATCTGGAAGGCTATAC 1190  
DB 1427 GTGCAATGTTGAGCTTCAAAAGGCTAGAAATAGCAACAATGCTCATAGGCAAGATGC 1486  
QY 1191 CTGATCATCTGAGCTCTTGCACAACAATCTTAAACAGTTTAAATGTTCAATGGGAAACAATTTA 1250  
DB 1487 CTAGTTCATTTCTGGGCTCTCCCTCAAGTTTATCTCGAATCTCAATCAACAAGTTGC 1546  
QY 1251 GTGGCACTATACCCGAGCAATTTCAAAGCTAGAAAGTATGACTTAATCTTATCTGTCA 1310  
DB 1547 AAGGCTCGAATTTCTTGAATTAGGAATGCCAAGATCATACGGCTATTGATATCCG 1606  
QY 1311 GCAACAATATCAAAAGTCCAAATCCCGTTGAGCTATCTGTATCCGTAATCTAGATATCAT 1370  
DB 1607 GTAACGTTTCTCCGCACTTACCTTCTGAGATAGGCTGTGGCTTAATCTTCTGTGA 1666  
QY 1371 TGGATCTTTTCAACAACAAGATTAATGATATCTTCTTCTTCCCTGATGATTTGGAGC 1430  
DB 1667 TTGATGTAGCCACATCAATCAATCAAGCTCTTCCAGCACTTTGGGTTGCTGTAACA 1726  
QY 1431 ATCTTCTCAAGATGAATCTGAGTAAATCAATTAATCTGCTGATTTCCAGCGCACTTG 1490  
DB 1727 AATTAAGTAAATGATCTTCTTCAAGATCAATCTTCCGATGACCTTCCACTGAGATAC 1786  
QY 1491 GAAATCTAAGAACATCATGAAATGATCTTCAATTAATGATATCTGCGGCCAATTC 1550  
DB 1787 TGTATGAGATGAGCTTACAGACTTAATCTGCAATTAACAGATTTCTGGGCTCTATTC 1846  
QY 1551 CAGAAAGCTTAAACAATTAACAATTAATTTGCTGAGACTGAAAAATTAATACCTGA 1610  
DB 1847 CTAAAGAGCTAGGGAGCTGCCAGTTCTGACATATCTGATCTTTCTGTTAATGCTTGA 1906  
QY 1611 CTGATATGTTGTTTATTAGCCAACTGTCTGATCTCACTGATTAATGATATCTCAAT 1670  
DB 1907 CAGGAGAAATCCCTCTGAAATTTGGCAATTTGAAGCTTAAAGTTTCAATCTTTCCGATTA 1966  
QY 1671 ACAACTCTGATGATATCTCTTGAACAATTAATCTTCAAGATTTTCAACAGACAGCT 1730  
DB 1967 ATCAGCTAATGCTGATTTCTTCTGCTTCAAGTCTC--AATTTTTCACAACTCAAGTT 2023  
QY 1731 TCATTTGCAATCTGCTTCTTCTTGGGATTTGCTTAACTCACCGTGTCAATTTCTGCT 1790  
DB 2024 TAATGGCAATCTCTGGCTTTTGGAGCAATGATGCTTTAAAGGCTTTAAGTCTGTTCT-- 2082  
QY 1851 TGAATCTTCTCATGCTTAAATGAGCTTGGCCGACCGGATATCTCTCTCTTTCTTG 1910  
DB 2143 TTTGCTTTGGCTGGGCTCATTTTGTGTAGGACTGGCTCTGTTTAAAGCAATACCGT 2202  
QY 1911 ATGATCACTTGAACAACAGTAACTTAATTCGACACGGAAGCTGTATCTTCAATATGA 1970  
DB 2203 GATTAACAATTAAGCTTAAGTAAAGTTTGTGGCGAAGCAATAGCTCTCTGAGAGCTG 2262  
QY 1971 ACATGCACTCAAGTTTACAGAGATATCAAG--AATGACAGAAATCTTAAGTGAAG 2029  
DB 2263 ACCACGTTTACCGAATTTGGGTTTCAAGAAATATGAATTTCTGATTTGATGACGAGAA 2322

2030 TATATCATTTGGGACGAGCATCAAGCATGTATACAAATGTGTTTGAAGAATTGTAA 2089  
2323 AATGTGATTTGGAAGTGTGATCAAGAAAAGTACAAAGCCACACTCGGGAATGGAA 2382  
2090 CCGGTTGCGATTAAAGCGCT-----TTACTCTCAACCCACAGTCA 2331  
2383 ACTGTGGCCATCAAGAGGCTGTGGACAAATGAAATGCTGAAGGCTCTACATCTGCAAT 2442  
2132 ATGAACAGTTTGAAGAAAGAACTGAGATGCTAGTACGATCAAGCAGCAAAATCTGTG 2191  
2443 GATTAATGATTCAGAGGCAAGGTTGAACCTTTGGGAAATATTAAGCATTAATAACATAGTG 2502  
2192 AGCCTCAAGCTTATTCCTCTCTCACTTGGGAGTCTCTGTTCTATGACTATTTGAA 2251  
2503 AACTCTGCTGTGCTGTGTCATGAGATTTCTTAATCTTTTGGATACGATCATGCTCT 2562  
2252 AATGTAGCCTCTGGAGATCTTTCTTCAATGAGCCCTACGAAGAAAAGCTCTTGAATGGAC 2311  
2563 AATGGAGTTTGGGGGATCTCTTCATGAGCC---CAAAGCTGGTGAACCTTAATTTGGCT 2619  
2312 ACACGGCTTAAGATAGATATGTCGACGACAAAGTTAGCTTATCTACACATGACTGT 2371  
2620 ACAGTTACAAAATGTCAGTTGAGCAGCTCAGGTTTGGCTTATTTGATCATGATGTGT 2679  
2372 AGTCAAGGATCATTCACAGAGACGTGAGTCCCAACATTTCTTGGACAAAGACTTA 2431  
2680 GTACTCTCTATCATCCATCGCATGTGAAGTCCACAAATATTCGTAGATGCTGATTTT 2739  
2432 GAGGCTGCTTGAACAGATTTTGGAAATGCGAAAAGCTT-----GTGTGTCAAAATCA 2485  
2740 GGTGCTGTGTGGCTGATTTTGGACTTCCAGAGTCTCTCAAGCTATGAGAGGAGATC 2799  
2486 CAACTTCACTTACATGATGAGGACGATAGTGTACATACACCCGAGTATGCTGAGT 2545  
2800 GATTTCTATGCTGCAATTTGCTGATCTTATGTTATATAGCTCCAGAAATGATACACT 2859  
2546 TCAAGGCTCACTGAGAAATCCGATGTCTACAGTTATGAAATAGCTTTCTTGAAGTTTGA 2605  
2860 CTCAAGGTGATGAGAAAGATGACATCTACAGTTTGGAGTGTGCTTCTTAGAGCTAGTG 2919  
2606 ACCCGAAGAAAGCGGTTGATGACGAAT 2633  
2920 ACCGGCAAGACGCGGTATTCAGAGATT 2947

RESULT 5  
US-09-353-585-4  
Sequence 4, Application US/09353585  
Patent No. 6287865  
GENERAL INFORMATION:  
APPLICANT: Dixon, Mark S  
Jones, Jonathan DG  
TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon & Vanderhye PC  
STREET: 8th Floor, 1100 No. 6287865th Glebe Road  
CITY: Arlington  
STATE: Virginia  
COUNTRY: United States of America  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/353,585  
FILING DATE: 15-Jul-1999  
CLASSIFICATION: C12N 15/29, 15/82, A01H 5/00, A01N 65/00, C12Q

1/68  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/930,277  
FILING DATE: 27-OCT-1997  
APPLICATION NUMBER: PCT/GB96/00785  
FILING DATE: 01-APR-1996  
APPLICATION NUMBER: GB 9506658.5  
FILING DATE: 31-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Ms Mary J Wilson  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 620-69  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3573 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Tomato  
STRAIN: CE2  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-353-585-4  
Query Match 6.9%; Score 220.2; DB 3; Length 3573;  
Best Local Similarity 48.0%; Pred. No. 6.2e-60;  
Matches 692; Conservative 0; Mismatches 743; Indels 6; Gaps 2;  
283 TGTGTGCTCTTAATTTGTCAGATTTGAATCTTGTGAGGAATCTCACTGCTATTTG 342  
280 TCTTGAATATCTTGATCTTGAAGAAACATATCTATGTACCATTCACCTAGATGG 339  
343 AGATCTCAAGAGTCTCTTGTCAATGATCTGCGAGTAATCGCTTGTGAGCAAAATCCC 402  
340 TAATCTCAAAATCTTGTCTATCTTGAATGAAACAACATCAATTTGAGGAACAATACC 399  
403 TGATGAGATTGGTACTGTTCTTTTGGCAAACTTAGACTTATCTTCAATGAATTAAG 462  
400 ACCAATATCGTTTACTAGCCAGCTTCAGATCATCCGATATTTCCACATCAATTAATA 459  
463 TGTGACATACCGTTTTCATTTGCAATTTGCAAGTGAAGCAACTGACAGCTGATTCGAAGA 522  
460 TGAATTTATTTCTTAAAGAAATAGGTTTACCTAAGGCTCTTACTAAGCTATCTTTGGGTAT 519  
523 TAACCAATGTATGAGACCGATCCCTTCAACACTTTTCAAGATTTCAAACTGAAATTTCT 582  
520 CAATTTCTTAGTGTTCCATTTCTGCTTCAAGTGGGAATCTGAACAATGCTTTT 579  
583 GGACTTGGCAGAAATTAATCACTAGTGTGATACCAAGACTTATTTACTGGAATGAGT 642  
580 GTATCTTTAACAATATACAGCTTTCTGCTCTATTTCTGAAAGAAATTAATTAACCTAAGATC 639  
643 TCTTCACTATCTTGGGTGAGGAGAAACAATAGTCGTAATATTTCTCAATTTTGG 702  
640 TCTTACTGACTGATTTGATGATTAATGCTCTTAATAGGCTCTAATTCCTGCTTCAATTTGG 699  
703 TCAACTGACTGCTTGTGATTTTGAAGTAAGTAAGAAACAACAGTTTGAAGTGTAGTATACC 762  
700 GAATATGAACAATCTGCTTTTGTGTTTCTTATGAAATACACTTTGCTGCTATGCTC 759  
763 TGAAGCATGAGAAATGACCTGCTTCCAGGTTTGGAGTTGCTCTCAATGAGCTAAC 822  
760 TGAAGAAATATGTACTTAAGATCTCTTACTTACTAGATTTGAGTGAAGATCTCTTAA 819  
823 TGTGAGATTCCTTTTGAATGAGCTTCCGCAAGTTGCAACATTAATCATGTC---AAG 879  
820 TGGCTTATTCCTGCTTCAATTTGGGAATTTGAACAACCTGCTTTTGTGTTTCTTTATGG 879



Db 2204 CAACCTTTCTAGTGTCCATCTCCTGTCAGTGGGAACTGAAACAATGCTTTT 2263  
QY 583 GGACTTGGCAACAATACTCAGTGTGATGCCAAGCTTATTACTGGAATGAGT 642  
Db 2264 GATCTTTTACAAATATCAGCTTTCTGGCTCTATTCTGAAAGAAATTAAGTACTTAAGATC 2323  
QY 643 TCTTCAGTATCTTGGTGGGAGAAACAATTAGTGTGTAACATTTCTCCAGATTGTG 702  
Db 2324 TCTTACGAGCTAGATTGAGTGTATATGCTTTAATAGGCTATTCTGCTTCATTTGGG 2383  
QY 703 TCACTGACTGTCTTTGTAATTTGACGTAAAGAAACAAGTTGACTGTAGTATACC 762  
Db 2384 GAATATGAAACAACCTGTCTTTTGTCTTAAATGAAATACAGCTTCTGCTCTATTACC 2443  
QY 763 TGAGAGATGGAATGCACTGCTCCAGGTTTGGACTTGTGCTTCAATACAGTAC 822  
Db 2444 TGAAGAAATATGTTACCTAAGATCTTACTTACCTAAGATTGAGTGAAGATGCTTTAA 2503  
QY 823 TGGTGAAGATCCCTTTTGACATCGGCTTCTGCAAGTTGCAACATTATCATTCG--AAG 879  
Db 2504 TGGCTCTATTCCTGCTTCATTTGGGAAATTTGAACAATTGCTTTTGTGTTCTTTATGG 2563  
QY 880 CAATCAACTCTCTGGGAAGATTCATGATGTTGTTCTATGCAAGCCCTTGCACTT 939  
Db 2564 AAATCAGCTTCTGGCTCTATTCTCTGAAGAAATAGTTTACCTAAGATCTCTTAATGCTCT 2623  
QY 940 AGATCTAAGTGGCACTTTGAGTGTATCTATCTCCGATTTCTGGAAATCTTACTT 999  
Db 2624 AGGTTTGAAGAGATCCTTTAATGAGCTCTATTCTGCTTCATTTGGGAAATCTGAAAA 2683  
QY 1000 CACCGAAGAAATGTAATTTGACAGATTAACAAGTACTGTTCAATTCACCTGAGCTTG 1059  
Db 2684 CTGTCTAGTGTGATCTTTGTAATATACAGCTTCTGGCTCTATCTGCTTCATTTGGG 2743  
QY 1060 AAACATGTCAAAATCCTCATTACTGGAATCAATGATTAATCATCTACGGTCTATACC 1119  
Db 2744 GAATCTGAACAACCTGTCTATGTTGATCTTTACAAATACAGCTTCTGCTCTATTTCC 2803  
QY 1120 ACCAGAGCTGGGAGTCTGACTGTTGATCTGAATGATGGCCAAACAATGATCGA 1179  
Db 2804 TGTCTCATTTGGGAGATCTGAACAATGCTGTATGTTTATCTTTTCAATATACGCTTTC 2863  
QY 1180 AGGACCTATCTGATCATCTGAGCTCTGACAAATCTTAAACAGCTTAAATGTTCAAG 1239  
Db 2864 TGGCTCTATTCCTGCTTCATTTGGGAAATCTGAACAACCTGTCTAAGTTGATCTCTCA 2293  
QY 1240 GAAACAATTTAGTGGCACTATCCCCGAGCTTTCAAAGCTAGAAGTATGATCTTCT 1289  
Db 2924 TAAATCAGCTTCTGGCTCTATTCTCTGAAGAAATAGTTACTGATTCCTCTTACTTATCT 2983  
QY 1300 TAACTCTCCAGCAACAATATCAAAAGTCCAAATCCCGGTTGAGCTATCTGATCGGTA 1359  
Db 2984 AGATTTAGTATATACCTCATTTAATGATTTATCTGCTTCATTTGGCAATATGAGCA 3043  
QY 1360 CTATAGATATGATCTTTCAACAACAAGATTAATGAAATCAATCTCTTCTCCCTGG 1419  
Db 3044 CTGGCTTTTGTGTTCTTATGAAAAATCAGCTGTAGCTCTGCTCTGAAGAAATAGG 3103  
QY 1420 TGATTTGAGCATTTTCTCAAGATGAATCTGAGTGAATCATATACTGTGTAGTTCC 1479  
Db 3104 TTACCTAAGTCTCTTAATGCTCTTGAATGAGTGAAGATGCTCTTAATGCTCTATTTCC 3163  
QY 1480 AGGCACTTTGGAATCTAAGAGCATCATGGAATATGATCTTCAATATATGATCTC 1539  
Db 3164 TGCTTCAATTTGGGAAATTTGAACAATGCTGTAGTGAATCTTTTAATATACGCTTTC 3223  
QY 1540 TGGCCCAATTTCAAGAGCTTTAAACAATTAAGAAATATTTTGTGAGACTGAAAA 1599  
Db 3224 TGGCTCTATTCCTGAAGAAATAGTTTACCTAAGTCTCTTAATGCTCTGATTTGAGTGA 3283  
QY 1600 TAAATACCTGACTG--TAAATGTTGTTCTTATGCAACCTGTCTCACTGATTT 1656  
Db 3284 GAAATGCTCTTAATGCTCTATTTCTGCTCAATGGGAAATTTGAACAACCTGTCTAAGTT 3343

QY 1657 GAATGATCTCATACAACTCTGATGATATCCCTAAGAAACAATTAATCTCAAGATT 1716  
Db 3344 GAATCTTTTATATATACAGCTTTCTGCTCTATTTCTGAAAGAAATAGTACTTAAGATC 3403  
QY 1717 T 1717  
Db 3404 T 3404  
RESULT 7  
US-09-180-439-7  
; Sequence 7, Application US/09180439  
; Patent No. 6225532  
; GENERAL INFORMATION:  
; APPLICANT: Dixon, Mark S  
; APPLICANT: Hatzixanthis, Kostas  
; APPLICANT: Jones, David A  
; TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof  
; FILE REFERENCE: 620 - 53  
; CURRENT APPLICATION NUMBER: US/09/180,439  
; EARLIER FILING DATE: 1998-12-06  
; EARLIER APPLICATION NUMBER: PCT/GB97/01249  
; EARLIER FILING DATE: 1997-05-08  
; EARLIER APPLICATION NUMBER: GB 9609681.3  
; EARLIER FILING DATE: 1996-05-09  
; EARLIER APPLICATION NUMBER: GB 9619924.5  
; EARLIER FILING DATE: 1996-09-24  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 4123  
; TYPE: DNA  
; ORGANISM: Lycopersicon esculentum  
US-09-180-439-7  
Query Match 6.9%; Score 217.6; DB 3; Length 4123;  
Best Local Similarity 48.2%; Pred. No. 4.8e-59;  
Matches 678; Conservative 0; Mismatches 724; Indels 6; Gaps 2;  
QY 292 TCTTAATTTCTCAGATTGTAATCTTGATGGAATATCTCAGCTGCTATTGGAATCTCA 351  
Db 950 TCTTGAATCTTGAACAACAATATCTCTGTACATCTCCAGAGATGTAATCTCAC 1009  
QY 352 GAGTCTTGTCAATGATGTGAGAGATATGCTGTCTGGAACAATCCCTGATGAT 411  
Db 1010 AAATCTGTCTATCTTGAATCTGAGTGAACAACATTCAGATTTGAGAAATTCACACAAAT 1069  
QY 412 TGGTGAATGTTCTTCTTGGCAAACTTGAATCTTATCTTCAATGAATTAAGTGTGACAT 471  
Db 1070 CGGTTCACCTAGCAAGCTTCAATCAATCCGATATTTAACAATCATTTAATGCTTTAT 1129  
QY 472 ACCGTTTTCGATTTCCAGTGTGAAGCACTTGAAGAGCTGATCTGAAGATTAACAAT 531  
Db 1130 TCTTGAAGAAATAGTTTACTTAAGTCTCTTAAGCTATCTTGGGTATCAACTTCT 1189  
QY 532 GATAGACGATCCCTTCAACACTTTCAAGATTTCAACCTGAATAATCTGAGCTTGGC 591  
Db 1190 TAGTGTCTATTCCTGCTTCATTTGGGCAATGAGCAACACTTGTCTTTTATTTCTTTA 1249  
QY 592 ACAGATTAACCTGAGTGTGAGATACCAAGACTTATTTACTGAAATGAAGTCTTCAGTA 651  
Db 1250 TGAATAATCAGCTTTCTGGCTTATTTCTGTAAGAAATAGTACTTAAGTCTCTACTTA 1309  
QY 652 TCTTGGGTCGAGAAACAATTAATGCTGTAACATTTCTCAGATTTGTGTCACTGAC 711  
Db 1310 GCTATCTTTGATATCACTTCTTATGTTGCTCATTTCTGCTTCAATTTGGGAAATCGAA 1369  
QY 712 TGGTCTTTGATTTTGAAGTAAACAACAGTGTGATGATGATGATGATGATGATGATGAT 771  
Db 1370 CAATCTGTCTTTTGTATCTTTTAAATATACAGCTTTCTGCTCTATTTCTGTAAGAAAT 1429



QY 772 AGGAATTCAGTCCCTCCAGGTTTGGATCTTGCTTCAATAGCTAACTGGAGAT 831  
DB 1430 AGGTACCTGAGGCTACTTACTAGCTATCTTGGATCACTTCTTATGGTTCCAT 1489  
QY 832 CCGTTTGGATGCGCTTCT--GCAAGTTGCAATATATATGCAAGGCAATCACT 888  
DB 1490 TCTGCTTCAATGGGGAATCAAACTGCTAGGATGATCTTAAATATAGCT 1549  
QY 889 CTCTGGGAATATCCATGATGATGCTGCTATGCAAGCCCTTGCACTTAAATCAAG 948  
DB 1550 TCTGCTTCAATGGGGAATCAAACTGCTAGGATGATCTTAAATATAGCT 1609  
QY 949 TGGCAACTGTTGATGATGATGATGCTGCTATGCAAGATCTTCACTTCAAGGAA 1008  
DB 1610 TGAAGATGCTTAAATGCTGCTATCTGCTTCTTATGGGAAATCAAACTGTTAT 1669  
QY 1009 ATTGATTTGACAGATCAAGCTGATGCTGATCACTGAGCTGGAACATATGTC 1068  
DB 1670 GTTGTATCTTAAATATGCTGCTTCTGCTATCTGAGGAAATAGGTTAAGCTAAG 1729  
QY 1069 AAAATCTTACTGGAATCAATGATATCATCTGAGGCTATATACCAAGCT 1128  
DB 1730 GTCTTACTTACTGATATGCTGATGAAATGCTTAAATGCTTAAATCTGCTTCT 1789  
QY 1129 TGGGAAGCTTACTGATGCTTGTGATGCAATGCTGCAATGATGATGGAAGCTAT 1188  
DB 1790 GGGGAATCTTAAATCTTCTGATGCTGATGCTTAAATATAGCTTCTGCTTAT 1849  
QY 1189 ACCTGATCATCTGAGCTTGTGCAAAATCTTAAATGCTTAAATGCTTAAATGCT 1248  
DB 1850 TCTGGAAGAAATAGGTTACTGATGCTTCTTACTTACTGATGCTTAAATGCTT 1909  
QY 1249 TATGTCATCTATACCCGAGCTTCTTCAAAAGCTGAAAGATGATGCTTAAATGCT 1308  
DB 1910 TATGTCATCTATACCCGAGCTTCTTCAAAAGCTGAAAGATGATGCTTAAATGCT 1369  
QY 1309 CAGCAATATCAAGATGCTTCAATGCTGATGCTGATGCTGATGCTGATGCTGATG 1368  
DB 1970 CATATATCACTTCTGCTGCTATCTGATGAAATAGCTTCTGATGCTTCTTACTGA 2029  
QY 1369 ATTGATCTTTCACACAAAGATTAATGGAATCTTCTTCTTCTTCTTCTTCTTCT 1428  
DB 2030 ACTATATTTGGGTAATATCTCTTATGCTGCTTCTTCTTCTTCTTCTTCTTCT 2089  
QY 1429 GATCTTCTCAAGATGCTGATGAAATCATATATGCTGATGCTGATGCTGATGCT 1488  
DB 2090 CAATCTGTTATGCTGATCTTATCAATATGCTGCTTCTTCTTCTTCTTCTTCT 2149  
QY 1489 TGGAAATCTTAAAGATGATGGAATATGCTTCTTCTTCTTCTTCTTCTTCTTCT 1548  
DB 2150 AGGTACCTGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2209  
QY 1549 TCCAGAGAGCTTAACTTCAATGATGAAATATGCTGAGCTGGAATATATATACCT 1608  
DB 2210 TCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2269  
QY 1609 GACTGG--TATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1665  
DB 2270 TCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2329  
QY 1666 TCATATCAACCTGATGATGATGCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1693  
DB 2330 TGATATGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2357

RESULT 8  
US-10-101-464A-308  
; Sequence 308, Application US/10101464A  
; Patent No. 6768041  
; GENERAL INFORMATION:  
; APPLICANT: Strabala, Timothy  
; APPLICANT: Nieuwenhuizen, Nicolaas  
; APPLICANT: Higgins, Colleen M.

; TITLE OF INVENTION: Compositions Isolated from Plant Cells  
; FILE REFERENCE: 11000.102062  
; CURRENT APPLICATION NUMBER: US/10/101,464A  
; PRIOR FILING DATE: 2002-03-18  
; PRIOR FILING DATE: 2000-11-01  
; PRIOR FILING DATE: 2000-11-01  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR FILING DATE: 1999-11-01  
; PRIOR FILING DATE: 2000-01-11  
; NUMBER OF SEQ. ID NOS: 989  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 308  
; LENGTH: 550  
; TYPE: DNA  
; ORGANISM: Pinus radiata  
US-10-101-464A-308

Query Match 6.8%; Score 217.2; DB 3; Length 550;  
Best Local Similarity 65.9%; Pared. No. 1.6e-59;  
Matches 315; Conservative 0; Mismatches 163; Indels 0; Gaps 0;

QY 2375 CCAAGATCATTTACAGAGAGCTGAAAGTGTCCACATTTCTTGGACAAAGCTTAGAG 2434  
DB 4 CCAAGATCATTTACAGAGAGCTGAAAGTGTCCACATTTCTTGGACAAAGCTTAGAG 63  
QY 2435 GCTGCTTACAGATTTTGGAAATAGGAAAGCTTGTGTGCAAGTCAATCTTCTCA 2494  
DB 64 GCACATTTGTGACATTTTGGCAATGCTGCAATGCTTCTTCTTCTTCTTCTTCTTCT 123  
QY 2495 ACTTACGATGAGGAGCAGATGATGATGATGATGATGATGATGATGATGATGATG 2554  
DB 124 ACTTACGATGAGGAGCAGATGATGATGATGATGATGATGATGATGATGATGATG 183  
QY 2555 ACTTACGATGAGGAGCAGATGATGATGATGATGATGATGATGATGATGATGATG 2614  
DB 184 AACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 243  
QY 2615 AAAGCGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2674  
DB 244 AAAGCGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 303  
QY 2675 GAAGTATGAAATGAGCAGATGATGATGATGATGATGATGATGATGATGATGATG 2734  
DB 304 GAAGTATGAAATGAGCAGATGATGATGATGATGATGATGATGATGATGATGATG 363  
QY 2735 AAGAAAGTTTCCATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2794  
DB 364 AAGAAAGTTTCCATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 423  
QY 2795 ATGACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2852  
DB 424 ATGACACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 481

RESULT 9  
US-10-101-464A-878  
; Sequence 878, Application US/10101464A  
; Patent No. 6768041  
; GENERAL INFORMATION:  
; APPLICANT: Strabala, Timothy  
; APPLICANT: Nieuwenhuizen, Nicolaas  
; APPLICANT: Higgins, Colleen M.  
; TITLE OF INVENTION: Compositions Isolated from Plant Cells  
; FILE REFERENCE: 11000.102062  
; CURRENT APPLICATION NUMBER: US/10/101,464A  
; CURRENT FILING DATE: 2002-03-18  
; PRIOR FILING DATE: 2000-11-01  
; PRIOR FILING DATE: 2000-11-01

PRIOR APPLICATION NUMBER: 09/228,986  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/162,866  
PRIOR FILING DATE: 1999-11-01  
PRIOR APPLICATION NUMBER: PCT/US00/00724  
PRIOR FILING DATE: 2000-01-11  
NUMBER OF SEQ ID NOS: 989  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 978  
LENGTH: 3432  
TYPE: DNA  
ORGANISM: Pinus radiata  
US-10-101-464A-878

Query Match 6.3%; Score 199.6; DB 3; Length 3432;  
Best Local Similarity 45.2%; Pred. No. 3e-53;  
Matches 1043; Conservative 0; Mismatches 1229; Indels 36; Gaps 7;

QY 344 GATCTCAAGAGTCCTTGTCAATGTATCTGCGAGTATCGCTTGTGCAAAATCCCT 403  
DB 562 GAGCTCTTCAAGCTTAAAGCATCTGAGATCTTGTGAAATAAATTAAGCGGTCGGTCCC 621  
QY 404 GATGAGATGTGTGACGTCTTCTTTCGAAAATTGACCTTATCTTCAATGAATTAAGT 463  
DB 622 CCGCGCTTCGGCGGCGCTGCGGGAATTCGAAGCTTAAATCTGCTCTCAATCTTCTCAAT 681  
QY 464 GGTGACATACCGTTTGTGATTTGGAAGTGAAGCACTTGAGAGCATTTGGAAGAAT 523  
DB 682 ACTACAAATTCGGCTTTGTAGTGATCTTCAAAATCTTTGAGCTTCAATTTGGCTTAC 741  
QY 524 AACCAATTTGATAGAACCGATCCCTTCAACATTTTCAAGATTCGAAATCTG 583  
DB 742 AATCTCTCACTGGAACGTATACCTCTGAGCTGGAAATCGAAGAGCTGCAAAATCTA 801  
QY 584 GACTTGCGACGAATTAACCTGAGTGTGAGATACCAAGATTTATTTCTGGAATGAAGTT 643  
DB 802 TGGCTGCGGCGGTGCAATCTGTCGGAATAATCCGAGACCTTGGGCAATCTCTCCGAG 861  
QY 644 CTTCAGATATCGGGGTTGCGAGAAACAATTTAGCGGTAAATTTCCAGATTTGTGT 703  
DB 862 CTAAACAACCTTGAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 921  
QY 704 CAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 763  
DB 922 AAGCTGGAACAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 981  
QY 764 GAGACGATAGGAATTCACCTGCTTCCAGGTTTGAATTTGATGATGATGATGATGATGATGAT 823  
DB 982 GTGCGCATGCGGCGAGCTTAAAGCAATGAAGGTTTATGCTTCCATGAATATGCTAGAC 1041  
QY 824 GGTGAGATTCCTTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 883  
DB 1042 GGTTCATTTCTTGGCGGAGCTGAGGAGCTTGAATCTGGAATCTTGAATCTTGAATCTTGA 1101  
QY 884 CAATCTCTGGAAGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 943  
DB 1102 AATCTGTTGGCAAAATACCTCCAGGCTTGGTTGTTTACGATCTCAAGAGATTTAAAG 1161  
QY 944 CTAAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1003  
DB 1162 CTCTTCTCAATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1221  
QY 1004 GAGAAATTTGATTTGCAAGTAAAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1063  
DB 1222 CTAGACCTGATATGCAAGACCTGATATCTGGAAGGCTTCTCCGATCTATGCAAA 1281  
QY 1064 ATGCAAAATCTCAATTAATCTGGAATCAATGATTAATCAATCAATCAATCAATCAATCAAT 1123  
DB 1282 AACAAAAGCTTGAATTTCTAGCATTTTCAACATGAGCTCGGTGATTTTACCTGAA 1341  
QY 1124 GAGCTTGGGAAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1183  
DB 1342 AGCTTGGGAACCTGCAAGAGCTTAAACAGAGTCCGCTAGGAGCAACAAATTTAAAGGC 1401

QY 1184 CTTATACCTGATCATCTGAGCTCTTGCAAAATCTAAACAGCTTAATGTTCAATGGGAAC 1243  
DB 1402 TCGGTACCCAGTTTATTTCTGGGACCTTCTCAAGCTCTCACTGCTGGAGCTCAAGGACAAAT 1461  
QY 1244 AAGTTAGTGGCACTATACCCGAGCATTTCAAAAGCTGAAAGTATGACTTACTTAAT 1303  
DB 1462 TATTTGAAGGATTTTCTCCCGCATTTGCCGAGCTTAAATCTCTCATGCTGCTG 1521  
QY 1304 CTGTCCAGCAAGATTAATCAAGAGTCCAAATCCGGTTGAGCTATCTGATCTGTAATCTTA 1363  
DB 1522 ATCAGGCGCAATATTAATTTAGGCGGAGCTGCTTACGAAATCTGATGACTGAGAACTTC 1581  
QY 1364 GATACATTTGATCTTTTCAACAACAAGATTAATGAAATCTTCTTCTTCTGATGAT 1423  
DB 1582 AGGAGATTAATGCTGACATATTAATTAATCACTGATGATGATGATGATGATGATGATGATGAT 1641  
QY 1424 TTGAGCATTTCTCAAGATGAACCTGATGAATATATTAATCTGATGATGATGATGATGATGAT 1483  
DB 1642 CTGCAATCTGCGGAAAGCTGAGCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 1701  
QY 1484 GACTTTGGAATATTAAGGACATCATGGAATGATCTTCAATTAATGATATCTGATGAT 1543  
DB 1544 CCAATTTCAAGAAAGCTTAAACCAATTAACAGAAATTAATTTGCTGAGACTGGAATAAT 1603  
QY 1702 GAATCAATCTGCAACAGCTTGAAGATCAATCTTCAAGAAACAGCTCTCCGT 1761  
DB 1762 TCGATTTCTGCGAGCTGCTGATCTTGTGCTTATTAATTAATGATCTCTGGAAT 1821  
QY 1604 AACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1663  
DB 1822 CTTCCTACCGGCGGATCTCTTCCAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1881  
QY 1664 TCTCATTAACAACCTCGAGTGTG-ATATCCCTAAGAACAAATTAATCTTCAAGATTTTCAAC 1722  
DB 1882 TCGGCAACCGCTTGTCTGCGGAGCTTCTTGGCTTTGAATTCGGATGATGAAAG 1941  
QY 1723 AGACAGCTTATTTGCAATCTGCTCTTGGCGATGATGATGATGATGATGATGATGATGATGATGAT 1782  
DB 1942 AGTTTCTGGAATAATCCGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2001  
QY 1783 TTTCTGCGAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1842  
DB 2002 TCTGAAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2061  
QY 1843 G--GGACTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1900  
DB 2062 TTTGAT 1960  
QY 1901 CTTTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1960  
DB 2122 AACTTGAACAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2181  
QY 1961 CTTTCTTGAACAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2020  
DB 2182 TTTTCAAGG--TTGGGATTCAGTGAATGAG-----ATCTGATGATGATGATGATGATGATGAT 2226  
QY 2021 AGTGAAGATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2080  
DB 2227 GATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2286  
QY 2081 AATTTAAACCGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2131  
DB 2287 AATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2346  
QY 2132 ATGAACAAGTTTGAACAAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 2191  
DB 2347 GATTAATGATTTTCAAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2406  
QY 2192 AGCTTACAACTTATTCCTCTCTCACTTGGGAGTCTTCTGTTCTTATGATGATGATGATGATGAT 2251  
DB 2407 AAGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2466

2252 AATGATAGCTCTGGATCTTCTTCAATGAGCCCTACGAGAAAAAGACTCTTGATGGAC 2311  
2467 AATGGAGTCTGGAAATCTTCTTCAATGAGCT--AAGCTAGTCTTCTGAGTGGCC 2523  
2312 ACAAGGCTTAAGATACATATGCTGACAGCAAGGTTTACCTTATACACATGACTGT 2371  
2524 ATAAATACAAAGATGCTCCCTTGGAGAGCTCAGGGGCTGGCATATCTTCAATGATGT 2583  
2372 AGTCCAGAGATCTTACAGAGAGCTGAGTGTCTCCCAACTTCTCTTGGACAAAGCTTA 2431  
2584 GATACCAATCATTTGTACAGAGAGCTGAAATCCAAATATATTTGTCTGATGAGATAT 2443  
2432 GAGGCTCGTTTGACAGATTTTGGATAGCGAAAAAGCTTG--TGTGTGCAAAATCA 2485  
2644 GGGGCTCATGTTGCTGATTTTGGTGTGCGAAGTTTCTGAGAGCTGCGGTAGTGAAGCT 2703  
2486 CATACTTCAACTACGTATGAGGAGCAGATAGTTTACATAGACCCGAGTATGCTGACT 2545  
2704 GATTTATGACTGCAATGCTGGGTCTATGGCTACATAGCTCAGAGTATGCTCAACT 2763  
2546 TCACGCTCAGTACAGAAATCCGATGCTACAGTTATGAAATAGTCTTCTTGAGTTTGA 2805  
2764 CTCAGAGTGAATGAAAAAGTGAATCTATATGTTTGGAGTTGTGATCTTGGAGCTGTA 2823  
2606 ACCGGAAGAAAGCCGTTGATGACGAAT 2633  
2824 ACTGGAGCGCGGCGGAGTATCCAGACT 2851

## RESULT 10

US-09-180-439-1  
Sequence 1, Application US/09180439

Patent No. 6225532  
GENERAL INFORMATION:

APPLICANT: Dixon, Mark S  
APPLICANT: Hatzixanthis, Kostas

APPLICANT: Jones, David A  
APPLICANT: Jones, Jonathan DG

TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof  
FILE REFERENCE: 620 - 53

CURRENT APPLICATION NUMBER: US/09/180,439  
CURRENT FILING DATE: 1998-12-06

EARLIER APPLICATION NUMBER: PCT/GB97/01249  
EARLIER FILING DATE: 1997-05-08

EARLIER APPLICATION NUMBER: GB 9609681.3  
EARLIER FILING DATE: 1996-05-09

EARLIER APPLICATION NUMBER: GB 9619924.5  
EARLIER FILING DATE: 1996-09-24

NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 3979  
TYPE: DNA

ORGANISM: Lycopersicon esculentum  
US-09-180-439-1

Query Match 6.2%; Score 195.4; DB 3; Length 3979;  
Best Local Similarity 48.2%; Pired. No. 7,8e-52;

Matches 615; Conservative 0; Mismatches 656; Indels 6; Gaps 2;

423 CTTCTTGGAAAATTAGACTTATCTTCAATGAAATTAAGTGGTGAATACCGTTTTCGA 482  
937 CTTTCTCGAATCTTGAATCTTACGAAACAATATCTGTGATACATTTCCACTGAGA 996  
483 TTTCGAAGTTGAACAATTGAGCAGCTGATTTCTGAAGATTAACAATGATGAGACGA 542  
997 TTGGTATCTCAACAATCTGTCTATCTTGACTTGAACCAATCAGATTTTCGAGAACAA 1056  
543 TCCCTTCAACACTTTCACAGATTTCCAAACTGAAATTTCTGGAGTTGGACAGAAATTAAC 602  
1057 TTCCACCAACAATTCGGTTCACTAGCCAGCTTCCAGATCATCCCATATATTAACAATCAT 1116  
603 TCAGTGTGATGATACCAAGACTTATTACTGAAATGAATGTTCTTCAGTATCTTGGGTGC 662

1117 TAAATGGCTTTATTCCTGAAGAAATAGCTTACCTAGAGTCTCTTACTAAGCTATCTTTGG 1176  
663 GAGAAACAACATTAATGCTGTAACATTTCTCAGATTTGTGTCAACTGACTGCTTTGGT 722  
1177 GTATCAACTTTCTTAACTGATGCTTATCTGCTTCAATGGGCAATATAGCAACTGTCTCT 1236  
723 ATTTTGAAGTAAACAACAGTTTGAAGTGTAGTATGATCTGAGAGATGAGAAATGCA 782  
1237 TTTTATTTCTTATGAAATTCAGCTTTCTGCTTTATCTCTGAGAAATAGTTTACCTTA 1296  
783 CTGCTTCCAGGTTTGTGAGCTTCTTCAATCAGCTTAACTGCTGAGATCCCTTTTGACA 842  
1297 GGTCTTAACTAAGCATATCTTTGATATCAACTTTCTTATGTTGTTCCATCTCTGTTCA 1356  
843 TCGGCTTCTG--CAAGTTGCAACTTATCATGCAAGCAATCAACTCTCTGGAGAGA 899  
1357 TGGGGAATCTGAACAATGCTTCTTTTGTATCTTACATATATCAGCTTTCTGGCTCTA 1416  
900 TTCCATCAGGATGCTGCTCATGCAAGCCCTTGCACTTTAGATCTAAGTGGCACTGT 959  
1417 TTCTGAAGAAATAGTTTACCTAAGTCACTTACCTATCTTTGGATCACTTTC 1476  
960 TGAGTGAATCTATCTCCGATTTCTGAAATCTTCACTTTCAACGAGAAATGTATTTTC 1019  
1477 TTAGTGTTCATCTCTGCTTCAATGGGATCTAACAACCTGTCTAGGTTGATCTTT 1536  
1020 ACAATTAACAGTCACTGTTCAATTCACCTGAGCTTGGAAACATGTCAAACTCCATT 1079  
1537 ACAATTAATAGCTTCTGCTCATTTCTGAGAAATATAGGTTTACCTAAGTCTCTTACT 1596  
1080 ACCTGGAATCAATGATATATCATCTCAGCGTATATACCAAGAGCTTGGGAAGCTTA 1139  
1597 ACCTAATTTGGTGAAGATGCTTAAATGCTTAAATGCTTAAATCTTTTATTTGGGAATCT 1656  
1140 CTGACTTGTGTTGATCTGAATGTGGCCAAATGATCTGGAAGAGCTTAACTGATCATC 1199  
1657 ACAATTTGCTAGTGTGATCTTCAATATATAGTTTCTGCTCTATCTCGAAGAAA 1716  
1200 TGAGCTCTTGCAACAATCTAACAAGTAAATGTTTCAATGAGAAACAAGTTTGTGCACT 1259  
1717 TAGGTTACCTAAGTCTCTTACTTACCTGATTTGGGAGATGCTCTTAAATGGCTCTA 1776  
1260 TACCCGAGATTTCAAAAGCTAAGATATGATACCTATATCTGTCCAGCAACAT 1319  
1777 TTCTGCTTCAATTTGGGAAATCTGAACAAGTTTATGTTGATCTTTTACATATATCAGC 1836  
1320 TCAAGATCCAAATCCCGTTGAGCTATCTGTAATCGTAATTAAGATTAAGATCTTT 1379  
1837 TTCTGCTCTATTTCTGTAAGAAATAGTTTACCTGAGTTCTCTTACTGAATATTTGG 1896  
1380 CCAACAACAAGATTAATGAAATCTTCTTCCCTTGTGATTTGAGACATCTTCTCA 1439  
1897 GTATATATCTCTTAAATGCTCTATCTGCTTCAATTTGGGAAATCTGAACAATCTTCT 1956  
1440 AGATGAATCTGATGAATATCAATATATACCTGCTATCTCAGCGGCACTTTGAAATCTTA 1499  
1957 TGTGATCTTTTAAATATATCAGCTTTCTGCTTATTTCTGAGAAATAGTTTACTCTGA 2016  
1500 GAAGCATCTGAAATATAGATCTTTCAATATATGATATCTTGGCCCAATTTGAGAGAGC 1559  
2017 GTTCTCTTACTGAACATATTTTGGTAATATACCTCTTATATGCTCTATTTCTGCTTCA 2076  
1560 TTAACCAATTAACAACATTAATTTTCTGAGACTGGAATATTAACCTGACTG--TA 1616  
2077 TGGGGAATCTAACAACATTTGTAGGTTTATCTTAAATATATCAGCTTTCTGGCTCTA 2136  
1617 ATGTTGTTTCAATTAAGCAATGCTCAGTCTCAGCTATTTGAATGATATCAATCAAC 1676  
2137 TTCTGCTTCAATTTGGCAATATGAGAAATCTGCAAACTGTTTCTCAGATATAGGATC 2196  
1677 TCGTAGGATATCTCT 1693

Db 2197 TCATTGGGGAATTCTT 2213

RESULT 11

US-09-180-439-2

Sequence 2, Application US/09180439

Patent No. 6225532

GENERAL INFORMATION:

APPLICANT: Dixon, Mark S

APPLICANT: Hatixanthia, Kostas

APPLICANT: Jones, David A

APPLICANT: Jones, Jonathan DG

TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof

FILE REFERENCE: 620 - 53

CURRENT APPLICATION NUMBER: US/09/180,439

EARLIER FILING DATE: 1998-12-06

EARLIER APPLICATION NUMBER: PCT/GB97/01249

EARLIER FILING DATE: 1997-05-08

EARLIER APPLICATION NUMBER: GB 9609681.3

EARLIER FILING DATE: 1996-05-09

EARLIER APPLICATION NUMBER: GB 9619924.5

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2

LENGTH: 3979

TYPE: DNA

ORGANISM: Lycopersicon esculentum

US-09-180-439-2

Query Match 6.2%; Score 195.4; DB 3; Length 3979;

Best Local Similarity 48.2%; Pred. No. 7.8e-52;

Matches 615; Conservative 0; Mismatches 656; Indels 6; Gaps 2;

QY 423 CTCTTTGGAACCTTGAATCTTCTCAATGATTAATGCTGACATACCGTTTTCGA 482

DB 937 CTTTCTCGGAATCTTGATCTTAGCAACAATATCTCTGTACCTTCCACTGAGA 996

QY 483 TTTGGAATGGAACAATCTGACAGCTGATTTGGAAGATAACAATGATGAGACGA 542

DB 997 TTGGTATCTCAAAATCTTGTCTATCTTGAACCTGGAACCAATCTTCAAGAACAA 1056

QY 543 TCCCTTCAACCTTTCACAGATTCACAACTGAAATTTGCACTTGGACAGAAATAC 602

DB 1057 TTCACACAAATCGGTTCACTAGCCAAAGCTCAGATCATCCGATTTTAACAATCAT 1116

QY 603 TCGTGTGATGATGACCAAGCTTATTTACTGGAATGAAGTTCTTCACTTGGGTGC 662

DB 1117 TAAATGCTTATTTCTGAAAGAAATAGTTAAGTCTCTTAACTAACTATCTTTGG 1176

QY 663 GAGGAAACAATTAAGTCGTAACTTTCTCAGATTTGTGTCAACTGACTGCTTTTGT 722

DB 1177 GTATCAACTTTCTTAAGGTCTTATCTCTGCTTATGGGCAATATGACCAACTGTCT 1236

QY 723 ATTTTGAAGTAACAACAGTTTGACTGTAGTATCTGAGAGATAGAAATTTGCA 782

DB 1237 TTTTATTTCTTTATGAAATACAGTTTCTGCTTATTTCTGAAAGAAATAGTTACTTA 1296

QY 783 CTGCTTCAAGTTTGAATGCTTCAATCAAGCACTGATGAGATGAGATGCTTTGACA 842

DB 1297 GGTCTCTTAAAGCTATCTTTGATATCAACTTTCTTATGTTTCCATTCCTGCTTCAT 1356

QY 843 TCGGCTTCTCTG---CAAGTTGAACATTTATCTTGAAGCAATCAACTCTCTGGAGAA 899

DB 1357 TGGGGAATCTGAACAATCTTCTTTTGTATCTTTATCAATATCACTTCTGCTCTTA 1416

QY 900 TTTCATCAAGTATGCTCTCATGCAAGCCCTTGCACTTAAATCTTAAGTGGCACTGT 959

DB 1417 TTCTGAAGAAATAGTTAAGTCAAGTCACTTAAAGTATCTTTGGGTATCAACTTTC 1476

QY 960 TGAATGATATATCTCCCGCATCTCTGGAATCTTATTTTACCGAAGAAATGATTTGC 1019

DB 1477 TTATGATTCATCTCTGCTTCAATGGGGAATCAACAATCTGTCTTAAAGTATCTTT 1536

QY 1020 ACAGTAACAGCTGACTGTTCAATTTCCACTGAGCTGGAAACATGTCAAAATCTCAT 1079

DB 1537 ACATATATAGCTTCTGGGTCTATTTCTGGAAGAAATAGGTTACCTAAGTCTTACTT 1596

QY 1080 ACTGGAATCAATGATATCATCTCAAGGCTATATPACCAAGCTTTGGAGCTTA 1139

DB 1597 ACCTAATTTGGGTGGAATGCTTAAAGGCTTATTTCTTCTTCAATGGGGAATCTTA 1656

QY 1140 CTGACTGTTTGAATCTGAATGAGCCAAATGATGATGAGAGCACTTATCTGATCATC 1199

DB 1657 ACAATTTGCTAGCTTGAATCTTAAATATAGCTTTCTGCTCTTATTTCTGAGAA 1716

QY 1200 TGAGCTCTTGCACAAATCTAAACAGCTTAAATGTTATGAGGAACAAGTTAGTGGCACTA 1259

DB 1717 TAGTTAACCAAGGCTCTTACTTACTGATTTGGGTGAGATGCTTAAATGGCTCTTA 1776

QY 1260 TACCCGAGCTTTCAAAGCTTGAAGATGATGACTTAACTTATCTGTCCAGCAACAATA 1319

DB 1777 TTCTCTCTTCAATGGGGAATCTGAAACATTTGTTATGTTGATCTTTTCAATATCAGC 1836

QY 1320 TCAAGGTCCAAATCCGGTTGAGCTATCTGTATCGTAACTTAAATGATGATCTTT 1379

DB 1837 TTCTGCTCTTATTTCTGAAAGAAATAGTTAAGCTTCTTACTGAACTATATTTGG 1896

QY 1380 CCAACAACAAGATTAATGGAATCATTTCTTCCCTTGGTGAATTTGAGCATCTTCTCA 1439

DB 1897 GTATTAATCTCTTAAATGCTCTATTTCTGCTTCAATGGGGAATCTGAACACTTGT 1956

QY 1440 AGATGAATCTGATGAAATCATATATCTGATGATTTCCAGGCACTTTGGAATCTTA 1499

DB 1957 TGTGATATCTTAAATTAACACTTTTGGCTCTATTTCTGAAAGAAATAGTTACTGTA 2016

QY 1500 GAGCATCATGGAATAGATCTTCAATATATATATCTTGGCCCAATTCGAAAGAGC 1559

DB 2017 GTTCTCTTACTGAATATTTTGGGTAATATCTTAAATGCTCTATTTCTGCTTCAAT 2076

QY 1560 TTAAACAATTAACAACATATTTTCTGAGACTGGAATAATTAACCTGACTG---TA 1616

DB 2077 TGGGAATCTTAACAACCTTGTAGGTTGATCTTTAAATATCAAGCTTTCTGGCTCTTA 2136

QY 1617 ATGTGCTTATTAAGCACTGCTCAATCTCACTGATTTGAATGATATCTCAATACAC 1676

DB 2137 TTCTCTCTTCAATTTGGCAATATGAGAAATCTGCAACTCTGTTTCAAGTAAAGATC 2196

QY 1677 TCGTAGTATATCCCT 1693

DB 2197 TCATTGGGGAATTCTT 2213

RESULT 12

US-09-228-986-5

Sequence 5, Application US/09228986

Patent No. 635198

GENERAL INFORMATION:

APPLICANT: Strabala, Timothy

APPLICANT: Nieuwenhuizen, Niels

TITLE OF INVENTION: Compositions isolated from Plant Cells

TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling

FILE REFERENCE: 11000/1020

CURRENT APPLICATION NUMBER: US/09/228,986

NUMBER OF SEQ ID NOS: 130

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 5

LENGTH: 3340

TYPE: DNA

ORGANISM: Pinus radiata

US-09-228-986-5

Query Match 5.5%; Score 173.2; DB 3; Length 3340;

Best Local Similarity 45.7%; Pred. No. 1.1e-44;

Matches 1015; Conservative 0; Mismatches 1133; Indels 72; Gaps 9;

OY 294 TTAATTGTCAGATTGGAATCTTGATGAGAGAAATCTACGCTATGAGATCTCAAGA 353  
 DB 477 TGACTCTCTCTTAACAACTCACGGGAAACATCCCCACAACATAGCTTCTCCCA 536  
 OY 354 GTCTCTTGTCATATGATCTGCGAGTAATGCTGTGTGGAACAATCTCGATGAGATTG 413  
 DB 537 ACCATAATATGATGCTCTGGGAAATTAACAATTTGACGGGAAACAATCCCGACTGTGG 596  
 OY 414 GTGACGTGTTCTTTGGCAAACTTAGACTTATCTTCATATGAATTAAGTGTGACATAC 473  
 DB 597 GAAACATATCTCTTTGACGACTTATCTTTGAGTCAAGGTAACTTCAGGGGAGTGTC 656  
 OY 474 CGTTTTCGATTGGAAGTGAAGCACTTGACGAGCTGATTTGGAAGATTAACCAATTGA 533  
 DB 657 CTTCGCAATTTGGGTAGGCTTAAGCCAGCTCATCGTTCTTGATCTGTTGGGAAACATCTCA 716  
 OY 534 TAGGACCGATCCCTTCAACCTTTCACAGATTCCAAACTGAAAATTTCTGACCTTGAC 593  
 DB 717 CGGGATGACATTCGCTCTGTGTTGCCAATGCAACAATCTTGAACATATGATATAGGTG 776  
 OY 594 AGAATTAACCTAGTGTGAGATACCAAGACTTATTTACTGGAATGAAGTTCTTCA----- 648  
 DB 777 ATTAACCAATTAAGTTGGCAATTCGCTCGATTTGTGTACCAAGAAAGACCAACCAAGTTAA 836  
 OY 649 -GTATCTGGGTTGCGAGGAAACAATTAGTCGGTAACTTTCTCCAGATTTGTGCAAC 707  
 DB 837 TGTATCTCGTCTGGGTCTTAATCAGCTAATGAGCCAGCTTCTTCAATCCCTTCAATT 896  
 OY 708 TGAATGATCTTTGGTATTTTGAAGTAAGAAACAAGTTGACTGTGATATACCTGAGA 767  
 DB 897 GTACCAAGTTACAAAGATTTGCTTACATATAACCAAGCTCAGCGGAATGTGCTATAG 956  
 OY 768 CGATAGGAATTCGACTGCTTCCAGGTTTGGACTTTGTCTCAATCAGCTAATCTGATG 827  
 DB 957 AGTGGGTAAATTTGACACATCTCCAGCGGCTTTCTTTGGCGGAAATTAATTTATTAAGC 1016  
 OY 828 AGATCCCTTT---TGACATCGGCTTCTCGAGTTGCAAC-----AT 866  
 DB 1017 GCACACCATGAGATGCCCATTTCTTATCTGCTTATGTAATCTGTTGATCTCAATATG 1076  
 OY 867 TATCATTTGCAAGGCAATCACTCTGCGGAAGATTCATCAATGATATG---TCTCATGC 923  
 DB 1077 TTAGCTTATCTGAGAAATTAATCTTCACTGGGCAATTTGCCGTTTCTATATAGGCACTCTCCA 1136  
 OY 924 AAGCCTTTCGACTTATGATCTAAGTGGCACTTTGTGAGTGAATCTATTTCTCCGATTC 983  
 DB 1137 AAAAATCTTACCAATTTAGACTTGGGTAGCAACGAATTTAGCTGAGAAATTAATCTCCGGCTA 1196  
 OY 984 TCGGAATCTTACTTTCAACGAGAAATTTGATTTGCAAGTAAAGCTGACGTGTTCA 1043  
 DB 1197 TTGGAATTTTAAGTACCTTAACATCTCTTAATTTAGAGCTAAATTTTTCAGGGCTCA 1256  
 OY 1044 TTTCACCTGAGCTTGGAAACATGCTCAAACTCCATTAACCTGAACTCAATGATATATC 1103  
 DB 1257 TCCCATCTTCACTTATTAATGCTTCAAGAGTTGGAAGGTTATATGATTTCCAAATAT 1316  
 OY 1104 TCAAGGCTATATACCAAGAGCTTGGAGCTTACTGACTTTGATCTGAATGTG 1163  
 DB 1317 TACAGGAACATTTCCAAATGGAATTTGGGACCTAAAGAGCTTAGCTTCTTATATCTTT 1376  
 OY 1164 CCAACCAATGATCTGAAAGGCTATACCTGATCATCTGAGCTTTGCACAAAATCTAAAC 1223  
 DB 1377 CTGGAATTAATTTGCTGGAATAATCCCTGATTTTGTGGCAACCTTCAGCAATTAAGAT 1436  
 OY 1224 GCTTAATTTGATGGAACAAGTTATGTCACATAACCCGAGCAATTTCAAAAGCTAG 1283  
 DB 1437 ATTATATCTTAATCATTAACAGTTATCAAGAGATATAATGAATTTAGGAAATGTG 1496  
 OY 1284 AAGATATGACTTAATCTGCTCCAGCAACAATATCAAGGTCCAAATCCGGTTGAGC 1343  
 DB 1497 TGAATCTTAATCTGATGATCTATATCAACAAGGCTTAGTGGGCAATTAATCTCAAGAGC 1556

OY 1344 TATCTGTATCGGTAACTTAGATACA---TTGATCTTTTCAACAACAGATAAATGAA 1400  
 DB 1557 TCGAGAGCCTTGAAATTTTAGCTTCTATTTTCAACTGTCTAAACAAATTTATTAAGTGCC 1516  
 OY 1401 TCATTCCTTCTTCCCTTGTGATTTGGACATCTTCAAGATGAACCTGAGTGAATTC 1460  
 DB 1617 ATGTACCTTTAGAACATGGAAGATTTGATATGCTTCAACCCATAGATATATTTCCGCAATC 1676  
 OY 1461 ATATACTGTGTATGTTTCCAGGGGACTTTGGAAATCTAAGAACATCATGAAATGATC 1520  
 DB 1677 AATTAATCGGTACATTTCCAAAGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1736  
 OY 1521 TTTCAATATATGATATCTCTGCGCCATTCAGAAAGCTTAAACATTAACAAATATA 1580  
 DB 1737 TTTCTTCAATGACACTTGAAGGTCCATTCAGTGTCAATCAGTGAACCTTCAATGCTTC 1796  
 OY 1581 TTTTGTGAGACTGGAATAATATACCTGAC---TGTAAATGTTGTTCTATAGCAACT 1637  
 DB 1797 AAGACCTAGATCTCTCTCCAAACAATTTGTGGGGTGAATACCTATATCACTAGCAAAATC 1856  
 OY 1638 GTCTAGTCTCACTGATTTGAATGTATCTCATPAACAACCTCGAGTATATCCCTAAG 1597  
 DB 1857 TCACAATGCTCATCACTTGAATTTTCTTTTAAACAAGTTGTCAAGGGAAGTCCTAAG 1916  
 OY 1698 ACAATTAATCTTCAAGATTTTTCACAGACAGCTTCAATGSCAAATCCGTGCTTTGGGCTA 1757  
 DB 1917 AAGGATTTTCAAAAATATTTGGGCGCACAGATTTATGGGAAATCTTGCTTATGTGAC 1976  
 OY 1758 GTTGGCTAAATCAGCGTGTATGATTTCTGTGAACGTGACAGTGTCAATCTTAGAG 1817  
 DB 1977 CTGGGTAATCTACCAACCGGTGTATGTCTATTAACATAAAGTGTGTAATCTCAAA 2036  
 OY 1818 CAGCTATTTCTGGAATAAGCTATTTGGGGACTTGTATCTCTTCAATGCTTAAATAGAG 1877  
 DB 2037 GAGTTATCAATCTGTTGTGTTGTGTAAGCAATGTTGATTTGTGTTTCTTCAATAT 2096  
 OY 1878 CTGGCGAGCGCATATCTCTCTCTTCTTGTGATGATCACTTGCAAAACAGTAATCT 1937  
 DB 2097 TGTGAGAAAGAAAT-----TGTAGGAATAATTTCAAGAGACATTTGTCTATC 2145  
 OY 1938 ATTGCACCGAAGCTGTATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1997  
 DB 2146 ATTAATATGTTGGGCAATGCAAGAAATCTCTATGCA-----GAGC 2183  
 OY 1998 TCAATGGAATGACAGAGATCTAATGAGAAATATCAATTTGGGCGACGAGATCAAGCA 2057  
 DB 2184 TGTCTTTCACAATAATGAAATTTAGATGCAAACTTTGTAGGAATTTGATTTTGGAA 2243  
 OY 2058 CTGTATCAAAATGTGTTTGAAGAAATTTGAACCGGTTGCGATTAAGCGGCTTTACTCTC 2117  
 DB 2244 AAGTGTACAAAGGATTTTGAATGATGCACAATGTTGTCTGATCAAGCTTCTCAATCTAC 2303  
 OY 2118 ACAACCAAGCTCAATGAACAGTTTGAACAGAACTGAGATGCTAATGATGATCAAGC 2177  
 DB 2304 AAAATGAAGGGGCTCAAAAGATTTTGAATGAAATGCAAAAGTTTGGTAGAGTTAGAG 2263  
 OY 2178 ACAGAAATCTTGTAGCTTCAAGCTTATTTCCCTCTCTCACTTTGGGAGTCTTGTCT 2237  
 DB 2364 ACCGGAATTTGATTCGGGTCAATTAATCTTCAATGATCTCCAAATCAAGCTTTGATAT 2423  
 OY 2238 ATGACTATTTGGAATAATGTTAGGCT---CTGGGATCTTCTTCAATGCGCTTACGAAGAAA 2294  
 DB 2424 TTTCATTAATGCCAAGAGAGCTTGAAGAAAGTGTATATCTCCATGATGAGAACAA 2483  
 OY 2295 AGACTTTGATTGGGACACAGCGCTTAAGATGATATGATGATGATGATGATGATGATGATGAT 2354  
 DB 2484 GTTGTGTAATTTGATTTCAAGGTGAAATATAGCAATATATATGCGCCAAAGGATGATCAT 2543  
 OY 2355 ATCTACACATGATCTATGATCAAGATCATTTCAAGACGATGATGATGATGATGATGATGATGAT 2414  
 DB 2544 ATCTCATATATATGCTTTGTGCAAGTATTTGATTTGATTTGAAACCAAAATGTGT 2603  
 OY 2415 TCTTGAACAACAACCTTAGAGGCTCGTTTGAACAGATTTTGAATTAAGGAAAGCTTGTGTG 2474

Db 2604 TGTGTGGTGAAGATATGACTGCATATTTATAGACTTTGGCATTTGCTACTATATAGTTTGG 2663

RESULT 13

US-10-101-464A-5

Sequence 5, Application US/10101464A

Patent No. 6768041

GENERAL INFORMATION:

APPLICANT: Strabala, Timothy

APPLICANT: Nieuwenhuizen, Nicolaas

APPLICANT: Higgins, Colleen M.

TITLE OF INVENTION: Compositions Isolated from Plant Cells

TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling

FILE REFERENCE: 11000.102002

CURRENT APPLICATION NUMBER: US/101/101.464A

CURRENT FILING DATE: 2002-03-18

PRIOR APPLICATION NUMBER: 09/704.302

PRIOR FILING DATE: 2000-11-01

PRIOR APPLICATION NUMBER: 09/228.986

PRIOR FILING DATE: 1999-01-12

PRIOR APPLICATION NUMBER: 60/162.866

PRIOR FILING DATE: 1999-11-01

PRIOR APPLICATION NUMBER: PCT/US00/00724

PRIOR FILING DATE: 2000-01-11

NUMBER OF SEQ ID NOS: 989

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5

LENGTH: 3340

TYPE: DNA

ORGANISM: Pinus radiata

US-10-101-464A-5

Query Match 5.5%; Score 173.2; DB 3; Length 3340;

Best Local Similarity 45.7%; Pred. No. 1.1e-44;

Matches 1015; Conservative 0; Mismatches 1133; Indels 72; Gaps 9;

Db 294 TTAATTTGTCAGATTTGAATCTTGATGAGAGAAATCTCACCTGCTATTTGAGATCTCAGA 353

477 TGACTCTCTCTTTAACAACCTCAGGGAAACATTCGCCACAACATGCTTCTCCCA 536

354 GTCTCTTTCATATGATCTGCGAGTAAATGCTTGTCTGACAAATCCCTGATGAGATTG 413

537 ACCTAATATGATGCTCTTGGGAATTAACATTTGACGGGAACATCCGAGCTGCTTG 596

414 GTGACTGTTCTTCTTGGCAAACTTACACTTATCTTCATGAAATTAAGTGAGACTAC 473

597 GAAACATATCTCTTGGCAGTACTTATCTTGAAGTCAAGGTAACCTTCAGGGCAGTCTC 656

474 CGTTTTCGATTTGGAAGTTGAAGCACTTGAGCAGCTGATTTGAGAGATTAACCAATTGA 533

657 CTTCGAAATGGGGTAGGCTAAGCAGCTCATCGTCTTGATCTGTTGGGAACATCTCA 716

534 TAGAGCCGATCCCTTCAACACTTTCACAGATTTCCAAACCTGAAATTTGAGCTTGGCAC 593

717 CGGAGATGATCCGCTCTTCTTGTCCAACTGCAACCAATCTTGAATTTGGAATTAAGTG 776

594 AGAATAACACAGTGGGAGATACCAAGACTTATTTACTGGAATGAAGTTCTTCA----- 648

777 ATTAACCAATTAAGTTGGCCACATTCCTGCAATTTGTTACCAAGAACACACCCAGTTAA 836

649 -GTATCTTGGGTTCCGAGAAACAATTTAGTGGTAAATTTCTCCAGATTTGTCTCAAC 707

837 TGATCTCCGCTCGGGGTGCTAATCAGCTAAGTGCAAGCTTCTTCAATTCCTCTCAATT 896

708 TGACTGCTCTTTGGTATTTTGGAGTAAGAAACAACAGTTGACTGGTATGATATCTGAGA 767

897 GTACCAAGTTACAAAGAGATTCCTTACATATAACAGCTCAGGGGAATGAGTGAGTG 956

768 CGATAGGAATTTGACATGCTCCAGGTTTGGACTTGTCTCAATCAGTAACTGAGTG 827

957 AGTTGGTAAATGACATCTCCAGCGGCTTTTCTTGGGGGAATTAATCTTAATTAAGCG 1016

Qy 828 AGATCCCTT-----TGACATCGGCTTCTGCAAGTTGCAAC-----AT 866

1017 GCAACACATGAGATGCCCATTTCTACTGCTCTTGTAGTACATGCTGATCAATATAG 1076

867 TATCATTTGCAAGCATTCACACTCTTGGGAAGTTCCATCAGATTTGG----TCTCATGC 923

1077 TAGACTTATCTGGAATTAACCTTCACAGGCAATTTGCCGTTTCTATAGGCACTCTCCA 1136

924 AAGCCCTTGACGCTTGAATCTAAGTGGCACTTGTGAGATGATCTATTCCTCCGATTC 983

1137 AAAAATCTTACCTTTTACCTTGGTGGTACCAAGCAATTTAGTGAAGAAATATCCTCCGCTA 1196

984 TCGGAATCTTACTTTCACCGAATAATGTTGATTTGACAGTAACAAGCTGACTGTTCAA 1043

1197 TTGGAATTTAAGTACCTTAATCTTCTTAATTTAGAGTAATTTTATACAGGGTCAA 1256

1044 TTCCACTGAGCTTGGAAACATGTCAAAATCTCATTAACCTGGAACCTCATGATATATC 1103

1257 TCCCATCTTCACTTATTTATGCTTCAGAAAGTTGAGGTTATATATGATTCCAATTAAT 1316

1104 TCAGGGTCAATATACCAAGCAGCTTGGGAAGCTTACTGACTGTTGATCTGATATGAG 1163

1317 TACAGGAAACATTCATGGAATTTGGGAGCTTAAAGACTTAAAGTCTTATATCTTT 1376

1164 CCAACATGATCTGGAAGGACTATACCTGATCATCTGAGCTCTTGCACAAATCTTAAAC 1223

1377 CTGGAATATATTTGTCTGGAATAATCCCTGATTTTGTGGCAACCTCCAGCAATTAAGAT 1436

1224 GCTTAATGTTCAATGGGAACATTTAGTGGCATATACCCGAGATTTCAAAAGCTAG 1283

1437 ATTTATATCTTATATCAATACAGATTTACAGAGATATTAATGCAATTTTAGGAAATG 1496

1284 AAGATATGACTTACTTAACTCTGTCAGCAACAATATCAAGGTTCCATCCCGTTGAGC 1343

1497 TGAATCTTACTGCTATGATCTATCATACACAGCTTATGGGCAATATCCTCAAGAGC 1556

1344 TATCTGATCGGTAACCTTATGATACA--TTGATCTTTTCAACAAACAGATTAATGAA 1400

1557 TCGCAGGCTTGCATAATTTAGCCTTCTATTTCAACTTGTCAAACTTATTAATTAAGTG 1616

1401 TCAATCTCTTCTTCTTGGTGGATTTGGAGCATTTCTCAAGATGAAGCTTGAAGTGAAT 1460

1617 ATGTACTTATTAAGATGGAAGGATTTGATGCTTCAAGCCATATATTTCCGCAATC 1676

1461 ATATTAATGATGATTTCCAGGCGACTTGGAAATCTTAAGACATCATGGAATATGATC 1520

1677 AAATTAATGCTATCTTCAAGATGCTTGGAAAGCTGGAAGATGATATCTGATATC 1736

1521 TTTCAATTAATGATATCTGCGCCAAATTCAGAAAGCTTAAACAATTAACAGACATTA 1580

1737 TTTCTTAATGATGCACTTGAAGGTCCAATTCAGGTGCAATCAGTGAACCTTAAAGTCT 1796

1581 TTTTGTGAGACTGGAATAATTAACCTGAC---TGGTAATGTTGATCTTAAGCCAACT 1637

1797 AAGACCTAATCTCTCTCCCAACAATTTGCGGTGAATTAATTAATCACTGACCAATC 1856

1638 GTCTAGCTCACTGATTAATGATATCTCAATAACAACCTCGTAGGTGATATCCCTAAG 1697

1857 TCAATATGCTCACTCACTTGAATTTTCTTTTAAACAAGTTGTCAGGGGAAGTCCCTAAG 1916

1698 ACAATAATCTTCAAGATTTTCAACAGACAGCTTCAATGGCAATCTCGGTCTTTGGGTA 1757

1917 AAGAGATTTTCAAAAATTAATGGGCCCAAGCAATTTATGGAATAATCTTGTATGTCAG 1976

1758 GTTGGCTAAATCAAGGCTGATGATCTCGTGAACCTGAACGAGTGAATCTTATGAG 1817

1977 CTGGGTAATCTTACACCGGCTGATGCTATTAACATTAATAAGTTTGAATCTCAAAA 2036

1818 CAGCTATTTTGGAAATGATTAATGGGGGACTTGTGATCTCTTCATGCTTATATAGCAG 1877

2037 GAGTTATCATACAGGTTGTTGTGTAGCAATTTGTATTTGTTGTTCTTGAATAT 2096

1878 CTGCGAGCCGATTAATCTCTCTCTTTTCTTGTATGATCATCTTGAACAAACAGTAATCT 1937



Db 2097 TGTGAGAAAGAT-----TGTAGAGAAATATTCAGAGAGACATGTGTCATC 2145  
Qy 1938 ATTGACACCGAGCTGTCATCTTCATATGAAACATGCACTCCACGTTTACGAGATA 1997  
Db 2146 ATTAAATGTGGGGCTGAGAAATCTCCATGCA-----GAGC 2183  
Qy 1998 TCATGAAATGACAGAAATCTAAGTAGAAGATATCATTTGGGACGAGCATCAAGCA 2057  
Db 2184 TCGTCAATGCAACAAATGAAATTTAGTATGCAAACTGTTAGAAATTTGGATTTGGAA 2243  
Qy 2058 CTGTATACAAATGTTTGAAGAAATTTGAACCGGTTGCAATTAACCGGCTTTACTCTC 2117  
Db 2244 AAGTGACAAAGGATTTTGAATGATGCGACAAATGGTGTGTCAGAGCTTCTCAATCTAC 2203  
Qy 2118 ACACCCACAGTAAATGAAACAGTTTGAACAGATCTCGAGATGCTAAGTACATCAAGC 2177  
Db 2304 AAATGAAAGGGCTCAAAAGATTTGATGAGAAATGCAAAATTTGGGTAGAGTTAGAC 2363  
Qy 2178 ACAGAAATCTTGAGCTTCAAGCTTATTCCTCTCTCACTTGGGAGTCTTCTGTTCT 2237  
Db 2364 ACCGGAATTTGATTCGGGTATATCTTCTGATTCAGATCTCAAAATCAAGCTTTGATAT 2423  
Qy 2238 ATGACTAATTTGAAAAATGTAAGCT---CTGGATCTTCTTCATGCGCCCTACAGAAATA 2294  
Db 2424 TTCATTAATGCAAAAGAGAGCTGAGAAAAGTGTTATATCCGATGATGAGAAACAA 2483  
Qy 2295 AGACTTGTATTTGGACACACCGCTTAAGTATGATATGTTGACACAGATTTAGCTT 2354  
Db 2484 GTTGTGTAATTTGATTCAAAGGTTGAAATGATATGCAATGATATGCGCCAAAGGATGACAT 2543  
Qy 2355 ATCTACCATGATGCTGATGCTCAAGATCATTCACAGAGACGTAAGTGTCCACATTC 2414  
Db 2544 ATCTCATATCTATCTTCTTGTGCAAGTATGATGATTTGAAACCAACAAATGTGT 2603  
Qy 2415 TCTTGACAAAGACTTGAAGGCTGCTTGAACAGATTTTGAATAGGAAAGCTGTGTG 2474  
Db 2604 TGTGGGTGAAGTATGATGATATTTAATACATTTGGCATTTGCTATGATATGTTTG 2663

RESULT 14  
US-09-180-439-5  
; Sequence 5, Application US/09180439  
; Patent No. 6235532  
; GENERAL INFORMATION:  
; APPLICANT: Dixon, Mark S  
; APPLICANT: Hatziathanis, Kostas  
; APPLICANT: Jones, David A  
; APPLICANT: Jones, Jonathan DG  
; TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof  
; FILE REFERENCE: 620 - 53  
; CURRENT APPLICATION NUMBER: US/09/180,439  
; CURRENT FILING DATE: 1998-12-06  
; EARLIER APPLICATION NUMBER: PCT/GB97/01249  
; EARLIER FILING DATE: 1997-05-08  
; EARLIER APPLICATION NUMBER: GB 9609681.3  
; EARLIER FILING DATE: 1996-05-09  
; EARLIER APPLICATION NUMBER: GB 9619924.5  
; EARLIER FILING DATE: 1996-09-24  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 3541  
; TYPE: DNA  
; ORGANISM: Lycopersicon esculentum  
US-09-180-439-5

Query Match 5.4%; Score 170.2; DB 3; Length 3541;

Best Local Similarity 48.0%; Pred. No. 1,1e-43;

Matches 518; Conservative 0; Mismatches 558; Indels 3; Gaps 1;

Qy 546 CTTCAACACTTTCACAGATTCACAACTGAAATTTCTGACCTTGGACAGAAATTAATCA 605

Db 865 CTTTCATTTTCATCCCTCCCTTTTCTCGAAGATCTGATCTTAGCAACAAATATCT 924  
Qy 606 GTGGTAGATACCAACACTTATTACTGATGAATGATTTCTTGATATCTTGGTTGGAG 665  
Db 925 CTGGTACCAATTCACCTGAGATTGGTAACTCAAAATCTGTCTATCTTGACCTTGAACA 984  
Qy 666 GAAACAACTTATGCGGTAACTTCTCCAGATTTGTGTCAACTGACGTGGCTTTGGTATT 725  
Db 985 CCAATGATTTTACGAAACAAATTCACCAAAATGCGTTTCACTAGCCAACTTCAGATCA 1044  
Qy 726 TTGACGTAAAGAAACAAACAGTTTGACTGTAGTATATCTGAGAGATGAGAAATTTGCACTG 785  
Db 1045 TCCGATATTTAAACAATTAATTAATGCTTATATCTGTAAGAAATATAGTTACTTAAGT 1104  
Qy 786 CCTTCAAGTTTGGACTTGTCTTACAAATCAGTATCTGTGTGATATCCCTTTTGAATCG 845  
Db 1105 CTCTTACTAAGCTATCTTGTGGTATCACTTCTTGTGTGTTCTATCTGCTTCAATGG 1164  
Qy 846 GCTTCCG---CAAGTTGCAACATTAATTCATTTGCAAGGCAATCACTCTGAGGAATTC 902  
Db 1165 GCAATATGACCAACTTGTCTTTTATTTCTTATGAAATACGCTTTCTGCTTATATTC 1224  
Qy 903 CATCAGTATGCTCTCATGCAAGCCCTTGACGCTTGAATCTAAGTGCACACTTGTGA 962  
Db 1225 CTGAAAGAAATAGTTACTAAGGCTCTTACTAAGCTATCTTGTGATATCAACTTCTTA 1284  
Qy 963 GTGGATCTATCTCTCCGATTTCCGAAATCTTACTTTCACCGAAATTTGATTTGACA 1022  
Db 1285 GTGGTTCACTCTCTGTTTCAATGGGAAATCTGAAACACTTGTCTTTTGTATCTTAA 1344  
Qy 1023 GTAAACAGCTGACTGTTTCACTTCCACTGAGCTTGAACATATGCAAACTTCATTAAC 1082  
Db 1345 ATATATAGCTTCTGCTTATTTCTGAAAGAAATAGTTATCTTAAGGCTCTTACTTAAC 1404  
Qy 1083 TGGAACTCATATATATCATCTCACCGGTATATMACACAGAGCTTGGAAAGCTTACTG 1142  
Db 1405 TAGATTTGAAAGAAATGCTTAAATGCTATATCTGCTTCAATTTGGGAAATCTGAACA 1464  
Qy 1143 ACTTGTATATCTGAATGTGGCCAAATGATCTGGAAGAGCTTATCTGATCATCTGA 1202  
Db 1465 ACTTGTATGTTGATCTTCTTCAATTAACACTTCTGCTTATCTTCAAGAAATAG 1524  
Qy 1203 GCTTTCGCAAAATCTAAACAGCTTAAATGTTCAATGGAACAAAGTTAGGCACTATAC 1262  
Db 1525 GTTACTTGAGTTCTCTTACTAATCTATATTTGGTATATCTCTTATATGACTTATTC 1584  
Qy 1263 CCGAGCAATTTCAAAAGCTAGAAAGTATGACTTACCTTATCTGTCCAGCAACATATCA 1322  
Db 1585 CTGCTTCAATTCGGAATATGAGAAATCTGCAAGCTGTCTTCAATGATTAACAACTCA 1644  
Qy 1323 AAGTTCATTCGGGTGAGCTATCTGTAATGCTTGAATCTTGAATCTTGTTC 1382  
Db 1645 TTGGGAAATTCCTTCAATTTGTGTCAATTTAATCACTAGAACTGTGTATATCCGA 1704  
Qy 1383 ACAACAAATTAATGGAATCATTCCTTCTTCCCTTGGGATTTGAGACATCTTCAAGA 1442  
Db 1705 GAAACAAATTTGAAGGAAAGTTCCGCAATGTTGGGTATATCACTGACCTTTGCTTT 1764  
Qy 1443 TGAATCTGAGAAATCATATATATCTGTATGTTCCAGGCACTTTGGAATCTTAAGA 1502  
Db 1765 TGTCAATGTCATTAATATGTTTCAATGAGAGCTCCCTTCAATTTTCAATTTAAT 1824  
Qy 1503 GCATCATGGAATATGATCTTTCAAAATATGATATCTTGGCCCAATTTCCAGAGACTTA 1562  
Db 1825 CACTAATAATCTTGAATTTTGGCAGAAACAACTGAGGAGCAATATACACATATGTTTG 1884  
Qy 1563 ACCAATTCAGAAACATTAATTTTGTGAGACTGGAATAATATATACCTGAGTGAATGTT 1621  
Db 1885 GCAATATTTAGTACCTCCAGGTTTGTGATATCAGAAATACAAACTTTTCTGGGACTCTT 1943

RESULT 15  
US-10-101-464A-837

```

; Sequence 837, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101.464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704.302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228.986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162.866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 837
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Pinus radiata
US-10-101-464A-837

```

Query Match 5.2%; Score 164.2; DB 3; Length 2691;

Best Local Similarity 48.1%; Pred. No. 8.3e-42;

Matches 497; Conservative 0; Mismatches 533; Indels 3; Gaps 1;

```

QY 679 CGGTACATTTCTCCAGATTGTGTCACAGCTGCTTGTGATTTGACGTAAGAA 738
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 465 CGGCTATATTCCAAAGAAATTGTTAATTGTAACGCTTCAACGATCGACCTTCCCA 524
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 739 CAACAGTTGACTGTGATGATTAACCTGAGACGATGAAATTGCACTGCTTCCAGTTT 798
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 525 TAATAGTTTACAGGGGATACCACTTCTATCGGCAACAGCGCTTGTGCAACGAT 584
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 799 GGACTGTGCTCAATCAGCTAACTGCTGAGATCCCTTTGACATGGGCTTCCG---CA 855
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 585 GAATCTTGAGAGAACCGATTGAGGGGTCTATCCGACGAAATTCGGCGCTGGTCCA 644
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 856 AGTGCACATTTATTCATTCGACGACATCACTCTGCGAAGATTCCATCAGTATGG 915
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 645 CTGGAATCTCTCAGTTGTACAGCATATCTGAGTGAAGCATCCCACTTCTCTCGC 704
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 916 TCTCATGCAAGCCCTTGCACTTTAGATCTAAGTGGCACTTGTGATGATCTATTC 975
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 705 CAACCTGCACTTCACTTATAAAATGAGCTGAGGACACAAATTTGATGCTCAATACC 764
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 976 TCCGATTTCTGGAAATCTTACTTCAACGAAATGTATTGCAAGTAACAAGCTGAC 1035
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 765 ATCAGAAATTCAGTCGCTTGTGTCAGTTGGAACACTTGTTCGATGACAAATAGTAA 824
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1036 TGGTTCAATTCACCTGAGCTTGGAACATGCAAAATCCATTACCTGGAACCTCAATGA 1095
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 825 TGGAGCATTTCCAGCTTCGATTAGTAACTCAGCTTCACTTCAATATTGGATATCAGCGA 884
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1096 TAATCAITCTCAGCGGTATATACCAACGAGCTTGGGAAGCTTAAGCTTGTGATCT 1155
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 885 CAACAGTTGAGTGTCCAAATACCATCAGATTCAGTCGCTGTCAGCTTGGAAATCACT 944
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1156 GAATGTGGCCCAATGATCTGGAAGGACCTATACCTGATCATCTGAGCTCTTGCAAAA 1215
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 945 CTACTTCACGACAAATAGTAAAGTGAAGACATCCCACTTTCTGTGCAACTGCACTTC 1004
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1216 TCTAAACAGCTTAATGTTGATGGAACAAGTTAGTGCACTAATCCCGAGCATTTCA 1275
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1005 GCTCTGCAATTTGGGGGCTAGCGGAAACAAATGAGTGTCAATCCCTTCGGTATGGG 1064
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1276 AAAGCTAAGAAAGTATGACTTAATCTGTCTCAGCAACAAATATCAAGGTCAATCCC 1335
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

DB 1065 TTGTATGAAAAACATATCATTTTATGATTTATCCAAACAATCTCTCACTGGCCATATCCC 1124
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1336 GGTGAGCTATCTCGATGCGTATGAGTAAGTAACTTTCACAAACAAGATTA 1395
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1125 TCCACCTATTTAAATTTGATCACTATTTTGGAGCTTAGCGATTAACAACCTTAG 1184
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1396 TGGATATCTTCTTCTCCCTTGGATTTGAGCATCTTCTGAGATGAAGTGAAGTAG 1455
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1185 AGGTAGCATTCGCCCATTTATTTACAAATAGTGAATGATGATCTCGACTTATCCAA 1244
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1456 AATCATATACGTGTGTAGTTCAGGCGACTTTGGAATCTAAGAACTCATGAAAT 1515
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1245 CAACAGTTAATGATCTCTCCGCGTAACATAGGTCATTAAGCAATCTCAATCTCT 1304
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1516 AGATCTTCAATATATGATATCTGAGCCCAATTCAGAAAGACTTAACCAATTAAGAA 1575
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1305 TGATTTATCAAAATTAACAATTTTCACTGATCTTCCACGTAACATAGTCAATTAAGCAA 1364
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1576 CATTAATTTGCTGAGACTGGAATAATAAAGCTGATGATGTTGTTCAATTAAGCAA 1635
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1365 TCTTTACTGCTGATCTATCAAGCAACAAATTCAGTGAATCTCTCCGCTTAGTAAAG 1424
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1636 CTGTCTCAGTCTCACTGTATGTAATGTATCTCAATTAACACTGTAGTATTCCTTA 1695
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1425 TCACTGGAATTAACAAGCTTATATCTATATATAATTAATTTGGAACATTAACCAA 1484
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1696 GAACAATTAACCTTC 1708
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1485 TAATATTAAGTTTC 1497
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Search completed: September 3, 2006, 18:19:03  
Job time : 413 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 5, 2006, 17:14:32 / Search time 1881 Seconds  
(without alignments)  
11772.388 Million cell updates/sec

Title: US-10-519-135-1  
Perfect score: 3176  
Sequence: 1 gttctctctcatgagact.....actctctataagttcttgc 3176

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues  
Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_8:\*

- 1: geneseqn180s:\*
- 2: geneseqn190s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002as:\*
- 7: geneseqn2002bs:\*
- 8: geneseqn2003as:\*
- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004as:\*
- 13: geneseqn2004bs:\*
- 14: geneseqn2005s:\*
- 15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3176	100.0	3176	12 ADI32613	Adi32613 Thale cre
2	3136.2	98.7	3176	2 AAT62124	Aat62124 Arabidops
3	3136.2	98.7	3176	14 AED28148	Aed28148 Arabidops
4	2930	92.3	2930	8 ADA68568	Ada68568 Arabidops
5	1486.6	46.8	2750	13 ADX30336	Adx30336 Plant ful
6	1161.8	36.6	3089	14 AED28154	Aed28154 Arabidops
7	1117.6	35.2	2901	12 ADI32621	Adi32621 Thale cre
8	1112.8	35.0	3100	14 AED28152	Aed28152 Arabidops
9	1102	34.7	9295	2 AAT62125	Aat62125 Arabidops
10	1074.6	33.8	2751	12 ADI32619	Adi32619 Thale cre
11	1050.8	33.1	2766	12 ADI32617	Adi32617 Sorghum t
12	1044.4	32.9	2796	8 ADA71018	Ada71018 Rice gene
13	1035.2	32.6	3000	12 ADI32615	Adi32615 Rice tran
14	1015.4	32.0	2533	13 ADX59740	Adx59740 Plant ful
15	995.8	31.4	1872	13 ADX27817	Adx27817 Plant ful
16	940.4	29.6	1859	13 ADX13059	Adx13059 Plant ful
17	915.4	28.8	2895	8 ADA71317	Ada71317 Rice gene
18	901.2	28.4	2315	12 ADI32656	Adi32656 Maize tra

19	758.6	23.9	2523	13 ADX60773	Adx60773 Plant ful
20	680	21.4	1798	13 ADX60599	Adx60599 Plant ful
21	625	19.7	650	6 ABO65951	Abog65951 Arabidops
22	552.4	17.4	1688	14 AEB67281	Aeb67281 Rice geno
23	543.4	17.1	1456	13 ADX35156	Adx35156 Plant ful
24	533.8	16.8	4356	3 AAA79736	Aa79736 Pinus rad
25	530.8	16.7	1273	12 ADI32633	Adi32633 Maize tra
26	515.6	16.2	522	10 ABR57642	Abx57642 Arabidops
27	489	15.4	501	10 ADP81647	Adp81647 Arabidops
28	488.6	15.4	1346	12 ADI32631	Adi32631 Bread whe
29	410.4	12.9	1416	13 ADX28952	Adx28952 Plant ful
30	371.2	11.7	1079	13 ADX37065	Adx37065 Plant ful
31	340.4	10.7	1121	13 ADX61629	Adx61629 Plant ful
32	339.6	10.7	584	13 ACR54994	Ac54994 Cotton an
33	306.8	9.7	683	12 ADI32648	Adi32648 Maize tra
34	306.8	9.7	683	12 ADI32655	Adi32655 Maize tra
35	299.2	9.4	636	12 ADI32623	Adi32623 Bread whe
36	275	8.7	6240	10 ADB84162	Adb84162 Gene exp
37	269.8	8.5	556	12 ADI32654	Adi32654 Maize tra
38	267.4	8.4	4686	8 ADA71282	Ada71282 Rice gene
39	265.8	8.4	558	12 ADI32652	Adi32652 Maize tra
40	263.8	8.3	549	12 ADI32628	Adi32628 Bread whe
41	260.4	8.2	719	12 ADI32630	Adi32630 Bread whe
42	248.4	7.8	3375	6 ABR212862	Ab212862 Arabidops
43	241.6	7.6	3330	8 ADA70802	Ada70802 Rice gene
44	241.6	7.6	3330	11 ACR26733	Ac26733 Rice abio
45	237.6	7.5	634	12 ADI32651	Adi32651 Maize tra

ALIGNMENTS

RESULT 1	AD132613	standard; DNA; 3176 BP.
ID	AD132613	
XX	AD132613;	
AC		
XX		
DT	22-APR-2004	(first entry)
XX		
DE	Thale cress transpiration efficiency-related ERECTA DNA.	
XX		
KM	plant; transpiration efficiency; ERECTA; breeding; genetic engineering;	
KW	thale cress; ds; gene; chromosome 2.	
XX		
OS	Arabidopsis thaliana.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	77..3007
FT		/tag= a
FT		/product= "thale cress transpiration efficiency-related ERECTA protein"
XX		
PN	W02004005555-A1.	
XX		
PD	15-JAN-2004.	
XX		
PF	02-JUL-2003; 2003WO-AU000854.	
XX		
PR	02-JUL-2002; 2002AU-00003339.	
XX		
PA	(AUSV ) UNIV AUSTRALIAN NAT.	
XX		
PI	Masle J, Farquhar GD, Gilmore SR,	
XX		
DR	WPI; 2004-091390/09.	
XX		
DX	P-PSDB; ADI32614.	
PT	Selecting plant having enhanced transpiration efficiency, useful for	
PT	producing plants with enhanced transcription efficiency comprising	
PT	selecting plant expressing a genetic marker linked to the ERECTA locus in	
XX	the genome of the plant.	

PS Claim 3; SEQ ID NO 1; 209pp; English.  
XX  
CC The invention relates to a novel method for selecting a plant having  
CC enhanced transpiration efficiency comprising detecting a genetic marker  
CC for transpiration efficiency, where the marker comprises a nucleotide  
CC sequence linked genetically to an ERBCTA locus in the genome of the plant  
CC and selecting a plant that comprises or expresses the genetic marker. The  
CC method of the invention may be useful for selecting a plant having  
CC enhanced transpiration efficiency. The isolated ERBCTA gene or allelic  
CC variant or protein-encoding region may be useful in the preparation of a  
CC genetic construct for modulating the transpiration efficiency of a plant.  
CC Furthermore, the ERBCTA genes may be useful for producing plants having  
CC enhanced transpiration efficiency by both traditional plant breeding and  
CC genetic engineering approaches. The current sequence is that of the chae  
CC cress ERBCTA DNA of the invention which is located on chromosome 2.  
XX  
SQ Sequence 3176 BP; 896 A; 660 C; 667 G; 953 T; 0 U; 0 Other:  
Query Match 100.0%; Score 3176; DB 12; Length 3176;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTTCTCTTCATGAGAGACTTGAAGCTTTAAAGTATATCTAATAAAGCAGTCGTTTGA 60  
DB 1 GTTCTCTTCATGAGAGACTTGAAGCTTTAAAGTATATCTAATAAAGCAGTCGTTTGA 60  
QY 61 AGACTGTGTGAGAAATGCTCTGTTAGAGATATGTTCTTGGGTTTCTCTCTG 120  
DB 61 AGACTGTGTGAGAAATGCTCTGTTAGAGATATGTTCTTGGGTTTCTCTCTG 120  
QY 121 CTGAGCTTAGTACTGCTGCTGAGAGAGAGCAAGTGTGAGATTAAGA 180  
DB 121 CTGAGCTTAGTACTGCTGCTGAGAGAGAGCAAGTGTGAGATTAAGA 180  
QY 121 CTGAGCTTAGTACTGCTGCTGAGAGAGAGCAAGTGTGAGATTAAGA 180  
DB 121 CTGAGCTTAGTACTGCTGCTGAGAGAGAGCAAGTGTGAGATTAAGA 180  
QY 181 GTCAATTGAAGATGGAACAATGTTCTTATGACTGACAACTTCACTTTGGATTA 240  
DB 181 GTCAATTGAAGATGGAACAATGTTCTTATGACTGACAACTTCACTTTGGATTA 240  
QY 241 TTGTGTCTGAGAGAGTGTCTTGAAGAAATGTCACCTTCAATGTGTGCTTAAATT 300  
DB 241 TTGTGTCTGAGAGAGTGTCTTGAAGAAATGTCACCTTCAATGTGTGCTTAAATT 300  
QY 301 GTCAATTTGATCTGAGAGATTAATGCTTGTGACAAATCCCTGATGAGATTGGTACTG 420  
DB 301 GTCAATTTGATCTGAGAGATTAATGCTTGTGACAAATCCCTGATGAGATTGGTACTG 420  
QY 421 TTCTCTTTTGGAAACTTGAAGCTTATGCTTGAAGATTAAGTGTGACATACCGTTTC 480  
DB 421 TTCTCTTTTGGAAACTTGAAGCTTATGCTTGAAGATTAAGTGTGACATACCGTTTC 480  
QY 481 GATTTCGAAGTTGAAGCACTTGAAGAGCTGATTCTGAAGATTAACCAATGATGAGACC 540  
DB 481 GATTTCGAAGTTGAAGCACTTGAAGAGCTGATTCTGAAGATTAACCAATGATGAGACC 540  
QY 541 GATCCCTTCAACACTTTCAAGATTCGAACCTGAAATTTCTGACCTTGGACAAGATTA 600  
DB 541 GATCCCTTCAACACTTTCAAGATTCGAACCTGAAATTTCTGACCTTGGACAAGATTA 600  
QY 601 ACTAGTGTGAGATTAACCAAGATTAATTAATGAGATTAAGTGTGACATGATGAGTT 660  
DB 601 ACTAGTGTGAGATTAACCAAGATTAATTAATGAGATTAAGTGTGACATGATGAGTT 660  
QY 661 GCGAGAAACAACCTTGAAGCTTGAAGATTTCTCAAGATTTGTGCACTGAGCTGTTG 720  
DB 661 GCGAGAAACAACCTTGAAGCTTGAAGATTTCTCAAGATTTGTGCACTGAGCTGTTG 720  
QY 721 GTATTTTGAAGTAAAGAAACAAGTTGACTGTGATACCTGAGAGATGAGAAATTG 780  
DB 721 GTATTTTGAAGTAAAGAAACAAGTTGACTGTGATACCTGAGAGATGAGAAATTG 780

QY 781 CACTGCTTCCAGGTTTGTGACTTGTCTTAACAATCAGCTAATCTGTGAGATCCCTTTTGA 840  
DB 781 CACTGCTTCCAGGTTTGTGACTTGTCTTAACAATCAGCTAATCTGTGAGATCCCTTTTGA 840  
QY 841 CATGCGCTTCTGCAAGTTCGCAACATTTATATTGCAAGGCAATCACTCTCTGGAAAGAT 900  
DB 841 CATGCGCTTCTGCAAGTTCGCAACATTTATATTGCAAGGCAATCACTCTCTGGAAAGAT 900  
QY 901 TCCATCAGATATGATGATCTGCAAGGCTTGGAGCTTATGATCTAAGTGGCAACTGTT 960  
DB 901 TCCATCAGATATGATGATCTGCAAGGCTTGGAGCTTATGATCTAAGTGGCAACTGTT 960  
QY 961 GAGTGAATCTATTCCTCCGATTCGGAATCTTACTTTTCAACGAGAAATTTGATTTGCA 1020  
DB 961 GAGTGAATCTATTCCTCCGATTCGGAATCTTACTTTTCAACGAGAAATTTGATTTGCA 1020  
QY 1021 CAGTAAACAGCTGACTGTTCAATTCACCTGAGCTTGGAAACATGCAAACTCCATTA 1080  
DB 1021 CAGTAAACAGCTGACTGTTCAATTCACCTGAGCTTGGAAACATGCAAACTCCATTA 1080  
QY 1081 CTTGGAACCTGAATGATATCATCTCAAGGCTCATATACCAAGAGCTTGGAGAGCTTAC 1140  
DB 1081 CTTGGAACCTGAATGATATCATCTCAAGGCTCATATACCAAGAGCTTGGAGAGCTTAC 1140  
QY 1141 TGACTTGTGATCTGATGATGTCGCAACAATGATCTGGAAGACCTATACCTGATCATCT 1200  
DB 1141 TGACTTGTGATGATGATGTCGCAACAATGATCTGGAAGACCTATACCTGATCATCT 1200  
QY 1201 GAGCTCTTGCAACAATTTAAACAGCTTTAAATGTTTCATGGAACAAGTTTGTGGCACTAT 1260  
DB 1201 GAGCTCTTGCAACAATTTAAACAGCTTTAAATGTTTCATGGAACAAGTTTGTGGCACTAT 1260  
QY 1261 ACCCGAGCAATTCMAAAGCTAGAAAGTATGACTTACCTTAATCTGTCGAGCAACAATAT 1320  
DB 1261 ACCCGAGCAATTCMAAAGCTAGAAAGTATGACTTACCTTAATCTGTCGAGCAACAATAT 1320  
QY 1321 CAAAGGTCCAATCCCGTTGAGCTATCTCGATTCGGTAACTTGAATCATTTGATCTTTG 1380  
DB 1321 CAAAGGTCCAATCCCGTTGAGCTATCTCGATTCGGTAACTTGAATCATTTGATCTTTG 1380  
QY 1381 CAACACAAGATTAATGATTAATCTCTTCTTCTGTTGGATTTGGAGCATCTTCTCA 1440  
DB 1381 CAACACAAGATTAATGATTAATCTCTTCTTCTGTTGGATTTGGAGCATCTTCTCA 1440  
QY 1441 GATGAATCTGAGTAAATGATTAATCTGAGTATGATCTGAGGAGACTTGGAAATCTAAG 1500  
DB 1441 GATGAATCTGAGTAAATGATTAATCTGAGTATGATCTGAGGAGACTTGGAAATCTAAG 1500  
QY 1501 AAGCATCATGAAATATGATCTTCAAAATATGATATCTGAGCCCAATTCAGAAAGACT 1560  
DB 1501 AAGCATCATGAAATATGATCTTCAAAATATGATATCTGAGCCCAATTCAGAAAGACT 1560  
QY 1561 TAAACCAATTAACAAGCAATATTTTGTGAGACTGGAAGAAATTAACCTGATGATATGT 1620  
DB 1561 TAAACCAATTAACAAGCAATATTTTGTGAGACTGGAAGAAATTAACCTGATGATATGT 1620  
QY 1621 TGGTTCATTTAGCCCAAGCTGCTCAGCTCTCACTGATTAAGTATCTATTAACAACCTG 1680  
DB 1621 TGGTTCATTTAGCCCAAGCTGCTCAGCTCTCACTGATTAAGTATCTATTAACAACCTG 1680  
QY 1681 AAGTGAATATCCCTTAAGAAACAATATCTTCAAGATTTTCAACGAGACACTTCAATTGCA 1740  
DB 1681 AAGTGAATATCCCTTAAGAAACAATATCTTCAAGATTTTCAACGAGACACTTCAATTGCA 1740  
QY 1741 TCTGTGTCTTGGCGGATGTTGGCTAAATCTACCGGTGATGATTTCTGTGAACTGTACG 1800  
DB 1741 TCTGTGTCTTGGCGGATGTTGGCTAAATCTACCGGTGATGATTTCTGTGAACTGTACG 1800  
QY 1801 AGTGTCAATCTCTAGACAGATATCTTGGAAATGATATGAGGAGACTTGTGATCTTCT 1860  
DB 1801 AGTGTCAATCTCTAGACAGATATCTTGGAAATGATATGAGGAGACTTGTGATCTTCT 1860

```

OY 1861 CATGCTCTTAATAGCAGCTTGCAGACCGCATATTCCTCTCTCTTCTTGATGATCACT 1920
DB 1861 CATGCTCTTAATAGCAGCTTGCAGACCGCATATTCCTCTCTCTTCTTGATGATCACT 1920
OY 1921 TGAACAAACGATACCTATTTCGACACCGAAGCTGCTATCTTCATATGAACTGGCACT 1980
DB 1921 TGAACAAACGATACCTATTTCGACACCGAAGCTGCTATCTTCATATGAACTGGCACT 1980
OY 1981 CCAAGTTTACGAGGATATCATGGAATGACAGAAATCTAAGTGAGAAATATCATTTG 2040
DB 1981 CCAAGTTTACGAGGATATCATGGAATGACAGAAATCTAAGTGAGAAATATCATTTG 2040
OY 2041 GCAAGGAGCATCAAGACCTGATATCAAAATGTTTGAAGATTTGAAACCGGTGGCAT 2100
DB 2041 GCAAGGAGCATCAAGACCTGATATCAAAATGTTTGAAGATTTGAAACCGGTGGCAT 2100
OY 2101 TAAAGCGCTTACTCTCACAACCCACAGTCATGAAACAGTTTGAACAGAACTCGAGAT 2160
DB 2101 TAAAGCGCTTACTCTCACAACCCACAGTCATGAAACAGTTTGAACAGAACTCGAGAT 2160
OY 2161 GCTAAGTAGATCAACGACGAAATCTGTGAGCCTTAAAGCTTATTCCTCTCTCACT 2220
DB 2161 GCTAAGTAGATCAACGACGAAATCTGTGAGCCTTAAAGCTTATTCCTCTCTCACT 2220
OY 2221 GGGGAGCTCTTCTGTCTATGACTATTGGAAGATGAGAGCTCTGGGATCTTTCATGG 2280
DB 2221 GGGGAGCTCTTCTGTCTATGACTATTGGAAGATGAGAGCTCTGGGATCTTTCATGG 2280
OY 2281 CCTACGAGAGAAAGACTCTTGAATGGGACACACGCGCTTAAATGACATATGATGTCAGC 2340
DB 2281 CCTACGAGAGAAAGACTCTTGAATGGGACACACGCGCTTAAATGACATATGATGTCAGC 2340
OY 2341 ACAAGGTTTAGCTTATCTACACATGACGTGATGCAAGGATCATTCACAGACGAGAA 2400
DB 2341 ACAAGGTTTAGCTTATCTACACATGACGTGATGCAAGGATCATTCACAGACGAGAA 2400
OY 2401 GTCTGCCAATCTCTGTGACAAAGACTTGAAGGCTCGTTTACAGATTTTGAATAGC 2460
DB 2401 GTCTGCCAATCTCTGTGACAAAGACTTGAAGGCTCGTTTACAGATTTTGAATAGC 2460
OY 2461 GAAAAGCTTGTGTCTCAAGTCAACATCTTCACTTACGTATGGGACGATAGGTTA 2520
DB 2461 GAAAAGCTTGTGTCTCAAGTCAACATCTTCACTTACGTATGGGACGATAGGTTA 2520
OY 2521 CATAGACCCCGAGTATGCTCGCACTTCAAGGCTCACTGAGAAATCCGATCTCAAGTTA 2580
DB 2521 CATAGACCCCGAGTATGCTCGCACTTCAAGGCTCACTGAGAAATCCGATCTCAAGTTA 2580
OY 2581 TGGATATGCTCTTCTGAGTTGTTAAACCGAAGAAAGCGTTGATGACGATCCAACT 2640
DB 2581 TGGATATGCTCTTCTGAGTTGTTAAACCGAAGAAAGCGTTGATGACGATCCAACT 2640
OY 2641 CCACCATCTGATATGTCAAAGACGGGGAACATGAAATGATGAAATGCAATCCAGA 2700
DB 2641 CCACCATCTGATATGTCAAAGACGGGGAACATGAAATGATGAAATGCAATCCAGA 2700
OY 2701 CATCATATGACCTGTAAGAAATCTCGTGTGGAAGAAAGTTTCCAAATGCACTCTT 2760
DB 2701 CATCATATGACCTGTAAGAAATCTCGTGTGGAAGAAAGTTTCCAAATGCACTCTT 2760
OY 2761 ATGCAACAAAGACACCGAATGATGACCCACATGACACGAGTGACTGTTCTGG 2820
DB 2761 ATGCAACAAAGACACCGAATGATGACCCACATGACACGAGTGACTGTTCTGG 2820
OY 2821 CAGTTTATATGCTATCGGAACACCTGCTGCACTGACAGCTCAGCGAGCTGGCTG 2880
DB 2821 CAGTTTATATGCTATCGGAACACCTGCTGCACTGACAGCTCAGCGAGCTGGCTG 2880
OY 2881 TTGCTGCTACGTGAGATGATGCAAAATCTCAGACCTCCCATTTCTGTAATGCTCTT 2940
DB 2881 TTGCTGCTACGTGAGATGATGCAAAATCTCAGACCTCCCATTTCTGTAATGCTCTT 2940
OY 2941 CATGAGTCTTCTGATGCTCAACTGTTTCTTGGTTGACAAAGTTATTTCTCAGAACAG 3000

```

```

DB 2941 CATGAGTCTTGTGATGCTCAACTGTTCTTCCGTTTGGACAAAGTATTTCTCAGAACAG 3000
OY 3001 TGAAGTATTTTGTGTAGAGAGAGAACTTTTAAAGGATATCTTTCGTTGCGCTTAAGCT 3060
DB 3001 TGAAGTATTTTGTGTAGAGAGAGAACTTTTAAAGGATATCTTTCGTTGCGCTTAAGCT 3060
OY 3061 GTTAAAAAATTAATGCTCATGTAAGTATTAATGACAGCTTATTAATTAAGACAAAG 3120
DB 3061 GTTAAAAAATTAATGCTCATGTAAGTATTAATGACAGCTTATTAATTAAGACAAAG 3120
OY 3121 TGTGTGTGTGAATATGCTCTTCAAGTGCACCTTAAGCTTCTTAAGTTCTTGGC 3176
DB 3121 TGTGTGTGTGAATATGCTCTTCAAGTGCACCTTAAGCTTCTTAAGTTCTTGGC 3176

RESULT 2
AAT62124
ID AAT62124 standard; cDNA to mRNA; 3176 BP.
XX
AC AAT62124;
XX
DT 10-JUN-1997 (first entry)
XX
DE Arabidopsis thaliana plant morphogenesis regulatory protein cDNA.
XX
KW plant; morphogenesis; regulation; short; stem; alteration; inflorescence;
XX extremeous; gene; expression; transformation; increase; control; form;
XX length; ds.
XX
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
FT CDS 51..2981
FT /tag= a
FT /note= "plant morphogenesis regulatory protein"
XX
PN JP09056382-A.
XX
PD 04-MAR-1997.
XX
PF 24-AUG-1995; 95JP-00216187.
XX
PR 24-AUG-1995; 95JP-00216187.
XX
PA (CHIK-) ZH CHIKYU KANKYO SANGYO GIJITSU KENKYU.
XX (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
XX WPI; 1997-206629/19.
XX DR P-PDSB; AAM13408.
XX
PT DNA encoding plant morphogenesis regulatory protein - useful to yield
XX plants with short stems or altered inflorescence.
XX
PS Claim 1; Page 6-10; 17pp; Japanese.
XX
CC The present sequence encodes an Arabidopsis thaliana plant morphogenesis
CC regulatory protein (MRP), which can be used to yield a plant with, e.g.
CC short stems or altered inflorescence. The MRP acts on a plant at a
CC specific site for a specific period, and can therefore be used to
CC regulate extraneous gene expression in a plant. The MRP's cDNA or genomic
CC DNA can be used to transform a plant to increase its MRP expression, and
CC therefore control the form (particularly stem length) of the plant
XX
SQ Sequence 3176 BP; 927 A; 654 C; 659 G; 936 T; 0 U; 0 Other:
XX
Query Match 98.7%; Score 3136.2; DB 2; Length 3176;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 318; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 27 CTTTAAAGTATATCTTAAAGACGAGCTGTTTAAAGCTGTGTGAGAAATGGCTCTGT 86
DB 1 CTTTAAAGTATATCTTAAAGACGAGCTGTTTAAAGCTGTGTGAGAAATGGCTCTGT 60

```

Oy	87	TTAGAGATATGTTCTTCTTGSGGTTCTCTTCTGCTGAAGCTTAACTAGCTACTGACATT	146
Db	61	TTAGAGATATGTTCTTCTTGSGGTTCTCTTCTGCTGAAGCTTAACTAGCTACTGACATT	120
Oy	147	CAGAGAGAGGAGCAACGTTGCTGAGAGATTAAAGACGATCAAAATGATGMAACATGTTTC	206
Db	121	CAGAGAGAGGAGCAACGTTGCTGAGAGATTAAAGAGTCATTAAGATGTGAACAATGTTTC	180
Oy	207	TTTATGACTGGAACAATTCACTTCGGAATTATTTGTCCTGAGAGGTGTCTTG	266
Db	181	TTTATGACTGGAACAATTCACTTCGGAATTATTTGTCCTGAGAGGTGTGTCTTG	240
Oy	267	AAAAATCACTTCATATGTGTGCTCTTAATTTGTCAATTTGAATCTTGATGAGAA	326
Db	241	AAAAATCACTTCATATGTGTGCTCTTAATTTGTCAATTTGAATCTTGATGAGAA	300
Oy	327	TCTCACTGCTATTGAGAGTCTCAAGAGCTCTTGTCAATTGATCTGCGAGGTAATCGCT	386
Db	301	TCTCACTGCTATTGAGAGTCTCAAGAGCTCTTGTCAATTGATCTGCGAGGTAATCGCT	360
Oy	387	TGTCGGAACAATCCCTGATGAGATGTGTGACGTGTCTTCTTGGAAAACTTGAATTAT	446
Db	361	TGTCGGAACAATCCCTGATGAGATGTGTGACGTGTCTTCTTGGAAAACTTGAATTAT	420
Oy	447	CCTTCAATGAATTAAGTGATGACATACCCTTTTGCATTTCCAAAGTTGAAGCAACTTGAAC	506
Db	421	CCTTCAATGAATTAAGTGATGACATACCCTTTTGCATTTCCAAAGTTGAAGCAACTTGAAC	480
Oy	507	AGCTGATTTCTGAAGATPAACCAATTTGATAGAGCCGATCCCTTCAACACTTTCACAGATTTC	566
Db	481	AGCTGATTTCTGAAGATPAACCAATTTGATAGAGCCGATCCCTTCAACACTTTCACAGATTTC	540
Oy	567	CAAACTGAAAAATTTGGAATTGGACAAGAAATPAACAGTGGTGAGATATCCACAGACTTA	626
Db	541	CAAACTGAAAAATTTGGAATTGGACAAGAAATPAACAGTGGTGAGATATCCACAGACTTA	600
Oy	627	TTTACTGGAATGAAGTTCTTCAGTATCTTGGGTTCGAGAGAAACAATTAGTCGCTATACA	686
Db	601	TTTACTGGAATGAAGTTCTTCAGTATCTTGGGTTCGAGAGAAACAATTAGTCGCTATACA	660
Oy	687	TTTTCACAGATTTGTGTCAACGTGACTGGCTTGTGGTATTTTGAACGTAAAGAAACAAGTT	746
Db	661	TTTTCACAGATTTGTGTCAACGTGACTGGCTTGTGGTATTTTGAACGTAAAGAAACAAGTT	720
Oy	747	TGACTGTAGTATATACCTGAGACGATAGAGAAATYGACATGCTCTTCAGGTTTTGACCTGT	806
Db	721	TGACTGTAGTATATACCTGAGACGATAGAGAAATYGACATGCTCTTCAGGTTTTGACCTGT	780
Oy	807	CCTAATATCAAGTATCTGTGAGATCCCTTTTGAATGSGCTCCCTGCAAGTTGGAACAT	866
Db	781	CCTAATATCAAGTATCTGTGAGATCCCTTTTGAATGSGCTCCCTGCAAGTTGGAACAT	840
Oy	867	TATCATTTCAAGGCAATCAACTCTCTGGGAGAGTTCCATCAGTGATTTGGTCTCATGCAAG	926
Db	841	TATCATTTCAAGGCAATCAACTCTCTGGGAGAGTTCCATCAGTGATTTGGTCTCATGCAAG	900
Oy	927	CCCTTGACGTCTTAGATCTAAGTGGCAACTTGTGATGATGTATCTTCCGCAATTCG	986
Db	901	CCCTTGACGTCTTAGATCTAAGTGGCAACTTGTGATGATGTATCTTCCGCAATTCG	960
Oy	987	GAAATCTTACTTTTCAACCGAGAAATTGTATTTGCAACAGTAAACAAGCTGACTGTTCAATTC	1044
Db	961	GAAATCTTACTTTTCAACCGAGAAATTGTATTTGCAACAGTAAACAAGCTGACTGTTCAATTC	1020
Oy	1047	CACCTGAGCTTGGAAACAATGTCAAAATCTCATTTACCTGGAATCTCAATGATATCATCTCA	1106
Db	1021	CACCTGAGCTTGGAAACAATGTCAAAATCTCATTTACCTGGAATCTCAATGATATCATCTCA	1080
Oy	1107	CGGGTCATATACCAACAAGCTTTGGGAAAGCTTACGATCTGTGTTGATCTGAATGTGGCCA	1166
Db	1081	CGGGTCATATACCAACAAGCTTTGGGAAAGCTTACGATCTGTGTTGATCTGAATGTGGCCA	1144

QY	1167	ACAAAGATCTGGANAGACCTTAATCCGTGATCATCTGAGCTCTTGCAACAAATCTTAAAGACT	1226
Db	1141	ACAAAGATCTGGANAGACCTTAATCCGTGATCATCTGAGCTCTTGCAACAAATCTTAAAGACT	1200
QY	1227	TAAATGTTCAATGGGAACAAGTTTAGTGGCACTAATCCCGAGCATTTCAAAGCTAGAAA	1286
Db	1201	TAAATGTTCAATGGGAACAAGTTTAGTGGCACTAATCCCGAGCATTTCAAAGCTAGAAA	1260
QY	1287	GTATGACTTAACCTTAATCTGTCCAGCAACAATATCAAAAGTCCAAATCCGGTTGACCTAT	1346
Db	1261	GTATGACTTAACCTTAATCTGTCCAGCAACAATATCAAAAGTCCAAATCCGGTTGACCTAT	1320
QY	1347	CTCGTATGGGTAACTTAAGTACATTGGATCTTTCCAAACAAGATTAATGGAAATCATTTG	1406
Db	1321	CTCGTATGGGTAACTTAAGTACATTGGATCTTTCCAAACAAGATTAATGGAAATCATTTG	1380
QY	1467	CTTCTCCCTGGTATTTGGAGCAATCTCTCAAGATGAATCTTAGTAAGAAATCATATAA	1466
Db	1381	CTTCTCCCTGGTATTTGGAGCAATCTTCTCAAGATGAATCTTAGTAAGAAATCATATAA	1440
QY	1467	CTGGTGTAGTTCCAGGCGACTTTGGAAATCTAAGAAAGCATGTGAATATAGATCTTTCAA	1526
Db	1441	CTGGTGTAGTTCCAGGCGACTTTGGAAATCTAAGAAAGCATGTGAATATAGATCTTTCAA	1500
QY	1527	ATAATGATATCTCTGGCCCAATTCAGAAAGACTTAAACCAATTAACGAACATATATTTGC	1586
Db	1501	ATAATGATATCTCTGGCCCAATTCAGAAAGACTTAAACCAATTAACGAACATATATTTGC	1560
QY	1587	TGAGACTGGAAAAATATAAAGCTGACGTGGTAAATGTTGGTTCATTAGGCAACGTGCTCAGTC	1646
Db	1561	TGAGACTGGAAAAATATAAAGCTGACGTGGTAAATGTTGGTTCATTAGGCAACGTGCTCAGTC	1620
QY	1647	TCACTGTATTTGAATGTATCTCTAAACAACCTGTAGTGTATATCCCTAAGAACAAATAACT	1706
Db	1621	TCACTGTATTTGAATGTATCTCTCTAAACAACCTGTAGTGTATATCCCTAAGAACAAATAACT	1680
QY	1707	TCTCAAGATTTTCAACAAGACCTTCATTGGCAATCTGTGCTTTTGCGGTAGTTGGCTAA	1766
Db	1681	TCTCAAGATTTTCAACAAGACCTTCATTGGCAATCTGTGCTTTTGCGGTAGTTGGCTAA	1740
QY	1767	ACTACCGGTGATGATTTCTGTGGAACCTGACGTACAGTGTCAATCTGTAGAGCACTATTTC	1826
Db	1741	ACTACCGGTGATGATTTCTGTGGAACCTGACGTGTCAATCTTGAAGCACTATTTC	1800
QY	1827	TTGGATATGATTTGGGGGACTTTGTGATCTTCTCAATGCTTTAATATAGACGTTGCGGAC	1886
Db	1801	TTGGATATGATTTGGGGGACTTTGTGATCTTCTCAATGCTTTAATATAGACGTTGCGGAC	1860
QY	1887	CGCATATATCTCTCTCTTTCTTTGATGATCATCTTGACAAACAGATTAATTTGACATC	1946
Db	1861	CGCATATATCTCTCTCTTTCTTTGATGATCATCTTGACAAACAGATTAATTTGACATC	1920
QY	1947	CGAAGCTGTATCTCTTCAATGAACAATGGCACTCAAGTTTAAACGAGATATCATAGAA	2006
Db	1921	CGAAGCTGTATCTCTTCAATGAACAATGGCACTCAAGTTTAAACGAGATATCATAGAA	1980
QY	2007	TGACAGAAATCTAAGTGAAGATATATCATTTGGGACCGAGCATCAAGCACTGTATACA	2066
Db	1981	TGACAGAAATCTAAGTGAAGATATATCATTTGGGACCGAGCATCAAGCACTGTATACA	2040
QY	2067	AATGTGTTTTGAAGATTTGTAACCGGTGGCATTAAGCGGCTTTAATCTCTACAAACCCAC	2126
Db	2041	AATGTGTTTTGAAGATTTGTAACCGGTGGCATTAAGCGGCTTTAATCTCTACAAACCCAC	2100
QY	2127	AGTCAATGAACAATTTGTAACAAGAACTCGAAGATGTAATGATCATCAAGCAAGAAATC	2186
Db	2101	AGTCAATGAACAAGTTTGAACAAGAACTCGAAGATGTAATGATCATCAAGCAAGAAATC	2160
QY	2187	TTGTAGAGCTCAAGACTTATTCCTCTCTCACTGGGGAGTCTTCTGTCTATAGACTAT	2246
Db	2161	TTGTAGAGCTCAAGACTTATTCCTCTCTCACTGGGGAGTCTTCTGTCTATAGACTAT	2220
QY	2247	TGGAAATAGTAGCCTCTGGGATCTTCTTCAATGCGCCCTTACGAAGAAAAAGACTTTGATT	2306



```
Db 2221 TGGAAATGTTACCTCTGGGATCTTCTCATATGAGCCCTTAGGAAAGAAAGAAAGCTTGTATT 2280
QY 2307 GGGACACACGGCTTAAAGATGATGATGTCAGACACAGGTTTATCTTATCTACACCATG 2366
Db 2281 GGGACACACGGCTTAAAGATGATGATGTCAGACACAGGTTTATCTTATCTACACCATG 2340
QY 2367 ACTGTAGTCCAAAGGATCTTACAGAGACGTCGAAGTCGTCAATCTCTTGGACAAAG 2426
Db 2341 ACTGTAGTCCAAAGGATCTTACAGAGACGTCGAAGTCGTCAATCTCTTGGACAAAG 2400
QY 2427 ACTTAGAGGCTCTTGGACAGATTTTGGAAATAGGAAAGCTTGTGTCTCAAGTCAC 2486
Db 2401 ACTTAGAGGCTCTTGGACAGATTTTGGAAATAGGAAAGCTTGTGTCTCAAGTCAC 2460
QY 2487 ATACTTCAACTTACGATGTCGACACGATAGGTTACATAGACCCCGAGATGCTCGACATT 2546
Db 2461 ATACTTCAACTTACGATGTCGACACGATAGGTTACATAGACCCCGAGATGCTCGACATT 2520
QY 2547 CACGGCTCACTGAGAAATCCGATGTCACGTTATGGAATAGTCCTTCTGAGTTGTTAA 2606
Db 2521 CACGGCTCACTGAGAAATCCGATGTCACGTTATGGAATAGTCCTTCTGAGTTGTTAA 2580
QY 2607 CCGAAGAGAAAGCGTTGATGACGAATCCATCTCCACATCTGATATGTCAAGACGG 2666
Db 2581 CCGAAGAGAAAGCGTTGATGACGAATCCATCTCCACATCTGATATGTCAAGACGG 2640
QY 2667 GGAACATGAATGATGAGAAATGCGAGATCCAGACATCAGATCGAGCTGTAAGATCTCG 2726
Db 2641 GGAACATGAATGATGAGAAATGCGAGATCCAGACATCAGATCGAGCTGTAAGATCTCG 2700
QY 2727 GTGTGTGTAAGAAAGTTTCCAACTGGCACTCCTATGACCAAAAGACAGCCGAATGATC 2786
Db 2701 GTGTGTGTAAGAAAGTTTCCAACTGGCACTCCTATGACCAAAAGACAGCCGAATGATC 2760
QY 2787 GACCCCAATGACACGAGTACTCGTGTCTCGGAGTTTATGCTATCGGAACAACAC 2846
Db 2761 GACCCCAATGACACGAGTACTCGTGTCTCGGAGTTTATGCTATCGGAACAACAC 2820
QY 2847 CTGCTGCGACTGACAGCTGACGAGCGCTGCTGTGCTGCTGATGATGATGCA 2906
Db 2821 CTGCTGCGACTGACAGCTGACGAGCGCTGCTGTGCTGCTGATGATGATGCA 2880
QY 2907 ATCTCAAGCTCCTCATTTCTGTAATGCTCTTCCATGATGCTTCTGATGCTCACTGT 2966
Db 2881 ATCTCAAGCTCCTCATTTCTGTAATGCTCTTCCATGATGCTTCTGATGCTCACTGT 2940
QY 2967 TTCTTCGTTTGGACAAAGTTATTTCTCAGAACAGTGAATGTTTTCGTTAGAGAGAA 3026
Db 2941 TTCTTCGTTTGGACAAAGTTATTTCTCAGAACAGTGAATGTTTTCGTTAGAGAGAA 3000
QY 3027 TCTTTAAACGGTATCTTTTCTGTCGTTGAGTAAAGCTGTTAGAAAAATTAATGCTCATGTAA 3086
Db 3001 TCTTTAAACGGTATCTTTTCTGTCGTTGAGTAAAGCTGTTAGAAAAATTAATGCTCATGTAA 3060
QY 3087 AGATATATGACACGCTTATTTATTTATTAAGCAAGTGTGTGTGAATATGTTCTTCAAGC 3146
Db 3061 AGATATATGACACGCTTATTTATTTATTAAGCAAGTGTGTGTGAATATGTTCTTCAAGC 3120
QY 3147 TGGCACTTGAATCTTCTATTA 3167
Db 3121 TGGCACTTGAATCTTCTATTA 3141
```

```
RESULT 3
AED28148
ID AED28148 standard; cdna; 3176 BP.
XX
AC AED28148;
XX
DT 01-DEC-2005 (first entry)
XX
DE Arabidopsis thaliana ERECTA protein encoding cdna.
```

```
XX
KW plant growth regulation; transgenic plant; crop improvement; transgene;
KW ERECTA; gene; ss.
XX
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
FT CDS 51..2981
FT /tag= a
FT /product= "Arabidopsis thaliana ERECTA protein"
XX
PN US2005223428-A1.
XX
PD 06-OCT-2005.
XX
PF 30-DEC-2004; 2004US-00027304.
XX
PR 01-APR-2004; 2004US-0558529P.
XX
PA (TORI/) TORI K U.
PA (SHPA/) SHPA E D.
XX
PI Torii KU, Shpak ED;
XX
DR WPI: 2005-675788/59.
DR P-PSDB; AED28149.
XX
PT Modulating plant height and organ shape comprises expressing, in plants,
PT a transgene encoding an ERECTA-like protein lacking an active kinase
XX domain.
XX
PS Disclosure; SEQ ID NO 1; 72pp; English.
XX
CC The present invention relates to a method for modulating plant height and
CC organ shape. The method involves expressing a transgene in a plant, where
CC the transgene encodes an ERECTA-like protein lacking an active kinase
CC domain and where expression of the transgene modulates plant height or
CC organ shape. ERECTA protein contains leucine-rich repeat receptor-like
CC kinase (LRR-RLK) with 20 consecutive leucine-rich repeats (LRR) and
CC functional Ser/Thr kinase activity. The invention is useful for producing
CC transgenic plant and for enhancing the yield of a crop plant. The present
CC sequence is the Arabidopsis thaliana ERECTA protein encoding cdna.
XX
SQ Sequence 3176 BP; 927 A; 654 C; 659 G; 936 T; 0 U; 0 Other;
XX
Query Match 98.7%; Score 3136.2; DB 14; Length 3176;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 3138; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 27 CTTTAAAGTATATCTAAAAAGCAGTGGTTTAAAGACTGTGTGAGAAATGCTCTGT 86
Db 1 CTTTAAAGTATATCTAAAAAGCAGTGGTTTAAAGACTGTGTGAGAAATGCTCTGT 60
QY 87 TTAGAGATATGTTCTTCTTGGGTTTCTTCTGCTGAGCTTAGAGTACTGTGACTT 146
Db 61 TTAGAGATATGTTCTTCTTGGGTTTCTTCTGCTGAGCTTAGAGTACTGTGACTT 120
QY 147 CAGAGAGGAGCAACGTTGCTGAGATTTAGAAAGTCAATCAAGATGGAACAATGTT 206
Db 121 CAGAGAGGAGCAACGTTGCTGAGATTTAGAAAGTCAATCAAGATGGAACAATGTT 180
QY 207 TTTATGACTGACACACTTACCTTCTTGGATTTATGTTGTGAGAGAGTGTCTTGTG 266
Db 181 TTTATGACTGACACACTTACCTTCTTGGATTTATGTTGTGAGAGAGTGTCTTGTG 240
QY 267 AAAATGTCACTTCAATGTTGTGCTCTTAATTTGTGCAGATTTGAATCTTGAAGAGAA 326
Db 241 AAAATGTCACTTCAATGTTGTGCTCTTAATTTGTGCAGATTTGAATCTTGAAGAGAA 300
QY 327 TCTCACTGCTAATGAGATCTCAAGAGTCTTGTGCAATGATCTGCAGGTAATGCT 386
Db 301 TCTCACTGCTAATGAGATCTCAAGAGTCTTGTGCAATGATCTGCAGGTAATGCT 360
```

OY	387	IGTCGGGCAAAATCCCTGATGAGATTGGTGACTGTTCTTTTCGAAAACCTTAGACTTAT	446
Db	361	TGTCGGGCAAAATCCCTGATGAGATTGGTGACTGTTCTTTTCGAAAACCTTAGACTTAT	420
OY	447	CCTTCAATGAATTAAGTGTGACATACCGTTTTGATTTCCAGTTGAAGCACTTGAGC	506
Db	421	CCTTCAATGAATTAAGTGTGACATACCGTTTTGATTTCCAGTTGAAGCACTTGAGC	480
OY	507	AGCTGATTCTGMAAGATACCAATTTGATAGNCCGATCCCTTCAACACTTTCAAGATTTC	566
Db	481	AGCTGATTCTGMAAGATACCAATTTGATAGNCCGATCCCTTCAACACTTTCAAGATTTC	540
OY	567	CAACCTGAAAATTTGGACTTGGCACAAGATAACTAGTGTGATTAACCAAGACTTA	626
Db	541	CAACCTGAAAATTTGGACTTGGCACAAGATAACTAGTGTGATTAACCAAGACTTA	600
OY	627	TTTACTGGAATGAACCTTCTGAGTACTTGGGTTGCGAGGAAACAACCTTACCGGTACA	686
Db	601	TTTACTGGAATGAACCTTCTGAGTACTTGGGTTGCGAGGAAACAACCTTACCGGTACA	660
OY	687	TTTCTCCAGATTTGTCGTAACGTGAGCTTTGGTATTTTTCAGCTAAGAAACAAGTT	746
Db	661	TTTCTCCAGATTTGTCGTAACGTGAGCTTTGGTATTTTTCAGCTAAGAAACAAGTT	720
OY	747	TGACTGTAGTATACCTTGAGACGATAGGAAATTCGACTGCTTCCAGGTTTGGACTTGT	806
Db	721	TGACTGTAGTATACCTTGAGACGATAGGAAATTCGACTGCTTCCAGGTTTGGACTTGT	780
OY	807	CCTAATACAGTACTGCTGTGAGTCCCTTTTGATATGGGCTCCTGCAAGTCGCAACAT	866
Db	781	CCTAATACAGTACTGCTGTGAGTCCCTTTTGATATGGGCTCCTGCAAGTCGCAACAT	840
OY	867	TATCATTTGCAAGGCAATCAACTCTCTGGGAAAGTTCCATAGTGAATTGCTCTCATGCAAG	926
Db	841	TATCATTTGCAAGGCAATCAACTCTCTGGGAAAGTTCCATAGTGAATTGCTCTCATGCAAG	900
OY	927	CCCTTGCAAGTCTTAGATCTAAGTGGCAACTGTTGATGATCTATTCCTCCGATTCTCG	986
Db	901	CCCTTGCAAGTCTTAGATCTAAGTGGCAACTGTTGATGATCTATTCCTCCGATTCTCG	960
OY	987	GAAATCTTACTTTGACCGAGAAATTGTAATTGACAGTAAACAAGCTGACGTGTCATTC	1046
Db	961	GAAATCTTACTTTGACCGAGAAATTGTAATTGACAGTAAACAAGCTGACGTGTCATTC	1020
OY	1047	CACCTGAGCTTGGAAACAATGTCGAAACTCCATTACCTGGAATCCTCATATATCATCTCA	1106
Db	1021	CACCTGAGCTTGGAAACAATGTCGAAACTCCATTACCTGGAATCCTCATATATCATCTCA	1080
OY	1107	CGGGTCATATACCAACCAAGCTTGGGAAAGCTTACTGACTGTTTGTATGTGAATGTGGCCA	1166
Db	1081	CGGGTCATATACCAACCAAGCTTGGGAAAGCTTACTGACTGTTTGTATGTGAATGTGGCCA	1140
OY	1167	ACAAATGATCTGGAAGGACCTATACCTGATCATCTGAGCTCTTGGCAAACTTAAACACT	1226
Db	1141	ACAAATGATCTGGAAGGACCTATACCTGATCATCTGAGCTCTTGGCAAACTTAAACACT	1200
OY	1227	TAAATGTTCAATGGGAACAAGTTTAGTGCACTATACCCGAGACTTTCAAAAGCTAGAAA	1286
Db	1201	TAAATGTTCAATGGGAACAAGTTTAGTGCACTATACCCGAGACTTTCAAAAGCTAGAAA	1260
OY	1287	GTAATGACTTAACTTATCTGTGACGCAACAATATCAAAAGTCCATCCCGTGTAGCTAT	1346
Db	1261	GTAATGACTTAACTTATCTGTGACGCAACAATATCAAAAGTCCATCCCGTGTAGCTAT	1320
OY	1347	CTCGATAGGGTAACTTAATATACATTGGATCTTTCCAAACAAGATAATGGATCATTC	1406
Db	1321	CTCGATAGGGTAACTTAATATACATTGGATCTTTCCAAACAAGATAATGGATCATTC	1380
OY	1407	CTTCTCCCTTGATTTTGGAGCACTTCTCAGATGAACCTTGATGATCATATATA	1466
Db	1381	CTTCTCCCTTGATTTTGGAGCACTTCTTCTCAGATGAATTAATGATGATCATATATA	1440
OY	1467	CTGGGTAGTTCCAGGCGACTTTGGAAATCTAAGAAGCATCATGGAAATAGATCTTTCAA	1526

Db	1441	CTGGGTGAGTTCACGGCAGCTTTGGAAAATCTAAGAAAGCATCATGAAAATPAGATCTTTCAA	1500
OY	1527	ATAATGATATCTCTGGCCCAATTCAGAAAGACCTTAAACAAATTACAGAAATATTTTGC	1586
Db	1501	ATPAAAGATATCTCTGGCCCAATTCAGAAAGACCTTAAACAAATTACAGAAATATTTTGC	1560
OY	1587	TGAGACTGGAAAATATATACTGACCTGGTAATGTGGTTTCATTAGCAACTGTCTCAGTC	1646
Db	1561	TGAGACTGGAAAATATATACTGACCTGGTAATGTGGTTTCATTAGCAACTGTCTCAGTC	1620
OY	1647	TCACGTATTTGAATGTATCTCTCAACAACCTGTGGGTATATCCCTAAGAACAAATPACT	1706
Db	1621	TCACGTATTTGAATGTATCTCTCAACAACCTGTGGGTATATCCCTAAGAACAAATPACT	1680
OY	1707	TCTCAAGATTTTTCACAGACAGCTTCATTGGCAATCTCGTCTTTGCGGTAGTTGGCTAA	1766
Db	1681	TCTCAAGATTTTTCACAGACAGCTTCATTGGCAATCTCGTCTTTGCGGTAGTTGGCTAA	1740
OY	1767	ACTCACCGTGTATGATTTCTGTGGAACCTGACAGATGTCATCTCTAAGACAGCTATTTC	1826
Db	1741	ACTCACCGTGTATGATTTCTGTGGAACCTGACAGATGTCATCTCTAAGACAGCTATTTC	1800
OY	1827	TTTGGAAATGCTATTGGGGGACCTTGGATTCCTTCTCATGGTCTTAAAGACAGCTTGGCCGAC	1886
Db	1801	TTTGGAAATGCTATTGGGGGACCTTGGATTCCTTCTCATGGTCTTAAAGACAGCTTGGCCGAC	1860
OY	1887	CGCATATAATCTCTCTCTTTCTTTCTTGAATGATCACTTGACAAACAGTAACTTATTGACAC	1946
Db	1861	CGCATATAATCTCTCTCTTTCTTTCTTGAATGATCACTTGACAAACAGTAACTTATTGACAC	1920
OY	1947	CGAAGCTGTCAATCCTTCATATGAAACATGGCACTCCACGTTTACGAGATATCATGAGAA	2006
Db	1921	CGAAGCTGTCAATCCTTCATATGAAACATGGCACTCCACGTTTACGAGATATCATGAGAA	1980
OY	2007	TGACAGAAATCTTAGTGAGAAATATCATTTGGGACGGAGATCAACACCTGTATPACA	2066
Db	1981	TGACAGAAATCTTAGTGAGAAATATCATTTGGGACGGAGATCAACACCTGTATPACA	2040
OY	2067	AATGAGTTTGTGAAGATTTGTAACCCGGTTGCGATTAAAGCGGCTTTTACTCTCACAAACCAC	2126
Db	2041	AATGAGTTTGTGAAGATTTGTAACCCGGTTGCGATTAAAGCGGCTTTTACTCTCACAAACCAC	2100
OY	2127	AGTCATATAACAGTTTGAACAGAACTTCGAGATGCTAATGATCATCAAGACAGAAATC	2186
Db	2101	AGTCATATAACAGTTTGAACAGAACTTCGAGATGCTAATGATCATCAAGACAGAAATC	2160
OY	2187	TTTGTAGCCTTACAGCTTATTCCTCTCTCTCACTTTGGGGAGTCTTCTGTCTTATGACTATT	2246
Db	2161	TTTGTAGCCTTACAGCTTATTCCTCTCTCTCACTTTGGGGAGTCTTCTGTCTTATGACTATT	2220
OY	2247	TGGAATAATGTGTAGCCTCTGGGATCTTCTTCAATGGCCCTACGAAGAAAAGAAAGCTCTGATT	2306
Db	2221	TGGAATAATGTGTAGCCTCTGGGATCTTCTTCAATGGCCCTACGAAGAAAAGAAAGCTCTGATT	2280
OY	2307	GGGACACACGGCTTAAGATAGCATATGTGACAGCAAAAGTTTACCTTATCTACACCATG	2366
Db	2281	GGGACACACGGCTTAAGATAGCATATGTGACAGCAAAAGTTTACCTTATCTACACCATG	2340
OY	2367	ACTGTATGTCCAAGGATTCATTTCAACAAGACGTGAATGTCCTTCTTGGACAAAG	2426
Db	2341	ACTGTATGTCCAAGGATTCATTTCAACAAGACGTGAATGTCCTTCTTGGACAAAG	2400
OY	2427	ACTTGAAGGCTCGTTTGAACAGATTTTGGAAATGCGAAAAGCTTGTGTGTCMAAGTCAC	2486
Db	2401	ACTTGAAGGCTCGTTTGAACAGATTTTGGAAATGCGAAAAGCTTGTGTGTCMAAGTCAC	2460
OY	2487	ATACTTCAACTTACGTGATGGGACAGATAGTTTACATAGACCCTCGATATGCTCGACTT	2546
Db	2461	ATACTTCAACTTACGTGATGGGACAGATAGTTTACATAGACCCTCGATATGCTCGACTT	2520
OY	2547	CACGGCTCACTGAGAAATCCCATGTCTACAGTTTATGGAATAGTCTTCTTGAAGTTGTTAA	2606

```
Db 2521 CACGGCTACTGAAATCCGATGCTCAAGTTATGGAATAGTCTTCTTGAGCTGTAA 2580
Oy 2607 CCGAAGAGAAAGCGCTTGATGAGCAATCCAATCCACATCTGATATGTCAAAGACG 2666
Db 2581 CCGAAGAGAAAGCGCTTGATGAGCAATCCAATCCACATCTGATATGTCAAAGACG 2640
Oy 2667 GGAACAATGAAAGTATGGAATGGCAGATCCAGACATCAATGACGCTGTAAAGATCG 2726
Db 2641 GGAACAATGAAAGTATGGAATGGCAGATCCAGACATCAATGACGCTGTAAAGATCG 2700
Oy 2727 GTGTGTTGAAAGATTTTCCAACTGGCACTCCTATGACCAAAAGACACCGAATGATC 2786
Db 2701 GTGTGTTGAAAGATTTTCCAACTGGCACTCCTATGACCAAAAGACACCGAATGATC 2760
Oy 2787 GACCCCAATGACCAAGGATCGGTCTCGGCACTTTTATGCTATCGGAACAACAC 2846
Db 2761 GACCCCAATGACCAAGGATCGGTCTCGGCACTTTTATGCTATCGGAACAACAC 2820
Oy 2847 CTGCTGCACTGACAGTCAGCAGCAGCTGCTGGTTCCTACGTGATGATGATGCA 2906
Db 2821 CTGCTGCACTGACAGTCAGCAGCAGCTGCTGGTTCCTACGTGATGATGATGCA 2880
Oy 2907 ATCTCAAGACTCTCTCAATCTGTCAATGCTCTTCCATGAGTCTTGATGCTCAACTGT 2966
Db 2881 ATCTCAAGACTCTCTCAATCTGTCAATGCTCTTCCATGAGTCTTGATGCTCAACTGT 2940
Oy 2967 TTTCTGGTTTGGAACAAGTATTTCTCAACAAGTATGTTTTCGTTAGAGAGAGAA 3026
Db 2941 TTTCTGGTTTGGAACAAGTATTTCTCAACAAGTATGTTTTCGTTAGAGAGAGAA 3000
Oy 3027 TCTTTAAACGATATCTTTTCTGTGCTTAAAGCTGTAGAAAATTAATGCTCATGTAA 3086
Db 3001 TCTTTAAACGATATCTTTTCTGTGCTTAAAGCTGTAGAAAATTAATGCTCATGTAA 3060
Oy 3087 AGTATTAATGCACTGCTTATTAATTAATTAACAAGTGTGTGTAATATGCTTCAAGAC 3146
Db 3061 AGTATTAATGCACTGCTTATTAATTAATTAACAAGTGTGTGTAATATGCTTCAAGAC 3120
Oy 3147 TGGCACTTAGACTTCTCTATTA 3167
Db 3121 TGGCACTTAGACTTCCAAAAA 3141

RESULT 4
ADA68568
ID ADA68568 standard; DNA; 2930 BP.
XX
AC ADA68568;
XX
DT 20-NOV-2003 (first entry)
XX
DE Arabidopsis thaliana gene, SEQ ID 480.
XX
KW plant; bacterial infection; fungal infection; viral infection; ds.
XX
OS Arabidopsis thaliana.
XX
PN WO2003000898-A1.
XX
PD 03-JAN-2003.
XX
PF 22-JUN-2001; 2001MO-IB001105.
XX
PR 22-JUN-2001; 2001MO-IB001105.
XX
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Qian S, Tao Y, Whitman S, Xie Z, Zhu T, Zou G;
XX WPI; 2003-175290/17.
XX
PT Identifying at least one gene involved in plant resistance or response to
```

```
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX
PS Claim 6; SEQ ID NO 480; 899pp; English.
XX
CC The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 2930 BP; 828 A; 625 C; 616 G; 861 T; 0 U; 0 Other;
Query Match 92.3%; Score 2930; DB 8; Length 2930;
Best Local Similarity 100.0%; Pred.No.0;
Matches 2930; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 77 ATGGCTCTGTTAGAGATATTTGTTCTTCTGCTGCTTCTCTGCTGCTGCTGCTGCTGCT 136
Db 1 ATGGCTCTGTTAGAGATATTTGTTCTTCTGCTGCTTCTCTGCTGCTGCTGCTGCTGCT 60
Oy 137 ACTGTGACTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 196
Db 61 ACTGTGACTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
Oy 197 AACAAATGTTCTTATGACTGAGCAACTTCACTTCTGAGATTAATGATGATGATGATG 256
Db 121 AACAAATGTTCTTATGACTGAGCAACTTCACTTCTGAGATTAATGATGATGATGATG 180
Oy 257 GTGTCTTGGAAGAAATGTCACCTTCAATGTTGTTGCTCTTAATTTGAGATTGAACTT 316
Db 181 GTGTCTTGGAAGAAATGTCACCTTCAATGTTGTTGCTCTTAATTTGAGATTGAACTT 240
Oy 317 GATGAGAAATGTCACCTGCTATGAGATCTCAAGAGTCTGTTGCAATGATGATGCGA 376
Db 241 GATGAGAAATGTCACCTGCTATGAGATCTCAAGAGTCTGTTGCAATGATGATGCGA 300
Oy 377 GGTAAATGCTGTGCTGAGCAAAATCCCTGATGATGATGATGATGATGATGATGATG 436
Db 301 GGTAAATGCTGTGCTGAGCAAAATCCCTGATGATGATGATGATGATGATGATGATG 360
Oy 437 TTAGACTATCTTCAATGAATTAATGATGATGATGATGATGATGATGATGATGATG 496
Db 361 TTAGACTATCTTCAATGAATTAATGATGATGATGATGATGATGATGATGATGATG 420
Oy 497 CAACCTGAGCAGCTGATTTGAGAAATTAACAATGATGATGATGATGATGATGATGAT 556
Db 421 CAACCTGAGCAGCTGATTTGAGAAATTAACAATGATGATGATGATGATGATGATGAT 480
Oy 557 TCACAGATTCCAAACTGAAATTTCTGCACTTGGCACAATAATTAATCTAGTGTGAGTA 616
Db 481 TCACAGATTCCAAACTGAAATTTCTGCACTTGGCACAATAATTAATCTAGTGTGAGTA 540
Oy 617 CCAAGACTATTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 676
Db 541 CCAAGACTATTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
Oy 677 GTGGTAAATTTCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 736
Db 601 GTGGTAAATTTCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Oy 737 AACAAAGTTTACAGTGTGATTAATCTGAGAGATGAGAAATGATGATGATGATGATGAT 796
Db 661 AACAAAGTTTACAGTGTGATTAATCTGAGAGATGAGAAATGATGATGATGATGATGAT 720
Oy 797 TTGACTGTCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 856
Db 720 TTGACTGTCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
```

Db 721 TTGGACTTGTCTACATCACTAAGTGTAGATCCCTTTTGACATCGGCTTCCTGCAA 780  
QY 857 GTTGCAACATTATCATTTGCAAGGCAATCACTCTCTGGGAAGATTCATGAGATTTGT 916  
Db 781 GTTGCAACATTATCATTTGCAAGGCAATCACTCTCTGGGAAGATTCATGAGATTTGT 840  
QY 917 CTCATGCAAGCCCTTGAGCTTTAGATCTAAGTGGCAACTGTGTAGTGGATCTATTCT 976  
Db 841 CTCATGCAAGCCCTTGAGCTTTAGATCTAAGTGGCAACTGTGTAGTGGATCTATTCT 900  
QY 977 CCGATTCTCGGAAATCTTACTTTTCAACGAAATTTGATTTGCAAGTAACTGACT 1036  
Db 901 CCGATTCTCGGAAATCTTACTTTTCAACGAAATTTGATTTGCAAGTAACTGACT 960  
QY 1037 GGTTCATTCCACTGAGCTTGGAACATGCAAAATCTCATTAACCTGGAACCTCAATGAT 1096  
Db 961 GGTTCATTCCACTGAGCTTGGAACATGCAAAATCTCATTAACCTGGAACCTCAATGAT 1020  
QY 1097 AATCATCTCAAGGCTCATATACCAACGAGCTTGGGAAGCTTACTGACTTTGTGATCTG 1156  
Db 1021 AATCATCTCAAGGCTCATATACCAACGAGCTTGGGAAGCTTACTGACTTTGTGATCTG 1080  
QY 1157 AATGTGGCCAACTAGATCTTGGAAGACCTATACCTGATCATCTGAGCTCTTGACAAAT 1216  
Db 1081 AATGTGGCCAACTAGATCTTGGAAGACCTATACCTGATCATCTGAGCTCTTGACAAAT 1140  
QY 1217 CTAAACAGCTTAATGTTCATGGGAACAAGTTTAGTGGCACTATACCCCGAGCATTTCAA 1276  
Db 1141 CTAAACAGCTTAATGTTCATGGGAACAAGTTTAGTGGCACTATACCCCGAGCATTTCAA 1200  
QY 1277 AAGCTAGAAAGTATGACTTACCTTAATCTGTCCAGCAACAATATCAAAAGGTCCAAATCCG 1336  
Db 1201 AAGCTAGAAAGTATGACTTACCTTAATCTGTCCAGCAACAATATCAAAAGGTCCAAATCCG 1260  
QY 1337 GTTGAAGTATCTGTATACGCTTAATGATACATTTGATCTTTTCAACAACAGATTAAT 1396  
Db 1261 GTTGAAGTATCTGTATACGCTTAATGATACATTTGATCTTTTCAACAACAGATTAAT 1320  
QY 1397 GGAATCACTTCCTCTTCCCTTGAGTATTTGGAGCATCTTCTCAAGATGAACCTTGAGTGA 1456  
Db 1321 GGAATCACTTCCTCTTCCCTTGAGTATTTGGAGCATCTTCTCAAGATGAACCTTGAGTGA 1380  
QY 1457 AATCATATACTGGTGTAGTTCAGGCGACTTTGGAAATCTAAGAACATCATGGAATA 1516  
Db 1381 AATCATATACTGGTGTAGTTCAGGCGACTTTGGAAATCTAAGAACATCATGGAATA 1440  
QY 1517 GATCTTTCAAAATATGATATCTCTGCGCCAAATTCAGAAAGCTTAACTTAACAGAAC 1576  
Db 1441 GATCTTTCAAAATATGATATCTCTGCGCCAAATTCAGAAAGCTTAACTTAACAGAAC 1500  
QY 1577 ATATATTTTGTGAGACTGGAATAATATACTGACTGTATATGTTGGTTCAATTAAGCCAA 1636  
Db 1501 ATATATTTTGTGAGACTGGAATAATATACTGACTGTATATGTTGGTTCAATTAAGCCAA 1560  
QY 1637 TGTCTCAGTCTCACTGTATTAATGATATCTCATTAACAACCTCGTAGTATATCCCTAAG 1696  
Db 1561 TGTCTCAGTCTCACTGTATTAATGATATCTCATTAACAACCTCGTAGTATATCCCTAAG 1620  
QY 1697 AACATATACTTTTCAGATTTTTCAGCAGACAGCTTCAATGGCAATCTCTGCTTTGGGCT 1756  
Db 1621 AACATATACTTTTCAGATTTTTCAGCAGACAGCTTCAATGGCAATCTCTGCTTTGGGCT 1680  
QY 1757 AGTTGGCTTAACACTACCGTGTCAATGTTCTGTGGAAGCTGTAGAGAGTCAATCTCTAGA 1816  
Db 1681 AGTTGGCTTAACACTACCGTGTCAATGTTCTGTGGAAGCTGTAGAGAGTCAATCTCTAGA 1740  
QY 1817 GCAGCTAATTTCTGGAATAGCTAATTTGGGGAAGCTTGTGATCTTCTCATGATCTTAATAGA 1876  
Db 1741 GCAGCTAATTTCTGGAATAGCTAATTTGGGGAAGCTTGTGATCTTCTCATGATCTTAATAGA 1800  
QY 1877 GCTTGGCCGACCGCATATCTCTCTCTTTTCTTATGATGATCATCTTGCAAAACAGTAACT 1936  
Db 1801 GCTTGGCCGACCGCATATCTCTCTCTTTTCTTATGATGATCATCTTGCAAAACAGTAACT 1860

QY 1937 TATTGCAACCGAAGCTCGTCACTCTTCAATATGAACTGGCACTCCGACGTTTACGAGAT 1996  
Db 1861 TATTGCAACCGAAGCTCGTCACTCTTCAATATGAACTGGCACTCCGACGTTTACGAGAT 1920  
QY 1997 ATCATGGAATGAACAGAAATCTTAAGTAGAAGTATATCATTTGGGACCGAGCATCAAGC 2056  
Db 1921 ATCATGGAATGAACAGAAATCTTAAGTAGAAGTATATCATTTGGGACCGAGCATCAAGC 1980  
QY 2057 ACTGTATACAAATGTCTTTTGAAGAAATGTAACCCGTTGCCGTTAAAGCGGCTTACTCT 2116  
Db 1981 ACTGTATACAAATGTCTTTTGAAGAAATGTAACCCGTTGCCGTTAAAGCGGCTTACTCT 2040  
QY 2117 CACAACCCACAGTCAATGAAACAGTTTGAACAGAACTCGAGATGCTTAAGTATACATCAAG 2176  
Db 2041 CACAACCCACAGTCAATGAAACAGTTTGAACAGAACTCGAGATGCTTAAGTATACATCAAG 2100  
QY 2177 CACAGAAATCTGTGAGCTTACAAAGCTTATCCCTCTCTCACTTTGGGAGCTTTCTGTTG 2236  
Db 2101 CACAGAAATCTGTGAGCTTACAAAGCTTATCCCTCTCTCACTTTGGGAGCTTTCTGTTG 2160  
QY 2237 TATGACTAATTTGGAATAATGTTAGCTCTGAGATCTTCACTGAGCCCTACGAGAAAGAG 2296  
Db 2161 TATGACTAATTTGGAATAATGTTAGCTCTGAGATCTTCACTGAGCCCTACGAGAAAGAG 2220  
QY 2297 ACTCTGATTTGGGACACACGCTTAAAGTATGATATGATGTCACACAGAGCTTTAGCTTAT 2356  
Db 2221 ACTCTGATTTGGGACACACGCTTAAAGTATGATATGATGTCACACAGAGCTTTAGCTTAT 2280  
QY 2357 CTACACCATGACTGTAGTCCAGAGATCATCTCACAGACGTAAGTGTCTCAACATTTCTC 2416  
Db 2281 CTACACCATGACTGTAGTCCAGAGATCATCTCACAGACGTAAGTGTCTCAACATTTCTC 2340  
QY 2417 TTGGAACAACACTTAGAGCTGCTTTGACAGATTTTGGAAATAGCGAAAGCTGTGTGTG 2476  
Db 2341 TTGGAACAACACTTAGAGCTGCTTTGACAGATTTTGGAAATAGCGAAAGCTGTGTGTG 2400  
QY 2477 TCAAAAGTCATATCTTCAACTTACGTATGAGTGGCAGCATAGTTTACATAGACCCCGATAT 2536  
Db 2401 TCAAAAGTCATATCTTCAACTTACGTATGAGTGGCAGCATAGTTTACATAGACCCCGATAT 2460  
QY 2537 GCTGCGACTTCACGCGCTCACTAGAAATCCGATGTCTACAGTTATGGAATGTCTTCTT 2596  
Db 2461 GCTGCGACTTCACGCGCTCACTAGAAATCCGATGTCTACAGTTATGGAATGTCTTCTT 2520  
QY 2597 GAGTTGTTAACCGGAGGAAGCGTTGATGAGAAATCCAAATCTCCACCACTGATTAATG 2656  
Db 2521 GAGTTGTTAACCGGAGGAAGCGTTGATGAGAAATCCAAATCTCCACCACTGATTAATG 2580  
QY 2657 TCAAAAGCGGGGAACAATGAAATGATGAAATGGCAGATTCAGACATCAACATGACGTGT 2716  
Db 2581 TCAAAAGCGGGGAACAATGAAATGATGAAATGGCAGATTCAGACATCAACATGACGTGT 2640  
QY 2717 AAAGATCTCGGTGTGTGGAAGAAATTTTCAACTGCGACTCTTAATGACACAAAGACAG 2776  
Db 2641 AAAGATCTCGGTGTGTGGAAGAAATTTTCAACTGCGACTCTTAATGACACAAAGACAG 2700  
QY 2777 CCGAATGATGAGCCCAATGACAACGAGTACAGTGTCTGCGGAGCTTTATGCTATCG 2836  
Db 2701 CCGAATGATGAGCCCAATGACAACGAGTACAGTGTCTGCGGAGCTTTATGCTATCG 2760  
QY 2837 GAAACAACACCTGCTGAGACTGACAGCTCAGCAGCGCTGCTGTTCTGTGCTACAGTCTGAT 2896  
Db 2761 GAAACAACACCTGCTGAGACTGACAGCTCAGCAGCGCTGCTGTTCTGTGCTACAGTCTGAT 2820  
QY 2897 GAGTATGCAAAATCTCAAGACTCTCTCATTTCTGTCAATTTGCTTTTCCATGAGTCTTGAT 2956  
Db 2821 GAGTATGCAAAATCTCAAGACTCTCTCATTTCTGTCAATTTGCTTTTCCATGAGTCTTGAT 2880  
QY 2957 GCTCAACTGTTTCTTGCGTTTGGACAAGTATTTCTCAGAAAGTAGATA 3006  
Db 2881 GCTCAACTGTTTCTTGCGTTTGGACAAGTATTTCTCAGAAAGTAGATA 2930

RESULT 5  
AD30336  
ID AD30336 standard; cDNA; 2750 BP.  
XX  
AC AD30336;  
XX  
DT 21-Apr-2005 (first entry)  
XX  
DE Plant full length insert polynucleotide seqid 13156.  
XX  
KW plant protectant; plant growth regulant; gene therapy; plant;  
KW recombinant DNA construct; physical array; plant breeding marker;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
KW growth rate; cell cycle pathway; disease resistance;  
KW galactomannan production; lignin production; plant growth regulator;  
KW yield; plant growth; plant development; seed oil; protein yield;  
KW protein content; gene; ss.  
XX  
OS Unidentified.  
XX  
PN US2004034888-A1.  
XX  
PD 19-FEB-2004.  
XX  
PE 28-Apr-2003; 2003US-00425114.  
XX  
PR 06-MAY-1999; 99US-00304517.  
PR 05-NOV-2001; 2001US-00985678.  
XX  
PA (LIU/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABAS/) TABASKA J E.  
PA (CAO/) CAO Y.  
XX  
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
XX  
DR WPI; 2004-180133/17.  
XX  
PT New recombinant DNA construct, useful for improving plant tolerance to  
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.  
XX  
PS Claim 1; SEQ ID NO 13156; 15pp; English.  
XX  
XX The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US patent office at  
CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for producing galactomannan,  
CC lignin or plant growth regulators, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carboxylate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This sequence represents a plant full length insert  
CC polynucleotide that can be used in the recombinant DNA construct of the  
XX invention.  
XX  
XX Sequence 2750 BP; 822 A; 572 C; 548 G; 808 T; 0 U; 0 Other;

Query Match 46.8%; Score 1486.6; DB 13; Length 2750;  
Best Local Similarity 74.8%; Pred. No. 0;  
Matches 1883; Conservative 0; Mismatches 619; Indels 15; Gaps 1;

QY 504 AGCAGCTGATTCGAGAAATTAACCAATTGATPAGACCGATCCCTTCAACACTTTCACAGA 563  
DB 1 AGAATCTGATTTTGAACAAACCAATGATGAGCAAAATCTTCAACTTTGCTCAGA 60  
QY 564 TTCCAAACTGAAATCTGGAATTTGGCAGACAAATAAAGTCACTGAGTACCAAGAC 623  
DB 61 TTCTGATTTGAAGATTTGACCTGGCTCAAAATAATCTTAGGGGAAATACCAAGGC 120  
QY 624 TTATTACTGGAATGAAGTTCTTCACTGATCTTGGGTTGCGAGAAACAACTAGTCGCTA 683  
DB 121 TTATATATTTGGAACGAAGTTTGGCAATATCTAGGCTTGAAGGGAAACAAATTTGGTTGTT 180  
QY 684 ACATTTCTCAGATTTGTGCACTGACCTGCTTTGGTATTTTGAAGTGAAGAACACA 743  
DB 181 CACTATACCAAGACATGTGCACTGATTAAGGCTGTGATTTTGAAGTGAAGAACATA 240  
QY 744 GTTTGACTGTGATGATACCTGAGACGATPAGAAATGCACTGCTTCAGGTTTGGACT 803  
DB 241 GCCTGACAGGAAGATTTCCAGAGAACATAGCAATTTGACCTTCAGGTTTGGATT 300  
QY 804 TGTCTTCAAAATCAGCTTACTGTGAGATCCCTTTTGAACATGCGCTTCTGCAAGTTGCA 863  
DB 301 TATCTTCAACCAACTAATCTGAGAGATACCATTCATATTTGATTTCTTCAAGTAGCA 360  
QY 864 CATTATGATTTGCAAGGCAATCACTCTGAGAAAGATTCATGATGATGCTCTCATG 923  
DB 361 CTGTGCTTTCGAAAGGCAATTAACCTCTTGACAAATTTCCACCGGTGATGCTCTCATG 420  
QY 924 AAGCCCTTGCAGTCTTATGATCTAAGTGGCAACTTGTGATGATCTAATCTCCGATTC 983  
DB 421 AAGCATTGCTGCTCTGACCTTGAAGCTGCACTTTGTTAAGTGAATGATCTCTCTATCT 480  
QY 984 TCGGAAATCTTACTTTCACCGAGAAATTTGATTTGCAACAGTAAACAAGCTGATGTTCAA 1043  
DB 481 TGGGAAATTTGACTTACACAGAAAAATTTGATTTGCAATGAAACAAGCTGATGCTGCTTCA 540  
QY 1044 TTCCACTGAGCTTGGAAACATGTCAAAATCTCATACCTGGAACATCAAGATATATATC 1103  
DB 541 TCCCTCCAGAGCTTGGAAATTTGATTTGCAATTTGGAATGGAATTAACCATTT 600  
QY 1104 TCAAGGCTCATATACCAACAGCTTGGAGAGCTTCTGCTGTTGATCTGAATGTG 1163  
DB 601 TAAATGACATATCCCGCCGAGCTTGGAAAGCTTACAGATCTGTTGAATCTTAATGTG 660  
QY 1164 CCAACAAATGATGGAAGACCTATACCTGATCATCTGAGCTTTGCAACAATCTAAACA 1223  
DB 661 CAAACAAATCTTGAAGGGCCAAATCTGATATCTAGCTCATGTAAATCTCAACA 720  
QY 1224 GCTTAATGTTCAATGGGAACAATTTAGTGGCATATCCCGAGACTTTCAAAAGCTAG 1283  
DB 721 GCTTCAATGATGACATGGCAACAAATTTGATGATCAATTTCCCTTTTGGCAAGTTTG 780  
QY 1284 AAGATGATCTTCACTTAATCTGTCCAGCAACAATTTCAAAAGGCTCAATCCGGTTGAG 1343  
DB 781 AGAGCATGACTTCTTGAATCTTTCTTCAACAATCTTCAAGGCGCAATTTCAATAGAAC 840  
QY 1344 TATCTGATGCTGATTAATCTTGAATGATGATCTTTTCAACAACAAGATTAATGATCA 1403  
DB 841 TGTGCGGAGATTTGCAATTTGATGATGATGATTTTCAACAATTAATCTTGTGTTTCA 900  
QY 1404 TTCTCTTCTTCTTCTTGGTATTTGGAGATCTTTTCAAGATGAACCTGATGATGAATCAT 1463  
DB 901 TCCCTTCTTCTTCTTGGTATTTGGAGATCTTTTCAAGATGAACCTGATGATGAATCAT 960  
QY 1464 TAACTGATGATTTCCAGGCGCACTTGAAGATTTAAGAGCATGAGAAATGATCTTT 1523  
DB 961 TAAAGATTTATTTCCAGGCGCACTTGAAGATTTAAGAGCATGAGAAATGATCTTT 1020  
QY 1524 CAATTAATGATTTCTGCGCAATTTCCAGAGAGCTTAAACAATTAACAAGATTAATTT 1583  
DB 1021 CAATTAATCAACTCTGCGCTGATTTCTGATGATTAAGTATGATGATTAAGTATGATAT 1080

QY 1584 TCGTGAAGCTGAAATTAATTAACCTGATGTTAGTGTCTATTAAGCAACTGTCTCA 1643  
 DB 1081 CTTTGAGACTTGAATAATTAACAATTAAGTGAAGTGTGGCATTCATTTCAAAATTTGACTTA 1140  
 QY 1644 GTCTCACTGATTAATGATATCTCATTAACAACCTCGTAGGTGATATCTCTTAAGAACATA 1703  
 DB 1141 GTCTCTCTCAACTTAATGATGCTCTTAACAACAATTAATTTGGTTATTCCTCAACGAGTACA 1200  
 QY 1704 ACTTCGAAAGTTTTCACAGACAGCTTCATTTGGCAATCCGATCTTTGGGGTGTGGC 1763  
 DB 1201 ACTTTACAGAGTTTCCCCCTGACAGTTTCATTTGAAAACTCGATCTTTTGTGTGATTTGGC 1260  
 QY 1764 TAAATCAGCCGTGTCATGATATCTGTGAACTGATGAGTGTCAATCTTAAGACAGCTA 1823  
 DB 1261 TGAATTTGCGGTGTCATGAGTGTGCGCCCTTCAAGCGAGTTACATTAATCTTAAGCTGCA 1320  
 QY 1824 TTTCTTGAATAGCTATTTGGGGGACTTGTGATCTTTTCATGCTCTTAATAGCAGCTTGGC 1883  
 DB 1321 TTTCTTGAATTAATCTTTGGTGTGCTGTGATCTTTATGTGTATGCTGTGCACTTGGC 1380  
 QY 1884 GACCGCAATATCCCTCCCTTTCTTGTATGAGTCACTTGAACAAACGATTAATTCGA 1943  
 DB 1381 GACCAATATGCTCTCTCTCTCTTCTGTGATGATTAATTAACAAACGATTAATTTCTCC 1440  
 QY 1944 CACCGAAGCTCGTCACTCTTCATATGAACATGACATCCAGTTTACGAGATATCATGA 2003  
 DB 1441 CCCCAAGGCTAGTATCTTCAATATGAATATGACATCAATGTTATGAAGATATCATGA 1500  
 QY 2004 GAATGACAGAAATCTTAAGTGAAGATTAATCATTTGGGACGAGCATCAAGCAGCTGAT 2063  
 DB 1501 GGATGACTGAAACCTGAGTGAAGATTAATTAATGATATGAGCATCAAGTACAGATTT 1560  
 QY 2064 ACAATGTTGTTTGAAGATTTGAACCGGTTGATGATTAAGCGGCTTTACTCTCAAC 2123  
 DB 1561 ATTAATGTTGTTTGAAGATTTGAACCGGTTGATGATTAAGCGGCTTTACTCTCAAC 1620  
 QY 2124 CACAGTCAATGAACAGTTTGAACAGAACTGAGATGCTTAAGTACATCAAGCAGCA 2183  
 DB 1621 CCCAATGATTAATGAAGATTTGAACCTGATGAGCGGTTGCGACATCAAGCAGCGGA 1680  
 QY 2184 ATCTTGTGAGCTTAAGAGCTTATTCCTCTCTCACTTTGGGAGTCTTGTCTTATGACT 2243  
 DB 1681 ATCTGTGAGCTTAAGAGCTTATTCCTCTCTCACTTTGGGAGTCTTGTCTTATGACT 1740  
 QY 2244 ATTTGGAATATGAGGCTCTGGGATCTTCTTCAATGAGCCCTAAGAGAAAAAGCTGTTG 2303  
 DB 1741 ACATGGAATATGAGGCTCTGGGATCTTCTTCAATGAGCCCTAAGAGAAAAAGCTTGTG 1800  
 QY 2304 ATTTGGAACACAGGCTTAAGATGACATATGATGAGCAGCAAGATTTAGCTTATCTACACC 2363  
 DB 1801 ACTGGAGAGCTGCTTAAGATTAAGCACTTGAAGCAGCAAGAGGCTTGTATCTACACC 1860  
 QY 2364 ATGACTGATGCTCAAGGATCTTACAGAGACGTTGAAGTGTCTCAACATTTCTTGGACA 2423  
 DB 1861 ATGATTCGCTGCTCAAGGATCTTACAGAGATGTTGAATCATCTTAACATCTTATGATG 1920  
 QY 2424 AAGACTTGAAGGCTGTTTGAAGATTTGGAATGAGCAAAAGCTTGTGTGCAAGT 2483  
 DB 1921 CAGACTTGAAGGCTGATCTCACTGATTTTGTGTATGAGCAAAAGCTTGTGTGCAAGT 1980  
 QY 2484 CACATACTTCAACTTACGATGATGAGCAGATAGTATCATATGACCCGAGTATGCTGCA 2543  
 DB 1981 CCCATTACTTCACTTACATTAATGAGCAAAATTTGCTATATGACCCGAGTATGCTGAA 2040  
 QY 2544 CTTTACGAGCTCACTGAAGATTCGATGCTTACAGTTATGAAATGTCTTTTGAAGTGT 2603  
 DB 2041 CTTTACGAGCTCACTGAAGATTCGATGCTTACAGTTATGAAATGTCTTTTGAAGTGT 2100  
 QY 2604 TAAACCGAAGAAAGCGTTGATGAGCAAGATTCATTCACCATGATATGCAAGA 2663  
 DB 2101 TAACTGGAAGAAAGCGTTGATGAGCAAGATTCATTCACCATGATATGCAAGG 2160  
 QY 2664 CCGGGAACAATGAAGTATGAGAAATGGCAGATCCAGACATCAATCAAGCTGTAAAGATC 2723

DB 2161 CAGCAACCAATGCAAGTATGAGAAACAGTTGATCCAGACATTAATGCAATGCAAGGACC 2220  
 QY 2724 TCGGTGTGGAAGAAAGTTTCCAACTGGCACTCCGATATGCAACAAAGACAGCCGATG 2783  
 DB 2221 TAGAGCTGTAAAAAGGTTTATCAGCTTGTCTTATTAATGCAAAAGAGGACGAGCTG 2280  
 QY 2784 ATGACCCCAATGCAACAGAGTACTGTGTCTGCGACATTTTATGCTATC----- 2835  
 DB 2281 ATAGGCCGAAATGCAAGAGTGAACAGTACTCCGAGACCTTGTGTCTCAAGCACC 2340  
 QY 2836 -----GGAACAACCACTGTGCGACTGACACGTCAGGACGCTGCGTGTGCT 2888  
 DB 2341 CACCAAGCAACTAGCTGACACTACACCTGCTTCAATCATGTGCAAGGTCACATGCT 2400  
 QY 2889 ACGTCAATGATATGCAATCTCAAGACTCCGATTCGTGATGCTGCTTCATGAGT 2948  
 DB 2401 ACGGATGATGATGCAAACTCAAGACTCACACTTGATGAACTGCTTCAATGAGCA 2460  
 QY 2949 CTTCTGATGCTCAACTGTTCTTCTGTTTGGACAGTTATTTCTCAGAACAGTGAAT 3005  
 DB 2461 CTTCAATGCTCAACTCTTCTCAAGTTTGGAGAAATCTCTCAAAACAGTGAAT 2517  
 RESULT 6  
 AED28154  
 ID AED28154 standard; cDNA; 3089 BP.  
 XX  
 AC AED28154;  
 XX  
 DT 01-DEC-2005 (first entry)  
 XX  
 DE Arabidopsis thaliana ERECTA paralog; ERL2 cDNA.  
 XX  
 KW Plant growth regulation; transgenic plant; crop improvement; transgene;  
 KW ERL2; gene; ss.  
 XX  
 OS Arabidopsis thaliana.  
 OS  
 XX  
 FH Key Location/Qualifiers  
 FT 186..3089  
 FT CDS /tag= a  
 FT /product= "Arabidopsis thaliana ERL2 protein"  
 XX  
 PN US2005223428-A1.  
 XX  
 PD 06-OCT-2005.  
 XX  
 PF 30-DEC-2004; 2004US-00027304.  
 PF  
 PR 01-APR-2004; 2004US-0558529P.  
 PR  
 XX  
 PA (TORI/) TORII K U.  
 PA (SHPA/) SHPAK B D.  
 XX  
 PI Torii KU, Shpak BD;  
 XX  
 DR WPI: 2005-675788/69.  
 DR P-PSDB: AED28155.  
 DR  
 XX  
 PT Modulating plant height and organ shape comprises expressing, in plants,  
 PT a transgene encoding an ERECTA-like protein lacking an active kinase  
 PT domain.  
 XX  
 PS Disclosure; SEQ ID NO 7; 72bp; English.  
 PS  
 CC The present invention relates to a method for modulating plant height and  
 CC organ shape. The method involves expressing a transgene in a plant, where  
 CC the transgene encodes an ERECTA-like protein lacking an active kinase  
 CC domain and where expression of the transgene modulates plant height or  
 CC organ shape. ERECTA protein contains leucine-rich repeat receptor-like  
 CC kinase (LRR-RLK) with 20 consecutive leucine-rich repeats (LRR) and  
 CC functional Ser/Thr kinase activity. The invention is useful for producing



transgenic plant and for enhancing the yield of a crop plant. The present sequence is the Arabidopsis thaliana ERECTA paralog, ER12 cDNA.

XX Sequence 3089 BP; 866 A; 682 C; 653 G; 888 T; 0 U; 0 Other;

Query Match 36.6%; Score 1161.8; DB 14; Length 3089;

Best Local Similarity 65.2%; Pred. No. 0;

Matches 1760; Conservative 0; Mismatches 927; Indels 12; Gaps 3;

```
QY 150 AGGAGGAGCAACCTTCTGTGAGATTGAAGAGTATTCAAGATGTGAACATGTTCTT 209
DB 274 ACGAAGAGAAAAGCTTATGCGATGAAGAGCTTCATTCAGCAAGTCGCGAATATGCTTC 333
QY 210 ATGACGACAACTTCACTTCTTGGATTATGTCGTGGAGAGGTCGTCCTTGAAA 269
DB 334 TTGATTGGAGCATGTTCAATACACAGCTTTTGTCTTGGAGGGTGCTTCTTGATATA 393
QY 270 ATGTCACCTTCAATGTTGTCCTTATATTGTTCAGATTGTAATCTTGATGAGAGAAATCT 329
DB 394 ACGTTACCTCAATGTTGTCCTTATCTGTCGAACCTGAAATCTTGATGAGAGATAT 453
QY 330 CACCTGCTATTGAGATCTCAAGATCTCTTGTCAATTGATCTGCGAGTATCGCTTGT 389
DB 454 CATCTGCCCTTGGAGATTGTGATGATCTGCAATCAATAGACTTGCAAGAAATTAATTGG 513
QY 390 CTGGAAGAAATCCCTGATGAGATTGGTGAAGTCTTCTTGGCAAAACTTGACTATCTT 449
DB 514 GTGTCAAAATTCAGATGAGATTGAAAAGTGTGTTCTCTGCTTATGTGATGATTTCTCA 573
QY 450 TCAATGAATTAAGTGTGACATACCGTTTTCGATTTGCAAGTTGAGCAACTTGAGAGC 509
DB 574 CCAATTTGTTGTTGAGAGACATACCGTTTTCATCTTCAATCACTGAACAGGTGAGTTTC 633
QY 510 TGATTTGAAAGATTAACCAATTGATAGACCGATCCCTTCAACCTTCAAGATTTCCA 569
DB 634 TGAACCTTAAGATTAATCAAGCTCACTGCTCAATACAGACAACTTCACTCAGATTTCAA 693
QY 570 ACCGGAATTTCTGGACTTGGCAGAGATAAATCACTGAGTGAGATGCAAGACTTATTT 629
DB 694 ACCTTAAGACCTTGACCTGCAAGAAACAGCTTACCTGAGATACCAAGATTACTCT 753
QY 630 ACTGGAATGAAGTCTTCAGATCTTGGGTTGCGAGAAACAATTGATGCGGTAACTT 689
DB 754 ACTGGAATGAAGTCTTCAGATCTTGGGTTGCGAGAAATGTTAACTGGAGATTTGT 813
QY 690 CTCCAGATTGTTGCACTGATCTGCTTTGTTGTTGACGTAAAGAAACAAGTTTGA 749
DB 814 CTCTGATATGTGTCAGCTGACGGGTCTGTGTACTTGTGATGTGAGAGCAACACTTA 873
QY 750 CTGTGATATACCTGAGACAGATAGGAAATGCACTGCTTCCAGCTTTTGGACTTGTCT 809
DB 874 CTGGAATCTATCCAGAGAGATTGGCAATGCAACAACTTTGAGATCTTGGATGATCTT 933
QY 810 ACAATGACTTAACCTGATGAGATCCCTTTTTCATCTGCTTCCAGTTGCAACTTAT 869
DB 934 ATATGATGATTAACCGAGATTAATACCTTAACAATATTTGTTTCTCCAGTACTCTGT 993
QY 870 CATTGCAAGCAATCAACTCTCTGGGAAAGATTCAATGATGATTTGTTCAATGCAAGCCC 929
DB 994 CACTTCAAGAGAAACAAGTTGACTGGCAGAAATTCGGAAGATGATGTTCTGATGAGGCTC 1053
QY 930 TTGAGCTTAAGATCTGATGAGCAACTTGTGATGATGATCTATCCCTGATCTTGGAA 989
DB 1054 TTGCTGATGATGATTTGATGATGATGATTAATTAATCTGGGCTTATTCACCAATATCTTGG 1113
QY 990 ATCTTACTTTCAACCGAGAAATTTGATTTGCAAGTAAACAAGTGAATGTTCAATTCAC 1049
DB 1114 ATCTGATTAATCAACGAGAAATCTGATCTCAATGCAAGTCAAGTCACTGCAAAATTCAC 1173
QY 1050 CTGAGCTTTGGAACATGTCAAAATCTCAATTAACCTGGAACCTCAATGATTAATCTTCAAG 1109
DB 1174 CCGAGCTAAGCAATATGTCAGCACTCAGCTAATTTGCAACTTAATGATTAATGATTAAGT 1233
```

```
QY 1110 GTCATATACCACAGAGCTTGGAGACTTACTGACTGTTTGTGATCTGAATGTGGCCACAGA 1169
DB 1234 GAAAGATCCCACTGAGCTTGGAGACTGGAACAATTTGTTGCAAGTGAATCTTGGCAACT 1293
QY 1170 ATGATCTGGAAGAGCTTAATCTGATCACTGATCTGCTTGGCAAAATCTTAACAGCTTAA 1229
DB 1294 ACAATCTTGGAGGCTGATTCATCTTAACATTAAGTTCTGTGTGCTTGGATCAATTTCA 1353
QY 1230 AATGTCATGGAACAAGATTGAGGACATTAACCCGAGATTTCAAAAGCTGGAAGATA 1289
DB 1354 ATGTCATGGAACCTTCTGATGAGAGCTGTATCACTTGAATTCGGAATCTTGAAGCT 1413
QY 1290 TGACTTAACCTTAATCTGTCCAGACAAATATCAAGGTCGAATCCCGTTGAGCTATCTC 1349
DB 1414 TGACTTATCTTAATCTTCTCTCAACAGTTTCAAGGGCAAAATATCTGCTGAGACTTGGCC 1473
QY 1350 GATTCGGTAACTTAATGATTAATGATCTTCCAAACAAGATTAATGATCAATTCCTT 1409
DB 1474 ATATCAATCAATCTGATTAATGATGATCTGTGCGCAACAAATTTCTGAGGCTCAATTCAT 1533
QY 1410 CTTCCTTGGTGAATTTGAGACATCTTCAAGATGAACCTTGAATGAATCAATTAATCTG 1469
DB 1534 TAAACATGATGATCTTGAACATCTTCTCATCTTAACCTTGAACAGAAATCAATCTGATG 1593
QY 1470 GTGTAGTTCAGGCGACTTGGAAATCTTAAGAGCATCAATGAATAGATCTTCAAAATA 1529
DB 1594 GCACATTCCTCGAGAAATTCGGAACCTCGGAACATCAATCAATCAATGATGTCTATTA 1553
QY 1530 ATGATATCTCTGGCCCAATTCAGAAAGCTTAACCAATTAACGAATCAATTAATTTCTGA 1589
DB 1654 ATTTCTTGGCGGTGATTAATCCAACTGAACCTTGGCAGATGCGAAGATTAATCTCTGTA 1713
QY 1590 GACTGGAATTAATTAACCTGATCTGATGATGATGATGATGATGATGATGATGATGATG 1646
DB 1714 TACTGAACAACAAGATTAATCAATGATGATGATGATGATGATGATGATGATGATGATG 1773
QY 1647 TCACTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1706
DB 1774 TTGCAATCTGGAACATCTCTTCAATTAATCTTCTGGAATTAATCCCACTTAAGAGACT 1833
QY 1707 TCTCAAGATTTTACAGAGACAGCTTCAATGGAATCTGCTTGGTGGTGGTGGTGGTGGT 1766
DB 1834 TTACAGATTTTCCCGGCGAGCTTCTTGGAAATCAATTTCTGCGGGAACTGGGTTG 1893
QY 1767 ACTCAACGTCATGATCTCTGTCGAATCTGATGATGATGATGATGATGATGATGATGATG 1826
DB 1894 GATCAATCTGTGGCCCATCTTAACCTTAAGTCAAGATGATGATGATGATGATGATGATG 1950
QY 1827 TTGGAATGATGATTTGGGGGACTGTGATCTTCTCAATGATGATGATGATGATGATGATG 1886
DB 1951 TTGATGATGATCTGCGTTTCACTCTCAATGATGATGATGATGATGATGATGATGATGATG 2010
QY 1887 CGCATTAATCTCTCTCTCTTCTTGTGATGATCACTTGAACAACAGTAACTTATTCGAC 1946
DB 2011 CAAGAGAGAGAGAAACAGCTTGAAGGCTTCAAAACAAAC-----CTGAAGGCTCA 2064
QY 1947 CGAAGCTGTCATCTTCAATTAATGAATGAGCACTCAAGCTTTACAGAGATTAATGAGAA 2006
DB 2065 CGAAGCTGTCATCTTCAATTAATGAATGAGCACTCAAGCTTTACAGAGATTAATGAGAA 2124
QY 2007 TGAACAGATCTTAAGGAGATTAATCAATTTGGGACGAGCATCAAGCATGATATCA 2066
DB 2125 TTACAGAAACCTGATGAGAAATCAATCAATTTGATGATGATGATGATGATGATGATGATG 2184
QY 2067 AATGTGTTTGAAGATTTGAACCGGTTGCAATTAAGCGGCTTATCTGCAACCCAC 2126
DB 2185 AGTGAACCTTCAAACTTCCCGACCTATTTGCAATTAAGGAACTCAATCAATCAATTCAC 2244
QY 2127 AGTCATGAAGAGCTTTGAACGAGACTGAGATGCTTAATGATCAATCAAGCAAGAAATC 2186
DB 2245 GCAACTTCGCGGATTTGAACGAGCTGAGCAATTTGGAGCAATCAACAGAAAC 2304
QY 2187 TTGTGAGCTTAACAGGATTAATCTCTCTCACTTGGGAGTCTTCTGTTCTATGATTAAT 2246
```



QY 731 GTAAGAAACAAGTTGAGTGTATACCTGAGACGATAGGAATGCACTGCTC 790  
DB 664 GTGAGAGAAATATCTAATCTGAGACCATCCGAGAGCATCGAAATGCAAGCTTT 723  
QY 791 CAGGTTTGGACCTTGTCTCAATCAGCTAACCTGTGATCCCTTTTGAATCGCTTC 850  
DB 724 CAATCTCTGACATCTTATTAATCAGATTAACAGGAGATTCCTTCAATATGGCTTC 783  
QY 851 CTGCAAGTTGCAATATCTATCTGCAAGGCAATCACTCTGTGGAAAGATTCCATGCTG 910  
DB 784 CTCCAAGTTCTCTCTGTCACTTCAAGGAAACAGATTGACGGGTAAATTCAGAAATT 843  
QY 911 ATTGCTTCAGAGAGCCCTTGGAGCTTATGATCTAAGTGGCAACTTGTGAGGCTCT 970  
DB 844 ATTGCTTATGACAGCTCTTGTCTTTGGATTGAGTACAAATGAGCTTTGTGCTCT 903  
QY 971 ATTCTCCGATCTCGGAAATCTTACTTTCACCGAGAAATTTATTTGACAGTAAACAG 1030  
DB 904 ATCCACCGATCTTGGCAATCTCTCATTTACCGGAAAGTTGATCTCCATGGCAATATG 963  
QY 1031 CTGACTGTCAATCTTCACTGAGCTTGGAAACATGTCAAAATCTCCATTAACCTGAACTC 1090  
DB 964 CTCACTGTCCAAATCCCTCTGAGCTTGGAAATATGTCAGTCTCACTTAATTTGCACTTA 1023  
QY 1091 AATGATATCATCTCAAGGGTCATATACCAACGAGCTTGGGAACTTACTGACTGCTT 1150  
DB 1024 AAGCAATATTAACCTAGTGGAACTATTCACCTGAGCTTGGAAAGCTGGAGCAATGTTT 1083  
QY 1151 GATCTGATGTGGCCCAACATGATCTGGAAGAGACTTATCTGATCTGAGCTTTCG 1210  
DB 1084 GAATGATCTTGGCAACCAACGTTTATGAGGGCCATACCATCCAACTTAATGTTCAATG 1143  
QY 1211 ACAATCTAAACAGCTTAAATGTTTATGAGGAAACAGTTTATGAGCACTATACCCGAGCA 1270  
DB 1144 GCAGCTTGAATCAATCAATGTTTCAATGAGGAACTCTTGAAGTATATTTCACTGAGCG 1203  
QY 1271 TTTCAAAAGTAGAAATGATGACTTACCTTAATCTGACAGCAACATTAACAAGTCCA 1330  
DB 1204 TTTGCGAATCTCGAGAGCTTGAATCTTAATCTTGTGCAACAAATTTCAAGGGGAAA 1263  
QY 1331 ATCCGCTTGAAGTATCTGATCTGATCGTAACTGATGATGATCTTTCACCAACAG 1390  
DB 1264 ATACGATTTGAGCTTGGACATATTAATCAATCTTGACAACTAATGCTGTGCGCAATTAAC 1323  
QY 1391 ATAAATGGAATCAATCTCTTCCCTTGTGATTTGAGACATCTTCTCAAGATGAACCTTG 1450  
DB 1324 TTTCTAGGGTCTATACCATTTAAGCTTGGGAGATCTTGAAACACTTCTCATATTAATCTT 1383  
QY 1451 AGTAGAAATCATATTAACCTGTGTAGTTTCAAGGCACTTGGAAATCTTAAGAACATCATG 1510  
DB 1384 AGCAAGAAACATCTGTAGTGAACATTAACCTGCAAGATTTGGGAACTTTCAGAACATTTGAG 1443  
QY 1511 GAATATGATCTTTCAATATATGATATCTGAGCCCAATTCAGAAAGACTTAAACCAATTA 1570  
DB 1444 ATGATTTGATATCAATCTGATCTGCTCGGAGTTATTTCCAACTGAACCTTGGCCAAATG 1503  
QY 1571 CAGACATTAATTTTGTGAGACTGGAATAATTAATTAACCTGATGTAATGTT---GGTTCA 1627  
DB 1504 CAAATTTTAAACTCTTAAATATTAAGCAACAAACAGCTTCATGGGAAATTTCCAGATCAG 1563  
QY 1628 TTAGGCAATCTGCTCACTGCTCACTGATTAATGATTAATCTAATTAACCACTCTGATGAT 1687  
DB 1564 CTTAAGCAATGCTTCACTTGTCAATCTGAATGCTCTTCAACCAATCTCTCCGGGATA 1623  
QY 1688 ATCCCTTAAGCAATTAATCTCTCAAGATTTTTCACAGACAGCTTCAATGCAATCTGCT 1747  
DB 1624 GTCCCAACCAATGAABAACTTCTGACGTTTGTCTCCAGCCAGCTTTGTGGAATTCATAT 1683  
QY 1748 CTTTGGGATGTTGGCTAAACTCAACGCTGATGATTTCTGTGAACCTGTAGAGATGCTCA 1807  
DB 1684 CTTTGTGGAACCTGGGTGATCTATTTGTGCTTCTTACGGAATCTCGA-----GTA 1737

QY 1808 ATCTTAGACAGACTATTTCTTGAATAGCTATTTGGGGGAACTTGTGATCTTCTCATGAGTC 1867  
DB 1738 TTCTCCAGAGGCTCTTGTGATCTGATTTGTTCTTGGGCTCATCTCTCTATGTATGATT 1797  
QY 1868 TTAATAGACGCTTGGCAGCCGATTAATCTCTCTCTTCTTGTGATGATCACTTGAACAA 1927  
DB 1798 TTCTTGGAGTTTAAACAATCAATGACAGAGAAAGATTTCTAACAAGCTC-----CTCA 1851  
QY 1928 CCAGTAACTTATTCGACACCGAAGCTCTGATCTTCTCATATGAATGAGCATGCACTCAAGTT 1987  
DB 1852 AAACAAGCTGAAGGTTTAAACCAAGCTTATGATTTCTCACATGAGCAATGCAATTCATPACA 1911  
QY 1988 TACAGGATATCATGAGAAATGACAGAGAAATCTAAGTAGAATATATTAATTTGGCCAGCA 2047  
DB 1912 TTTGATGATATCATGAGAGTACGATGAGATCTTAAAGAAAGTTTATATGATATGAT 1971  
QY 2048 GCATCAAGCAGCTGATPACAAATGTGTTTGAAGAAATTTGAACCGGTTGCAATTAACGG 2107  
DB 1972 GCTTCTAGCAGCGGTATACAAATGTGCAATTAAGTTCCCGACCTATTTGCCATTAAGCGCA 2031  
QY 2108 CTTTACTCTACAAACCCACAGTCAATGAAACAGTTTGAACAGAACTCGAGATGCTAAT 2167  
DB 2032 CTCTACATATGATATCCGATTAACCTTGGCGAAATTTTGAACAGAACTTGAACATTTGG 2091  
QY 2168 AGCATCAAGCAGAGAAATCTTGTGAGCTTACAAAGCTTATTTCCCTCTCACTTGGGAGT 2227  
DB 2092 AGCATTAAGCAGAAACATATGACATGATGATGATATGCTTGTCTCTACTGAGCAAC 2151  
QY 2228 CTTCTGTCTATGATCTATTTGGAATTTGAGTGGCTCTGAGATCTTTCATGAGCCCTAGC 2287  
DB 2152 CTTCTTTTCTATGATCAATATGAGAAATGATGATCACTTTGGGACCTTCTTATGGGTCAATG 2211  
QY 2288 AAAAAAAGACTTGTATTTGAGACACAGCGCTTAATATGATATGATGATGATGATGATGAT 2347  
DB 2212 AAAAAAGTAAAGTTTATTTGAGAGCAAGTTGAATGATGATGATGATGATGATGATGATGAT 2271  
QY 2348 TTAGCTTATCTACACCATGAGTACTGATCCAAAGGATATTTCAACAGAGCTGAAGTGTCC 2407  
DB 2272 CTAGCTTATCTTACCAAGATTTGATCTCTCTGATATTTACCTGATATCACTGATATGATG 2331  
QY 2408 AACATCTCTTGGACAAAGACTTGAAGGCTCTTTGACAGATTTTGAATTTGGAATTTGGAATTT 2467  
DB 2332 AACATCTCTTGAATGATGATGATTTGCAAGCAATTTATCTGATTTGGGATTTGCTAAGAG 2291  
QY 2468 TTGTGTGTCAAAAGTCAATCACTTCACTTACGTATGAGGCAAGTATGATGATGATGATG 2527  
DB 2392 ATACCAAGCTTGAAGAAACCATGCTCTGATGATGATGATGATGATGATGATGATGATGAT 2451  
QY 2528 CCGAGTATGCTGCACTTCAAGGCTCAGTGAAGAAATTCGATGATGATGATGATGATGATGAT 2587  
DB 2452 CAGAGTATGCTGTGATCTTCAAGATCAATGAGAAATCCGATATATACAGCTTCCGATAT 2511  
QY 2588 GTCTTCTTGTAGTTTGAACCCGAGAGAAAGCGTTGATGAGCAATCTCAATCTCCAACT 2647  
DB 2512 GTTCTTCTTGAAGTTCTCACTGAGAGAAAGCAAGTGTATGAGAACTTAACCTTGAATCA 2571  
QY 2648 CTGATATGTCAAAGACGGGGAACATGAATGATGAGAAATGAGCAATCAAGATCAAGATCA 2707  
DB 2572 CTGATATTTGTCAAAAGCTGATGATTAATCTGATGATGAGAGCAAGTGTATCTCAAGGTT 2631  
QY 2708 TCGAGTATTAAGATCTGAGTGTGAGAGAAAGTTTCACTGAGCACTCCATGAGCACC 2767  
DB 2632 GTGACTTGTATGAGCTTGGACATTAACAGAAAGCAATTTCAAGTGTCTCTTATATGACA 2691  
QY 2768 AAAAGACAGCCGAATGATGACCAACATGACACAGTACTGATGATCTCGGCACTTTT 2827  
DB 2692 AAGCGAAACCTTTAAGAGACCCACAAATGCTTGAAGTCTTGAAGGTTCTGAGCTCTCTT 2751  
QY 2828 ATGCTATCGGAACACCAACC 2847  
DB 2752 GTCCCATCTCTGCAAGTAC 2771

```
RESULT 8
AED28152
ID AED28152 standard; cDNA; 3100 BP.
XX
AC AED28152;
XX
DT 01-DEC-2005 (first entry)
XX
DE Arabidopsis thaliana ERECTA paralog, ERL1 cDNA.
XX
KW Plant growth regulation; transgenic plant; crop improvement; transgene;
XX ERL1; gene; ss.
XX
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
FT CDS 200..3100
FT /tag= a
FT /product= "Arabidopsis thaliana ERL1 protein"
XX
PN US2005223428-A1.
XX
PD 06-OCT-2005.
XX
PF 30-DEC-2004; 2004US-00027304.
XX
PR 01-APR-2004; 2004US-0558529P.
XX
PA (TORI/) TORII K U.
XX (SHPA/) SHPAK E D.
XX
PI Torii KU, Shpak ED;
XX
WP1; 2005-675788/69.
XX
DR P-PSDB; AED28153.
XX
XX
XX Modulating plant height and organ shape comprises expressing, in plants,
PT a transgene encoding an ERECTA-like protein lacking an active kinase
PT domain.
XX
XX Disclosure; SEQ ID NO 5; 72pp; English.
XX
XX
XX The present invention relates to a method for modulating plant height and
CC organ shape. The method involves expressing a transgene in a plant, where
CC the transgene encodes an ERECTA-like protein lacking an active kinase
CC domain and where expression of the transgene modulates plant height or
CC organ shape. ERECTA protein contains leucine-rich repeat receptor-like
CC kinase (LRR-RLK) with 20 consecutive leucine-rich repeats (LRR) and
CC functional Ser/Thr kinase activity. The invention is useful for producing
CC transgenic plant and for enhancing the yield of a crop plant. The present
CC sequence is the Arabidopsis thaliana ERECTA paralog, ERL1 cDNA.
XX
XX
SQ Sequence 3100 BP; 874 A; 647 C; 650 G; 929 T; 0 U; 0 Other;
XX
Query Match 35.0%; Score 1112.8; DB 14; Length 3100;
Best Local Similarity 63.9%; Pred. No. 0;
Matches 1738; Conservative 0; Mismatches 967; Indels 15; Gaps 3;
XX
QY 131 GTAGCTACTGTGACTTCAGAGAGAGAGCAAGCTTGGCTGGAGATTAAAGTCAATTCAA 190
DB GTTGGCTTCGGCTATGAAACAAGAGGAAAGCTCTGATGGCGATAAAAGGCTCTTTGAGC 322
QY 191 GATGTGAACAATGTTCTTTATGACTGGAGCAACTTCACTTCTTGATTTATGTGTGG 250
DB AACTTAGTAATATGCTTTTGGATTGGAGCATGTTCAACAAGTACTGTGTCTTGG 382
QY 251 AGAGGTGTCTTGTGAAATGTCACTTCAATGTGTGTCTTAAATTTGTCAATTTG 310
DB CGAGGTGTTTTCTCGACAACGTTAGCTACTCCGTGTCTCTGAAATTTGTCAAGTCTG 442
QY 311 AATTTGATGGAATAATCTCACTGCTATTGGAGATCTCAAGAGTCTTCTCAATTGAT 370
DB AATCTTGAGGAGAGATATCTCCAGCTATTGGAGCCCTAACGAAATTTGCAATTAATGAC 502
```

```
QY 371 CTCGAGATATCGCTTGTCTGGACAAATCCCTGATGAGATTGGTACTGTTCTTTG 430
DB TTGCAAGATTAATACTAGACAGGTCAAAATCCAGATGAGATTGGAACTGTGTTCTTT 562
QY 431 CAAAACCTTAGACTTATCTTCAATGAATTAAGTGTGACATACCGTTTTCGATTGCAAG 490
DB GTTTATCTGGATTGTCCGAGAAATCTGTTATATGAGACATACCTTTCATCTCTAA 622
QY 491 TTGAGCAATTGAGCAGCTGATTTCTGAAGAAATACCAATGATATGAGACCGATCCCTCA 560
DB CTCAGCAGCTTAAACTCTGAATCTGAAGAAACAATCAGCTCACAGGTCTTGTAACGCA 682
QY 551 ACACTTTCACAGATTCCTCAAACTGAAAATTTCTGACTTGGACAGATAAATCACTGATGT 610
DB ACCTTAACCCAGATTCCTCAAACTTGAAGACTTGATCTTGCTGGCATATCTAAGGGT 742
QY 611 GAGATACCAAGACTTATTTATCTGAAATGAAGTTCCTTCAATCTTGAGTTGCGAGAAAC 670
DB GAGATATCGAGATTGCTTTACTGGAATGAAGTTTTCAGATATCTTGGAATACGAGGAAT 802
QY 671 AACTTACTCGGTAAACATTTCTCAGATTTGTGCAATGACGTGCTTGTGATTTTGAAC 730
DB ATGTGACTGGAACGTTATCTTCTGATATGTGTGACGTAACGGTTTGTGTACTTTGAT 862
QY 731 GTAAGAAACAACAGTTTGAAGTGTAGATATCTGAGACGATAGAAAATTCAGTGCCTTC 790
DB GTGAGAGGAATATATCTAATCTGAACCATCCGGAGAGCATGGAAATTCACAAAGCTTT 922
QY 791 CAGGTTTGGACTTGTGCTCAATCAATCACTGATACGTGTGAGATCCCTTTTGACATCCGCTTC 850
DB CAATCTCTGACATATCTTATATCAAGATTAACGAGAGATTTCTTACATATCCGCTTC 982
QY 851 CTCGAGTTGCAACATTTATCATTTGCAAGCAATCACTCTCTGGAAGATTTCATCAGTG 910
DB CTCGAGTTGCTACTCTGTACTTCAAGGAAACAGATTCGCGGTGAATTTCCAGAAAGTT 1042
QY 911 ATTGCTCTCAATGCAAGCCCTTGGAGCTTATGATCTAATGAGGCAACTTGTGATGATCT 970
DB ATTGCTCTATGACAGGCTCTGCGTTTGTGATTTGATGATGACAAATGACGTTGTGGTCT 1102
QY 971 ATTCTCCGATTTCTCGGAATCTTACTTTCACCGAGAAATTTGATTTGACAGATTAACAG 1030
DB ATCCCAACCGAATCTTGGCAATCTCTCATTTACCGGAAAGTTGATCTCCATGCAATATG 1162
QY 1031 CTGACTGCTTCAATTCACCTGAGCTTGGAAACATGCAAAATCCATTACTGGAATCTC 1090
DB CTGACTGCTCAATCCCTCTGAGCTTGGAAATATGTCACGCTTCAGCTATTGGACGTA 1222
QY 1091 AATGATATATCATCTCAAGGCTCATATPACCAACAGCTTGGAGAGCTTACTGACTGTTC 1150
DB AAGCAATATTAACATGAGGAACTATTCACCTGAGCTTGGAAAGCTGGAGCAATGCTTT 1282
QY 1151 GATCTGAATGTGGCAACAATGATCTGGAAGACCTTACTGATATCTGAGCTGTTCG 1210
DB CTGACTGCTCAATCCCTCTGAGCTTGGAAATATGTCACGCTTCAGCTATTGGACGTA 1222
QY 1163 CTGACTGCTCAATCCCTCTGAGCTTGGAAATATGTCACGCTTCAGCTATTGGACGTA 1222
DB 1223 AAGCAATATTAACATGAGGAACTATTCACCTGAGCTTGGAAAGCTGGAGCAATGCTTT 1282
QY 1211 ACAATCTAACAAGCTTAAATGTTCAATGGAGCAAGTTTGTGCACTATATCCCGAGCA 1270
DB 1271 TTTCAAAAGCTAAGAAATATGACTTAACTTATCTGTCCAGACAATATCAAAAGTCCA 1330
DB 1343 GCAAGCTTGAATCAATTCATTAATGTTTCATGGAACCTCTTGAGTGAATCTTCCACTGGCG 1402
QY 1403 TTTCGCAATCTCGGAGCTTGAATTAATCTTAATCTTTCGTCGAACAATTTCAAGGGAAA 1462
DB 1331 ATCCCGGTGAGCTATCTGATACGATTAATCTGATACATTTGATCTTTCGAACAACAG 1390
DB 1463 ATACCAAGTTAGCTTGAACATATTAATCAATCTTGACAACTAATCTGTCTGCAATTAAC 1522
QY 1391 ATAATGGAATCAATTCCTTCTGCTGATGATTTGGAGCATCTTCAAGATGAATCTTG 1450
DB 1523 TTCTCAGGCTCTAATACATTAAAGCTTGGAGATCTTGAACACCTTCTCAATTAATCTTT 1582
```

1451 AGTAAATCATATTAACGTGTAGTTCAGGCGACTTTGGAAATCTAAGAGCATCATG 1510  
1583 AGGAGAAACCATCTTACTAGCAATTAACCTGAGAGTTGGAACTTCGAGAGATTCCAG 1642  
1511 GAAATGATCTTTCAATTAATGATATCTGCGCCCAATTCAGAGAGCTTTAACCAATTA 1570  
1643 ATGATGATGATATCAATCAATCTGCTCCGAGATTATCCAACTGAACCTTGGCAATTTG 1702  
1571 CAGAACTAATTTTGGGAGACTGGAATAATTAACCTGACTGATATGTT---GGTTCA 1627  
1703 CAGAAATTAACCTTTAATTAATTAAGACAACAAGCTTCAATGGGAAATTTCCAGATCAG 1762  
1628 TTAGCCAACTGCTCACTGCTCACTGATTAATGATATCTCATATAACAACCTGATAGTAT 1687  
1763 CTTAACGAAGCTTCACTCTTGTCAATCTGAATCTCTTCAACAAATCTCTCCGGATA 1822  
1688 ATCCCTAAGAACATTAATCTTCAAGATTTTCAACAGACAGCTTCATTTGCAATCTGCTG 1747  
1823 GTCCCAACCAATGAAAACTTCTCAGCTTTTGTCTCAGCCAGCTTTGTGGAAATCCATAT 1882  
1748 CTTTGGGTAGTGTGGCTAACTCAGCGGTGATGATTTCTGTGGAATGTACAGAGTGTCA 1807  
1883 CTTTGTGGAACTGGGTGGATCTAATTTGTGTCTTTACGAAATCTCA-----GTA 1936  
1808 ATCTTAGAGCACTAATCTTGGAAATAGCTAATGGGGGACTTGGATCTTCTCATGTGC 1867  
1937 TTCTCCAGAGGTGCTTGTGATCTGATTTCTTGGCGTCACTCTCCTATATGATAT 1996  
1868 TTAATAGCAGCTTCCGACCGCATTAATCTCTCTTTCTTGAATGATCACTTGACAA 1927  
1997 TTCTTGCAGATTACAATCAATGACAGAGAGAAATTTCAAGAGCTC-----CTCA 2050  
1928 CCACTAATCTTATTCGACCGGAGCTGCTGATCTCTCATATGAAACATGGACCTCCAGTT 1987  
2051 AAACAAGCTGAAGGTTTAACCAAGCTGATATCTTCCACATGACATGGAATTCATACAA 2110  
1988 TACGAGATATCATGAGATGACAGAGAAATCTAAGTAGAATATCATTTGGGACGGA 2047  
2111 TTTGATGATATCATGAGAGTGAAGTGAATCTTAACGAAAGTTTAAATTGATATGT 2170  
2048 GCATCAAGCAGCTGATTAACAATGTGTTTGAAGAAATGTAACCGGTGCGATTAACGG 2107  
2171 GCTTCTAGCAGCGTATATCAATGTGCAATTAAGTTCCGACCTAATTTGCCATTAAGCGA 2230  
2108 CTTTATCTTCAACAACCGACAGTCAATGAACAGTTTGAACAGAACTCGAGATGCTAAT 2167  
2231 CTCTCAACATAGTATCGCATTAACCTGGGAAATTTGAGACAGAACTTGAGACCATTTGG 2290  
2168 AGCATCAAGCAGAAATCTTGTGAGGCTCAAGCTTATCCCTCTCTCACTTGGGAGT 2227  
2291 AGCATTTAGGCAAGAAACATAGTCAAGCTTTCATGATATGCTTGTCTCTACTGGGAC 2350  
2228 CTTCTGTTCTATGACTAATTTGAAATGATAGCTCTGGAGTCTTCTCATGGCCCTACG 2287  
2351 CTTCTTTTATGACTATGAAATGATGATCACTTTGGACCTTCTTCAATGGGTATTTG 2410  
2288 AAAAAAAGACTCTTGATTTGGGACACACGCTTAAGATAGATATGATGACACAAAGT 2347  
2411 AAAAAAGTGAAGCTTGGTTGGGAGACAAAGTTGAAGATACCGGTGGAGCTGCACAAAGA 2470  
2348 TTAGCTTATCTACACCATGACTGATCCAAAGATCTTACAGAGACGTGAAGTGCCTCC 2407  
2471 CTAGCCATTTTACCCAGATTTGATCTCTCGAATCTTACCGTGAATCAAGTATCTCG 2530  
2408 AACATTTCTTGGACAAAGACTTGAAGGCTCGTTTGAACAGATTTTGGAAATAGCGAAAGC 2467  
2531 AACATATCTTGTATGAGATTTGAAAGCACATTAATCTGATTTGGGATTTGCTAAGAGC 2590  
2468 TTGTGTGTGTCAAAGTACATCTTCACTTAAGTATGATGAGCGATAGCTTACATAGAC 2527  
2591 ATACCAAGTACGAAACCCATGCTCGACTTAATGTTTGGGAAACAATGGTATATATAGAC 2650  
2528 CCGAGTATGCTGCACTTCAACGGCTCACTGAGAAATCCGATGTCTACAGTTATGAAATA 2587

2651 CCAGAGATGCTGTACTTACGAATCAATGAGAAATCCGATATATACAGCTTGGTATT 2710  
2588 GTCTCTTGTAGTGTGTTAAACCGAGAAAGCCGTGATGAGCAATCCAACTCCACAT 2647  
2711 GTCTCTTGTAGTGTGTTCACTGGGAAAGAAAGCATGTGAATTAACAACTTAATTTGCA 2770  
2648 CTGATATGTCAAAGACGGGAAACATGAAATGATGAAATGGCAGATCCAGACATCACA 2707  
2771 CTGATATTTGTCAAAGCTGATGATTAATCTGATGAAAGCATTAATCCAGAGTTACT 2830  
2708 TCAGCTGTAAAGATCTCGGTGTGTAAGAAAGTTTCCAACTGCACTCTATGACCC 2767  
2831 GTGACTTGTATGACTTTGGGACATATCAGGAAGACATTTACGTGCTCTTATACACA 2890  
2768 AAAAGACGCCGATATGAGACCCCAATGACACAGTACTGTGTTCTCGGACAGTTT 2827  
2891 AAGCGAAACCTTTTAAAGAGACCCCAATGCTTGAAGTCTTGAAGGTTGCTCTCTT 2950  
2828 ATGCTATCGGAACACACACC 2847  
2951 GTCCATCTCTGCAAGTTAGC 2970

RESULT 9  
AAT62125  
ID AAT62125 standard; DNA: 9295 BP.  
XX  
AC AAT62125;  
XX  
XX 10-JUN-1997 (first entry)  
DE Arabidopsis thaliana plant morphogenesis regulatory protein DNA.  
XX  
KW Plant; morphogenesis; regulation; short; stem; alteration; inflorescence;  
KW extraneous; gene; expression; transformation; increase; control; form;  
KW length; ds.  
OS Arabidopsis thaliana.  
XX  
XX Location/Qualifiers  
FH exon  
FT 1803..1881  
FT /tag= a  
FT 1882..2227  
FT /tag= b  
FT 2228..2366  
FT /tag= c  
FT 2367..2467  
FT /tag= d  
FT 2468..2539  
FT /tag= e  
FT 2540..2643  
FT /tag= f  
FT 2644..2715  
FT /tag= g  
FT 2716..2809  
FT /tag= h  
FT 2810..2878  
FT /tag= i  
FT 2879..2968  
FT /tag= j  
FT 2969..3040  
FT /tag= k  
FT 3041..3118  
FT /tag= l  
FT 3119..3190  
FT /tag= m  
FT 3191..3266  
FT /tag= n  
FT 3267..3338  
FT /tag= o  
FT 3339..3421  
FT /tag= p  
FT intron

```

FT exon 3422..3493 /*cag= g
FT intron 3494..3586 /*cag= r
FT exon 3587..3655 /*cag= b
FT intron 3656..3740 /*cag= c
FT exon 3741..3812 /*cag= u
FT intron 3813..3888 /*cag= v
FT exon 3889..3960 /*cag= w
FT intron 3961..4048 /*cag= x
FT exon 4049..4120 /*cag= y
FT intron 4121..4209 /*cag= z
FT exon 4210..4281 /*cag= aa
FT intron 4282..4349 /*cag= ab
FT exon 4350..4421 /*cag= ac
FT intron 4422..4508 /*cag= ad
FT exon 4509..4580 /*cag= ae
FT intron 4581..4706 /*cag= af
FT exon 4707..4778 /*cag= ag
FT intron 4779..4860 /*cag= ah
FT exon 4861..4932 /*cag= ai
FT intron 4933..5018 /*cag= aj
FT exon 5019..5090 /*cag= ak
FT intron 5091..5176 /*cag= al
FT exon 5177..5248 /*cag= am
FT intron 5249..5412 /*cag= an
FT exon 5413..5481 /*cag= ao
FT intron 5482..5576 /*cag= ap
FT exon 5577..5648 /*cag= aq
FT intron 5649..5726 /*cag= ar
FT exon 5727..5800 /*cag= as
FT intron 5801..5882 /*cag= at
FT exon 5883..6011 /*cag= au
FT intron 6012..6095 /*cag= av
FT exon 6096..6443 /*cag= ax
FT intron 6444..6519 /*cag= ay
FT exon 6520..6512 /*cag= az
FT intron 6891..6974 /*cag= aa
FT exon 6975..7328

```

```

FT /*cag= ba
XX JP09056382-A..
PN
XX
XX
XX 04-MAR-1997.
PD
XX
XX 24-AUG-1995; 95JP-00216187.
PE
XX
XX 24-AUG-1995; 95JP-00216187.
PR
XX
XX (CHIK-) ZH CHIKU KANKYO SANGYO GIJITSU KENKYU.
PA (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
XX
XX WPI; 1997-206629/19.
DR
XX
XX DNA encoding plant morphogenesis regulatory protein - useful to yield
PT plants with short stems or altered inflorescence.
PT
XX
XX Claim 6; Page 12-15; 17pp; Japanese.
PS
XX
XX The present sequence encodes an Arabidopsis thaliana plant morphogenesis
CC regulatory protein (MRP), which can be used to yield a plant with, e.g.
CC short stems or altered inflorescence. The MRP acts on a plant at a
CC specific site for a specific period, and can therefore be used to
CC regulate extraneous gene expression in a plant. The MRP's cDNA or genomic
CC DNA can be used to transform a plant to increase its MRP expression, and
CC therefore control the form (particularly stem length) of the plant
XX
SQ Sequence 9295 BP; 2873 A; 1581 C; 1602 G; 3239 T; 0 U; 0 Other;

Query Match 34.7%; Score 1102; DB 2; Length 9295;
Best Local Similarity 84.9%; Pred. No. 4e-312;
Matches 1376; Conservative 0; Mismatches 0; Indels 244; Gaps 3;

QY 1801 AGTGTCAATCTCTAGACGACTATTCTTGAATAGCTATGGGGACTGTGATCCCTCT 1860
DB 5881 AGTGTCAATCTCTAGACGACTATTCTTGAATAGCTATGGGGACTGTGATCCCTCT 5940
QY 1861 CATGCTCTTATAGACGCTTGGCCGACGATTAATCCCTCTTCTTGTGATGATCACT 1920
DB 5941 CATGCTCTTATAGACGCTTGGCCGACGATTAATCCCTCTTCTTGTGATGATCACT 6000
QY 1921 TGACAAAC----- 1928
DB 6001 TGACAAACGAGTCTACTCTCAAAACACTTTCGAATGTTCTTCACTTCAATGTAATC 6060
QY 1929 -----CAGTAACCTTATTCGACACGGAAGCTCGT 1956
DB 6061 CAATAGTTAATCCTTAATTTCTGTGTGACATGTAATTCGACACGGAAGCTCGT 6120
QY 1957 CATCTTCATATGAACTGACACTCCACGTTTACGAGATATCATGAGATGACAGAGAA 2016
DB 6121 CATCTTCATATGAACTGACACTCCACGTTTACGAGATATCATGAGATGACAGAGAA 6180
QY 2017 TCTAAGTGAAGATATATCATTTGGGACCGGACGATCAAGACCTGTATCAATATGTTT 2076
DB 6181 TCTAAGTGAAGATATATCATTTGGGACCGGACGATCAAGACCTGTATCAATATGTTT 6240
QY 2077 GAAGAATTTGAACCGGTTCCGATTAAGCGGCTTCTCTCAACCCCAAGTCATGAA 2136
DB 6241 GAAGAATTTGAACCGGTTCCGATTAAGCGGCTTCTCTCAACCCCAAGTCATGAA 6300
QY 2137 ACAGTTTGAAGACGAACTGAGATGCTAAGTACATCAAGACAGAAATCTTGAGCCT 2196
DB 6301 ACAGTTTGAAGACGAACTGAGATGCTAAGTACATCAAGACAGAAATCTTGAGCCT 6360
QY 2197 ACAAGCTTATTCCTCTCTCACTTGGGAGCTTCTGTCTATGACTATTGGAAAAATG 2256
DB 6361 ACAAGCTTATTCCTCTCTCACTTGGGAGCTTCTGTCTATGACTATTGGAAAAATG 6420
QY 2257 TAGCCTCTGGGATCTTCTTCAAT----- 2278
DB 6421 TAGCCTCTGGGATCTTCTTCAATGTAAGTCTCATCCGCAAAATAGAAAAATTATTGAAT 6480

```





QY 348 TCAAGACTCTTGTCAATTGATCTCGAGGTAATCCGTTGTCGACAAATCCCTGATG 407  
DB 182 TGAATGATCTGCATCAATAGACTTGGAGGAAATTAATTGGGTGCTCAATTCGACAT 241  
QY 408 AGATTGTCATCTCTTCTTTCGAAAATTAGACTTATCTTCAATGAAATTAAGTGTG 467  
DB 242 AGATTGGAAACTGTGTTCTCTGCTTATGTGAGATTTCTCCACCAATTTGTGTTGAG 301  
QY 468 ACATACGCTTTTGATTTGCAAGTTGAAGCACTTGACAGCTGATTCGTAAGAAATAAC 527  
DB 302 ACATACGCTTTTCAATCTTAACTCAAAACAGCT----- 335  
QY 528 AATTGATAGACCGATCCCTTCAACACTTTCACAGATTCCAAACTGAAAAATTCGACT 587  
DB 336 -----GACCTTAACTCAGATTCCAAACTTAAAGCCCTTGACC 373  
QY 588 TGGCAGCAATTAACCTCAGTGTGAGATCCAAAGACTTATTTACTGGAAATGAATCTTTC 647  
DB 374 TCGCAAGAAACAGACTTACGTGTAGATACCAAGTTACTCTACGGAAATGAATTTTAC 433  
QY 648 AGTATCTTGGGTTGCGAGAAACAATTAGTCGGTAACTTCTCCAGATTTGTGCAAC 707  
DB 434 AGATCTCGGTTTACGTGGAAATATGTTAACTGGGACATGTCTCTGATATGTGTGAC 493  
QY 708 TGACTGTCTTTGGTATTTTGAAGTAAGAAACAACAGTTTGACTGTAGATATACCTGAGA 767  
DB 494 TGAAGGCTGTGTGTACTTTGATGTGAGGCAACACCTTACCTGGAACATATCCCAAGA 553  
QY 768 CGATAGAAATTTGACCTGCTTCAAGTTTGGACTTGTCTACAAATCAGCTAACCTGTG 827  
DB 554 GCATTTGCAATTTGACAGACTTTAGATCTTGAATGATCTTAAATCAAGATTAACCGGAG 613  
QY 828 AGATCCCTTTTGAATGATGCGCTTCTGCAAGTTGCAACATTAATCAATGCAAGGCAATCAAC 887  
DB 614 TTATACCTTCAATATTTGTTTCTTCCAGTAGTACTCTGTCACTTCMAAGAAACAAGT 673  
QY 888 TCTCTGGGAAGATTTCATCACTGATGTGTCTCATGCAAGCCCTTGACAGCTTATGATCTAA 947  
DB 674 TGACTGGCAGAAATCCGGAAGTATGTGTCTGATGCAAGGCTCTTGATATTTGATTTGA 733  
QY 948 GTGGCACTTGTGAGTGTATCTATCTCTCGGATTTCTCGAAATCTTACTTTTCCCGAGA 1007  
DB 734 GTGCAATGAAATTAATCTGGGCTTATTCACCAATTAATCTTGGGAATCTGTCACTTCGAAA 793  
QY 1008 AATGTATTTTGCACAGTAAACAAGCTGACTGTTCAATTTCCACTGAGCTTGGAAACAAGT 1067  
DB 794 AACTGTATCTCCAGAGCAACAAGCTCACTGSAACAATCCACCGAGCTAGGCAATATGT 853  
QY 1068 CAAAACCTCCATTACCTTGAAGCTCAATGATTAATCTTCAAGGTCATTAACACACAGAGC 1127  
DB 854 CACGACTCAGCTATTGCAACTAATATGATAATGAACTAGTGGAAAGATCCCACTGAGC 913  
QY 1128 TTGGGAAGCTTACCTGACTGTTTGAATCTGAAATGTGGCAACAAGATCTGGAAGAGACTTA 1187  
DB 914 TTGGGAAGCTGGAACAATGTTCGAATCTGGAATCTTGGCAACAACAATCTGTGAGGCTGA 973  
QY 1188 TACCTGATCATCTGAGCTCTTGCACAAATCTAAACAGCTTAAATGTTCATGSGAAACAAGT 1247  
DB 974 TTCCATCTAATCAATTAAGTTCTGTGCTGCTGCTTGAATCAATTCATTAAGTGAACCTTCT 1033  
QY 1248 TTAAGTCACTAATACCCCGAGACTTTCAAAAGCTGAAAGATATGACTTAATCTTATCTGT 1307  
DB 1034 TGAAGTGAAGCTGTACCACTTGAATTCGGAAATCTTGGAAAGCTTGAATTAATCTTATCTT 1093  
QY 1308 CCAGCAACAATATTAAGAGTCCAAATCCCGGTTGAGCTATCTCGATAGGTAATCTTAATA 1367  
DB 1094 CTTCAAAACAGTTTCAAGGCAAAATTAACCTGAGCTTGGCCATATCATCATCTTATATA 1153  
QY 1368 CATTTGATCTTTCCAAACAAGATTAATGGAATCAATCTTCTTCCCTTGGTATTTGG 1427  
DB 1154 CATTTGATCTGTCTGGCAACAATTTCTCAGGCTCAATTCATTAACACTTGTGTATCTTG 1213  
QY 1428 AGCATCTTCTCAAGATGAATTTGAGTAGAAATCATATTAATCTGTGTAGTTCCAGGCACT 1487

DB 1214 AGCATCTTCTCACTTAACTTGAGCAGAATCATCTGATGACATGCGACATTCGCGAGAA 1273  
QY 1488 TTGGAATCTTAAGACATCATGGAATATGATCTTTTCAATTAATGATATCTGCGCCA 1547  
DB 1274 TCGGAACCTCCGAGAGATCAATCATGATGTGATTAATTAATTTCTTGGCGGTGA 1333  
QY 1548 TTCCAGAGAGCTTAAACCAATTAACAGAACATATTTTGTGAGACTGGAATTAATTAAC 1607  
DB 1334 TTCCAACTGAACCTTGGCAGTTGCAGAACATAAATCTGTGATACGTGAACAACAAGA 1393  
QY 1608 TGAAGTAAATGT---TGTTCATTAGCCCACTGTCTCAGTCTCACTGTATTTGAATGTAT 1664  
DB 1394 TTCAATGGGAAATCCCTGATCAGCTAACTAATCAGCTGTCACTGTGCAATCTGAACATCT 1453  
QY 1665 CTCATAACAACCTGATAGTATATCCCTAAGAACATTAATCTTCAAGATTTTCAACAG 1724  
DB 1454 CTTCAATTAATCTTTCTGGAATTAATCCACCTTGAAGAACTTTACAGCTTTTCCCGG 1513  
QY 1725 ACAGCTTCAATTTGGCAATCTCTGTCTTTCGCGTAGTTGGCTAACTCAACCGTTCATGAT 1784  
DB 1514 CCAAGCTTCTTGGAAATTCATTTCTGTGGGGAACGTGGGTGATCAATCTGTGGCCAT 1573  
QY 1785 CTGTGCAACTGTACGAGTGTCAATCTTAGACAGCTATTTCTTGGAAATGCTATTTGGG 1844  
DB 1574 CTTTACCTTAATGACAAAGT---ATTCAACAGAGTTGGCGGATTTGTATGTGTTCTGCGTT 1630  
QY 1845 GACTGTGATCTTTCATGAGTCTTAAATAGCAGCTTGGCCGACCGCATTAATCTCTCTCT 1904  
DB 1631 TCATCACTCTCATATGATGATATATTTCAATTCGCTTTTCAAGTCAAAAGCAGCAAAACAG 1690  
QY 1905 TTCTTGAATGATCATCTGCAAAACAGTAATTAATTCGACACCGAAGCTGTATCTCTTC 1964  
DB 1691 TCTTGAAGGCTCTTCAAAACAAC-----CTGAAGGTCACAGAACTGTGATTTCTTC 1744  
QY 1965 ATATGAACATGAGCACTCCAGCTTTAGAGGATATCATGAGAAATGACAGAGAAATCTTAAGT 2024  
DB 1745 ACATGACATGGCTATTTCAACAGCTTTGATGATATCATAGAGATTAACAGAAACCTGAGT 1804  
QY 2025 AGAATATATCATTTGGGACGAGACATCAAGCACTGATATCAATGTGTTTGAAGAT 2084  
DB 1805 AGAATATCATATTTGATAGGTAGGTGCTTTAGCAACAGTTTCAAGTGCACCTCCAAAATCT 1864  
QY 2085 GTAAACCGGTTTGCATTAAGACGGCTTTACTGTCAAAACCAAGTCAATGAATAACGTTTG 2144  
DB 1865 CCGACCTATTTGCATTAAGCAATCTAATCAGATATCCACCAACTTCCGCGAGTTTG 1924  
QY 2145 AAACAGAACTCGAGATGCTTAAGTATGACATCAAGACAGAAATCTTTGAGGCTTCAAGCTT 2204  
DB 1925 AAACAGAGCTCGAGACCATTTGGAGCATGACACAGAAACATGTAAAGCTTGCACGAGT 1984  
QY 2205 ATTCCCTCTCACTTGGGAGGCTTCTGTCTATGACTATTTGGAATAGTATGAGCTCT 2264  
DB 1985 ACGCTTATCTCCCTTTTGGCACTCTCTTCTACAGACTACATGGAATAATGGCTCTCTTT 2044  
QY 2265 GGAATCTTCTTCAATGCGCTTACGAAAGAAAAGACTTGAATTTGGGACACAGGCTTTAAG 2324  
DB 2045 GGAATCTTCTCAATGGGCTCGGGAAGAAAGGTGAAGCTTGAAGCTTGGGAAACAAGGCTGA 2104  
QY 2325 TAGATATGTGTGACGACCAAGTTTATAGCTTATCTACACATGACTGTATGCAAGATCA 2384  
DB 2105 TAGCTGTGAGGCTGCGCAAGAGCTTGATATCTTCAACATGACTGACACTTAAGATTA 2164  
QY 2385 TTCAAGAGAGCTGAAGTCTTCCAAACAATCTCTTGGACAAAGACTTGAAGGCTGTGTTGA 2444  
DB 2165 TCCATGAGAGACTCAAGTCAATCAAACTATCTCTTGAATGGAATTTGGAAGCCGCTTTGT 2224  
QY 2445 CAGATTTTGGAAATAGCGAAAGCTTGTGTGTCAAAGTCAATTAATCTTAATCACTTACGTA 2504  
DB 2225 CAGATTTTGGGATTTGCAAGAGCATACAGCCACAAATCTTATGTCTTCAACCTATGTTTC 2284  
QY 2505 TGGGACGATAGGTTACATAGACCCCGAGATATGTCTGCACTTACCGGCTCACTGAAGAA 2564

Db 2285 TTGGAACCATTTGATATATATGACCCAGATATGCTCGAAGCTTGGAGAGAGT 2344  
 Qy 2565 CCGATGCTACAGTTATGAAATAGTCTCTTGTAGTTGTTAAACCCGAAGAAAGCCGTTG 2624  
 Db 2345 CTGATATCTACAGTTTGGATTTGTCTCTTGTAGTTTAAACCCGAAGAGGCTGTGG 2404  
 Qy 2625 ATGACGAATCAATCTTCACCATCTGATTAATGTCMAAGACGGGGAACATGAATGATGG 2684  
 Db 2405 ATAAACGAGCCAACTTGATCAATGATGATCTATCAAAAGGCGGATGATTAACAGATATGG 2464  
 Qy 2685 AAATGCAAGTCCAGACATACATCCAGTGAAGATCTCGGTGTGTGAAGAAAGTTT 2744  
 Db 2465 AACCTGTGATGAGAGGTCTCAGTGTCTGATGACCTGAGACATCAATGAAGAAACAT 2524  
 Qy 2745 TCCAACTGAGCATCTCATGACCAAAAGACGCGAATGATCGACCAATGACACAGG 2804  
 Db 2525 TTGAGCTAGTCTCTTGTGTGACCAAGGAAATCTTTGGAGAGACCAACATGAGAGG 2584  
 Qy 2805 TGACTCGTGTCTTCGCGAGTTTATGCTATCGGAACAACCA 2845  
 Db 2585 TCTCTAGGAGTTCTGCTCTCACTGTCCCGTCTCCACCTCCA 2625

RESULT 11  
 ADI32617  
 ID ADI32617 standard; DNA; 2766 BP.  
 XX ADI32617;

22-APR-2004 (first entry)

Sorghum transpiration efficiency-related ERECTA DNA.

plant; transpiration efficiency; ERECTA; breeding; genetic engineering;  
 sorghum; ds; gene.

Sorghum bicolor.

Key Location/Qualifiers

FT CDS 1..2766  
 FT /tag= a  
 FT /product= "Sorghum transpiration efficiency-related  
 ERECTA protein"

MO2004005555-A1.

15-JAN-2004.

02-JUL-2003; 2003MO-AU000854.

02-JUL-2002; 2002AU-00003339.

(AUSU) UNIV AUSTRALIAN NAT.

Masle J, Farquhar GD, Gilmore SR;

WPI: 2004-091390/09.

P-PSDB; ADI32618.

PT Selecting plant having enhanced transpiration efficiency, useful for  
 PT selecting plant with enhanced transcription efficiency comprising  
 PT selecting plant expressing a genetic marker linked to the ERECTA locus in  
 PT the genome of the plant.

Claim 3; SEQ ID NO 5; 209pp; English.

CC The invention relates to a novel method for selecting a plant having  
 CC enhanced transpiration efficiency comprising detecting a genetic marker  
 CC for transpiration efficiency, where the marker comprises a nucleotide  
 CC sequence linked genetically to an ERECTA locus in the genome of the plant  
 CC and selecting a plant that comprises or expresses the genetic marker. The  
 CC method of the invention may be useful for selecting a plant having  
 CC enhanced transpiration efficiency. The isolated ERECTA gene or allelic

CC variant or protein-encoding region may be useful in the preparation of a  
 CC genetic construct for modulating the transpiration efficiency of a plant.  
 CC Furthermore, the ERECTA genes may be useful for producing plants having  
 CC enhanced transpiration efficiency by both traditional plant breeding and  
 CC genetic engineering approaches. The current sequence is that of the  
 CC sorghum ERECTA DNA of the invention.

Sequence 2766 BP; 716 A; 697 C; 646 G; 707 T; 0 U; 0 Other;

Query Match 33.1%; Score 1050.8; DB 12; Length 2766;  
 Best Local Similarity 63.4%; Pred. No. 2.3e-297;  
 Matches 1845; Conservative 0; Mismatches 882; Indels 185; Gaps 8;

Qy 112 TCTCTCTGCTTGAAGTTAGTACTGATCTGATCTGATGAGAGGAGCAAGTTGCTGA 171  
 Db 24 TCTCTGCTGCT 83  
 Qy 172 GATTAAGAAAGTCAATCAAAAGATGGAACAATGTTCTTTATGACTGGAACAATTCACCTTC 231  
 Db 84 GATCAAGAAAGTCTCTCGCAAGCGTGGCAACGTAATGATGAGATGGCGCGGAC----- 138  
 Qy 232 TTGGAATTAATGATGATGAGAGAGTGTCTGTGAAATATGTAATCTCAATGTTGTTC 291  
 Db 139 ---GACTACTGCTCTGCGCGCGCGCTCTGTCGCAACGTCACATTCGCCCTGCTGC 194  
 Qy 292 TCTTAATTTGTCAGATTGATGATGAGAGAAATCTGACCTGATTTGAGATCTCA 351  
 Db 195 GCTCAACCTCTCTGCGCTCAACCTTGAAGCGAGATCTTCAAGCCGTGGACGCTCA 254  
 Qy 352 GAGTCTCTTGTCAATGATCTGAGAGATGATGCTGTGTGCAAAATCCGTAGAT 411  
 Db 255 GAGCTCGTCTCATGATCTGAATCAATGAGGCTATCGGGCAATCCGTATGAGAT 314  
 Qy 412 TGATGACTGTTCTTCTTGGCAAACTTAGACTTATCTTCAATGATTAAGTGTACAT 471  
 Db 315 TGATGATGTTATCACTTAGAGACGCTGACCTTTTTCACCAACTTGAATGAGCAAT 374  
 Qy 472 ACCGTTTTCGATTTGCAAGTTGAGCACTGAGCAGTATTTCAATGATTAACCAAT 531  
 Db 375 ACCATTTTCTATATCAAACTGAGACCTGAGAACTTGATTTGAACAACACAGCT 434  
 Qy 435 GATTGTGCGATCCCATCAATGTCACAGCTCCCAAAATTTGAATTTGATTTGGC 494  
 Qy 532 GATGAGACCGATCCCTTCAACACTTTCACAGATTCGAAACCTGAAATTTCTGACTTGGC 591  
 Db 495 ACAGATTAATCACTGAGTGTGAGATACCAAGACTTATTTCTGGAATGAAAGTTCTTGA 651  
 Qy 592 ACAGATTAATCACTGAGTGTGAGATACCAAGACTTATTTCTGGAATGAAAGTTCTTGA 651  
 Db 495 ACAGATTAATCACTGAGTGTGAGATACCAAGACTTATTTCTGGAATGAAAGTTCTTGA 654  
 Qy 652 TCTTGGGTTGCGAGAAACAATGATGATTTCCAGATTTGTCTCACTGAC 711  
 Db 555 TC----- 556  
 Qy 712 TGATCTTGTGATTTTGAAGTAAGAAACAAGTTTGAAGTGTGATATCTGAGACGAT 771  
 Db 557 -----TTGATGTGAAGAAACAATGATGATGATGATGATGATGATGATGATGAT 602  
 Qy 772 AGGAATTCGACTGCTTCAGGTTTGGACTTTGCTTCAATCACTTAACCTGATGAT 831  
 Db 603 TGGAAGTCTTAACAAGTTTCAAGTCTTGAATTTGCTTCAACCGCTTCACTGAGACCAAT 662  
 Qy 832 CCGTTTGAATGCGGTTCTGCAAGTTGCAACATTAATGAGCAAGCAATCTTC 891  
 Db 663 CCATTCACATTTGATTTCTTCAAGTGTCTACACTTCTTCAAGTGTCTTCAAGTGTCT 722  
 Qy 892 TGGAAGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 951  
 Db 723 CGGTCAATTTCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 782  
 Qy 952 CAATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1011  
 Db 783 CAACCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 842

QY 1012 GATATTCACAGTACAGAGCTGATGCTGATTCACCTGAGCTTGGAAAAATGTCMAA 1071  
DB 843 GTACATCCAGGCAATTAAGTTAACTGGGTGATACCAACAGAGTTAGAAATATGTCAAC 902  
QY 1072 ACTCCATTACCTGGAACTCAATGATTAATCTCAAGGGTCAATATACCAAGAGCTTGG 1131  
DB 903 ACTTCATTACCTGAACTGAAACGATTAATCACTTACGGGGTCAATTCACACAGAGCTTGG 962  
QY 1132 GAAGCTTACTGACTGTTGTTGATGCAATGTGGCCAAATGATGTGGAAAGACCTATACC 1191  
DB 963 AAGGCTACAGGGCTTTGTTGACTGAACTTGGCAATACCACTGGAAAGAACCAATTC 1022  
QY 1192 TGATCATCTGAGCTCTTGACAAATCTTAAACAGCTTAATGTTTCATGSGAACAGATTAG 1251  
DB 1023 TGACACCTTAAGTTCAATGTGTAATCTCAATAGCTTCAATGCTTATGGCAACAAGTTAAA 1082  
QY 1252 TGGCACTATACCCCGAGCAATTTCAAAAGCTAGAAAGTATGACTTAACTTATCTGTCCAG 1311  
DB 1083 TGGGACCAATTCCTGTCGTGGCGGAAACTTGAAAGCATGACCTTATTAATCTGTATC 1142  
QY 1312 CAACAATATCAAAAGGTCCAATCCCGTTGAGCTATCGTATGSGTAACTTAGATCATT 1371  
DB 1143 AAACCTCATATAGTGCTCTATTCTATTGAGTTATCAAGGATCAACAATTTGGACAGCT 1202  
QY 1372 GGAATCTTCCAAACAAGATAAATGGAATCATTCCTTCCCTTGGTGAATTTGAGCA 1431  
DB 1203 GGAATTTATCCGTAAACATGATGACTGGTCCAAATTCATCATTAATGGACGCTTAGACA 1262  
QY 1432 TCTTCTCAAGTGAATCTTGAGTAAATTCATATACCTGGTGAATTCAGAGCACTTTGG 1491  
DB 1263 TCTATTGAGACTTAATCTTGAGCAAAATGTGCTAGTGGATTCATCCCGGGAGTTTGG 1322  
QY 1492 AAATCTAAGAAGCATCTGGAATAATAGATCTTCAAAATATGATATCTGAGCCCAATTC 1551  
DB 1323 TAATTTGAGAGGTGTCAAGAGATTGATTAATCTTAATATCACTGTGGCTGATTC 1382  
QY 1552 AGAAGACTTAACCAATTAACAGAAATATATTTGCTGAGACTGGAAAAATAAATCACTGAC 1611  
DB 1383 TCAAGAACTTGAATGCTGCAAAACATGATGTTGC----- 1417  
QY 1612 TGGTAATGTTGGTTCAATTAAGCAACGTCTCAGTCTACTGTATGTAATGTATCTATA 1671  
DB 1418 -----TAAATGTGCTGTAACA 1433  
QY 1672 CAACCTGATAGGTATATCCCTAAGAACAAATTAATCTTCAAGATTTTACACAGACGCT 1731  
DB 1434 TAATTTGGCTGGTGTTCCTCTGTAACAACACTTCAACAGGTTTTCACCTGACAGCTT 1493  
QY 1732 CATTTGCAATCTGTGCTTGTGCGGTAGTGGCTAACTCACCGTGTGATGATTTCTGTCG 1791  
DB 1494 TTTAGGTAAATCTGGACTGTGTGTAATCTGGCTTGTTGTCGTGCTTCCACTGGCCA 1553  
QY 1792 AACCTGACAGGTCAATCTCTAGAGCACTATTTCTTGGAAATAGCTATTTGGGGGACTTGT 1851  
DB 1554 CCAAGGAAACCGGCTATCTCAAAAGCTGCAATATGTGTTGCTGTGGGTGACTTGT 1613  
QY 1852 GATCCTTCTGATGATTTAAATAGAGCTTGGCCAGCCGATATCTCTCTCTTTTCTTGA 1911  
DB 1614 TATCTCTTATGATCTTTAGTACTGTTTGGAGGCCACATGCTCACCTGCTTTTAAAGA 1673  
QY 1912 TGGATCACTTGAACAACCAAGTAATTAATGTGACACCGAAGCTGCTCATCTTCATATGAA 1971  
DB 1674 TGTCACTGTAAAGCAAGCAAGTAAATGTCTCCCCAAGCTGTGATCTCTTATATGAA 1733  
QY 1972 CATGGCACTGCAGCTTACAGAGATATCATGAGAAATGACAGAAATGTAAGTGAAGTA 2031  
DB 1734 CATGGCCCTTCACTATACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1793  
QY 2032 TATCATTTGGGCAAGGACATCAACACTGATATCAAAATGTGTTTGAAGATTTAAACC 2091  
DB 1794 CATCATTTGATACGGGGGCTCAAGTACAGTTTAAATGTGTCTTAAAGATTTGCAACC 1853  
QY 2092 GGTTCGATTAAGCGGCTTACTCTCAAAACCAAGCTCAATGAAACAGTTTGAACAGA 2151

DB 1854 GGTGGCAATTAATAAAGCTGATATCCACTAACCCACAGAGCTTAAAGAAATTTGAAACTGA 1913  
QY 2152 ACTCGAATGCTAATAGATATCAAGACAGAAATCTTTGAGGCTTCAAGCTTATTCCT 2211  
DB 1914 GCTTGAAGACTGTGTGATCAACAGACCGGAATCTATGTCAGCTTCAAGGACTCAAT 1973  
QY 2212 CTCTCACTTGGGAGTCTTCTGTCTATGACTATTTGGAATAATGTAAGCTCTGGGATCT 2271  
DB 1974 ATCACGTTGGGAACCTCTCTTTATATATATATGAAATGTGGAGCTTATGGGATGT 2033  
QY 2272 TCTTCAT--GGCCCTACGAAGAAAAAGCTTTGATTTGGGACACAGGCTTAAAGTAC 2328  
DB 2034 TTTACATGAAGGTTCATCCAAAGAAAAAAGCTTGAACGGGAACTGCTACGAGATTGG 2093  
QY 2329 ATATGGGACGACAAAGTTTACTATCTACACCAATGACTGATGATCCAAAGATCATTTCA 2388  
DB 2094 TCTTGTGACGCTCAAGGCTTGTCTTACCTTCAACATGACTGCAATCCGATTAATTC 2153  
QY 2389 CAGAGACGTGAAGTGTCTCCAACTTCTTTGACAAAGACTTAGAGGCTGTTTGAACAG 2448  
DB 2154 TCGGAGTGAATTAATCAAGAATATCTCTTGAACAAAGATTAGAGGCCCATCTTACAG 2213  
QY 2449 TTTTGAATGCGAAAAAGCTTGTGTGTCAAACTCAATCTTCAATTTAGTGG 2508  
DB 2214 CTTTGAATGCTAAGGCTTATGTGTCTCAAAAACCTCAACATCAACTATGTCAATGG 2273  
QY 2509 CACGATAGTTACTATGACCCCGATGATGCTGCACCTTACAGGCTCACTGAGAAATCCGA 2568  
DB 2274 AACTATTTGCTAATGATGATCTGATGACCCGCACTTCCGCTCAACGAAAGCTGA 2333  
QY 2569 TGTCTACA--GTTATGGAATGATCTTCTTGAATTTTAAACCCGAAAGAAACCGTTGATG 2627  
DB 2334 TGTCTACAGGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2393  
QY 2628 ACGAATTCATCTCCACATCTATATGTCAAAGACGGGGAACATGAAAGTATGAAA 2687  
DB 2394 ACGAATTC-----TATCGAAGACGGCAACGAGATCATGATGAT 2434  
QY 2688 TGGCAGATCCAGACATCAATGACATGATGATGATGATGATGATGATGATGATGATGAT 2747  
DB 2435 CCGTGAACCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2494  
QY 2748 AACTGGCACTCTATGACCAAAAGACAGCGAATGATGACCCACATGACAGTGA 2807  
DB 2495 AGCTGGGCTCTTTTGAACCAAGGCAACCTTGACCGAGCGAGATGACAGAGTGG 2554  
QY 2808 CTGTGTTCTGGCAAGTTTATGCTATCGGAACAACCACTGCTGGACTG----- 2858  
DB 2555 TGGCGCTCTGGAATGCTGCTGTAACCCGGAACCGGCGCAAGCGGTGCGCACAG 2614  
QY 2859 ACAAGTACAGGACGCTGGCTGTTGCTGATGATGATGATGATGATGATGATGATGATGAT 2918  
DB 2615 TGGCGAGCCGTGCAAGCCGTGCAAGCTTACATCAACGATGATGATGATGATGATGATGAT 2674  
QY 2919 CTGATTTCTGCAATGCTC---TTCCATGATGCTTCTGATGCTCAATGCTTCTTCTG 2975  
DB 2675 CCGGCGCTCTCTCTGGGCAACCTGACAGCACTGCGAGCGGAGCTGTCTCTCAAGT 2734  
QY 2976 TTGGAACAAGTTATTTCTCAGAAACAGTGAAGT 3007  
DB 2735 TCGGCGAGGCACTCTGCAAGAACATGGAAGT 2766

RESULT 12  
ADA71018 standard; DNA; 2796 BP.  
ID ADA71018  
XX ADA71018;  
AC  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Rice gene, SEQ ID 4341.

XX Plant: bacterial infection; fungal infection; viral infection; rice;  
KM gene; ds.  
XX  
XX Oryza sativa.  
XX OS  
XX MO2003000898-A1.  
XX  
XX PD 03-JUN-2003.  
XX  
XX PF 22-JUN-2001; 2001MO-IB001105.  
XX  
XX PR 22-JUN-2001; 2001MO-IB001105.  
XX  
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y,  
PI Katagiri F, Qian S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;  
XX  
XX MPI, 2003-175290/17.  
XX  
XX Identifying at least one gene involved in plant resistance or response to  
PT pathogenic infection for conferring resistance or tolerance to a plant to  
PT bacterial, fungal or viral infection by determining or detecting plant  
PT gene expression.  
XX  
XX Claim 6, SEQ ID NO 4341; 899pp; English.  
XX  
XX The present invention relates to a method (M1) for identifying genes  
CC involved in plant resistance or response to pathogenic infection. M1  
CC comprises identifying a gene whose expression is significantly altered in  
CC the incompatible interaction of plant gene expression relative to  
CC expression of the gene in an uninfected plant, in a mutant plant that  
CC does not express a gene associated with response to pathogenic infection,  
CC or in a corresponding incompatible or compatible interaction. (M1) is  
CC useful for conferring resistance to resistance to a plant to  
CC bacterial, fungal or viral infection. The present sequence was used to  
CC illustrate the invention.  
SQ Sequence 2796 BP; 729 A; 659 C; 635 G; 773 T; 0 U; 0 Other;  
Query Match 32.9%; Score 1044.4; DB 8; Length 2796;  
Best Local Similarity 62.9%; Pred. No. 1.8e-295;  
Matches 1832; Conservative 0; Mismatches 911; Indels 171; Gaps 7;  
QY 112 TCTCTTCTGCTTGAAGTTAGTACTGCTGACTTGAAGAGGAGCAAGTGTCTGA 171  
DB 36 TCTCGTCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 95  
QY 172 GATTAGAAGTCTTAAAGATGTGAACAATGTTCTTTTATGATGACGACAACTTCACTTC 231  
DB 96 GATCAAGAAAGTCTTCCGCAATGTGACAAAGTACTGATGATGGCCCGCGGC----- 150  
QY 232 TTCGATTAATTTGCTGAGAGAGTGTGCTTGTGAAGATGTCACCTTCAATGTTGTC 291  
DB 151 ----GACTACTGCTGCTGAGGCGCTCTCTGCGACAAAGTACTGCTGAGCTGCGCCG 206  
QY 292 TCTTAATTTGTCAGATTGAAATCTTGAATGGAAGAAATCTCACTGCTAATTTGAGATCTCA 351  
DB 207 GCTCAACCTATCCGGGCTCAACTCGAGGCGAGATCTCCGGCGTGGCAGGTTGAA 266  
QY 352 GAGTCTCTTGTCAAT---TGATCTGAGAGTATCGCTTGTCTGAGCAAAATCCCTGATGA 408  
DB 267 GGGCAATGCTCGATGATGAGAAAGCGTGTGTGATCTTGTGTTTGGAAAAATGTG 326  
QY 409 GATTGTGACGCTGCTTCTTTTGCAGAAACTTGAAGCTTATCCTTCAATGATTAAGTGATGA 468  
DB 327 GCTTGTGCTGCTTGTGAGCTGCGAGTAACTTTGACTTGAAGTCAAAATGGGCTGTCTGGCA 386  
QY 469 CATACCGTTTGCATTTGCAAGTTGAAGCAACTTGAAGCAAGTATTTGAAAGATTAACA 528  
DB 387 GATCCCTGATGATTTGGCGATTTGTCATCATCAAAAAAATCTGATATTTGAAGAAACAACA 446

QY 529 ATTGATAGACGACGATCCCTTCAACACTTTACAGATTTCCAAACCTGAAATTTGACACTT 588  
DB 447 ACTGATCGAGATATCCATCAACGCTCTCACAGCTCCCAATTTTGAAGATTTTGACTT 506  
QY 589 GGCACAGAAATPAACTGAGTGTGAGATACCAAGACTTATTTACTGAAATGAAGTCTTCA 648  
DB 507 GGCACAGAAATPAACTGAGTGTGAGATACCAAGACTTATTTACTGAAATGAAGTCTTCA 566  
QY 649 GATATCTTGGTGTGAGGAAACAACCTAGTGGTAAATTTCTCCAGATTTGTGTCACT 708  
DB 567 ATACTTGGGATTTAGCGGTATATTTAGAGGACACATCTCCCGAGATATATGCGCAGTT 626  
QY 709 GACTGCTTGGTATTTTGAAGTAAAGAAACAACAGTTGACGTGATATACCTGAGAC 768  
DB 627 GACTGGGCTTTGATA----- 641  
QY 769 GATAGAAATTTGACACTGCTTCCAGGTTTGTGACTTGTCTTCAATACAGTAACTGTGTA 828  
DB 642 -----CTTGATTTGTCTTCAATTAATCTTCTGATC 674  
QY 829 GATCCCTTTGACATGCGCTTCTGCAAGTTGCAACATTAATCTTGAAGGCAATCACT 888  
DB 675 AATTCCTTTCACATTTGTTTCTTACAGATTTGCACTATCTTTCAGAGGAAACATGTT 734  
QY 889 CTCTGGAAAGATTCCATCAAGTATGCTCATGCAAGCCCTTGAAGCTTTAGATCTAAG 948  
DB 735 TACTGTCTTATTCATGATTTTGAATTTGACTTATGAGGCTCTGCTGTACTGATCTGAG 794  
QY 949 TGGCAACTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1008  
DB 795 TTACAAACCAATTTGCTGCTGCTTATTCATGATGATGATGATGATGATGATGATGATGAT 854  
QY 1009 ATTGATTTGACAGATTAACAAGTCTGCTGATTAATTCACCTGAGCTTGAAGCAATGTC 1068  
DB 855 GCTGATATGACAGGCAATTAAGTAAAGGTTCAAGGTTCAATGACCTTGAAGTATGTC 914  
QY 1069 AAATCCCAATTTACCTGGAATCAATGATATATCTCAGGGGCTATATCCACAGAGCT 1128  
DB 915 AACCTTCAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 974  
QY 1129 TGGGAAGCTTACTGACTTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1188  
DB 975 CGGAAAGCTTAACAGGTTTATTTGACTTAACCTTGAAGAAACAACCTTGAAGTCAAT 1034  
QY 1189 AACTGATCACTGAGCTCTTGGCAAAATCTTAAACAGCTTAAATGTTCAATGGAACAAGTT 1248  
DB 1035 CCTGATTAACATTAAGCTCATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1094  
QY 1249 TGTGGCACTATTAACCCGAGCAATTCAAAGCTAAGAAAGTATGATGATGATGATGATGAT 1308  
DB 1095 AAATGGACCAATTCCTCTTCAATGATTAACCTTGAAGGATGATGATGATGATGATGATGAT 1154  
QY 1309 CAGCAACAATATCAAGGTCATCCCGTGTGAGCTATCTGATGCTGATGATGATGATGATGAT 1368  
DB 1155 ATCAAAATTTTCAAGGTTTATTTCTATTTAGATGATGATGATGATGATGATGATGATGATGAT 1214  
QY 1369 ATTGATCTTTTCCACACAAGATTAATGAATCAATCTTCTTCCCTTGTGATTTGCA 1428  
DB 1215 CTTT----- 1218  
QY 1429 GCATCTTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1488  
DB 1219 -----AATCTTGAACAATGCTCTAGTAGATTTATTTCTGCAAAAT 1262  
QY 1489 TGGAAATCTAAGAGCATATGAAATATGATCTTTTCAATTAATGATATCTTGGCCCAAT 1548  
DB 1263 TGGCAACTTGAAGAGATATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1322  
QY 1549 TCCAGAAAGCTTAAACCAATTAACAGAACTAATTTTGTGAGCTGAGAAATATATTAACCT 1608  
DB 1323 TCTTCAGAAAGCTTGAAGATCTGAAATCTGATGATGATGATGATGATGATGATGATGATGATGAT 1382  
QY 1609 GACTGTATATGTTGTTTCAATTGACCAACTGTCTCAAGTCTCACTGATGATGATGATGATGAT 1668

Db	1383	AACGGGGATGTCCTTCTACTGATGAATGCGCTTACGCTCTCAATCTTAAATGTATCCTA	1442
Oy	1669	TAAACAACCTCGTAGGTGATATCCCTTAAGAACAAATATCTTCAAGATTTTCAACAGACAG	1728
Db	1443	TAAATATTTGGCTGCTGTGTGTATACCTACTGATACAACTTCTCACGGTTTTGCTGACAG	1502
Oy	1729	CTTCATTGGCAATCTGTGTCCTTTGGCGTAGTTGGCTAAACTCACCGTCATGTATTCG	1788
Db	1503	CTTTTGGGTAAATCCAGGACTTTTGGGATATTGGCTGTGTTCTTCGTGTCGCTCATCTGG	1562
Oy	1789	TCGAACGTACGAGTCATCTCTAGAGCAGCTATTCTTGGAATAGTATATTGGGGACT	1848
Db	1563	CCATTCACAGAAACCATATATCTCAAGGCTGCATATCTTGAAATGTCCGTGGGTGGGCT	1622
Oy	1849	TGTGATCCTTCTCAATGTCCTTAATATGACGCTTGCCGACCGGATATATCTCCTCTTTTCT	1908
Db	1623	TGTTATCTCTCTGATGATCTTATGTACCGGTGTGCAAGGCTCTATGTCCACTGTTTTCA	1682
Oy	1909	TGATGATCACTTGA CAACACAGTAATTAATTCGACACGGAAGCTGTATCTTTCAT	1968
Db	1683	AGATGTCTCTGTATAGCAAAACAGTAGAGAAATGTTCCCCCAAGCTGGTTATCTTCATAT	1742
Oy	1969	GAACATGGCACTCCACGTTTACGAGGATATCATAGAAATGACAGAAATCTAAGTAGAA	2028
Db	1743	GAACCTTTCCCTTCTTTGTATACGAGGATATATGACGATGACTGAAACCTGAAGTAGAA	1802
Oy	2029	GTATTCATTGGGACCGAGGATCAAGACATGATACAAATGTGTTTGAAGATTGTA	2088
Db	1803	GTACATCATGGGTATGGAGATCCAGACCGGTTTATATATATGTGTTTGAAGAACCGCA	1862
Oy	2089	ACCGGTTCGATTAAGCGGCTTTACTCTCACAAACCACAGTCAATGAAACAAGTTGAAC	2148
Db	1863	ACCAATGGCAGTAAAAAAGCTATATAGCCCATATCA CAGAGCTTCAAGGAATTTGAAAC	1922
Oy	2149	AGAACTCGAGATGCTAAGTAGATTAAGACACAGAAATCTTGTAGCCTTACAACTTATTC	2208
Db	1923	TGAGCTTGAGACTGTGTAGATCTMAAACCCGGAATATAGTCAGTCTTCAAGGATATTC	1982
Oy	2209	CCTCTCTCACTTGGGAGTCTCTGTCTATAGCATTAATTGGAAAAATGTACCTCTGGGA	2268
Db	1983	CCTATCTCTGTTGGAAAATCTTCTCTTACGATTAATCATGAAAAATGGAAGCCTCTGGGA	2042
Oy	2269	TCTTCTTCAT--GGCCCTACGAAAGAAAAAGACTCTTGATTTGGGACACACGGCTTAAGAT	2325
Db	2043	TGTTTTCATGAAGGTCCAACTCAAGAAAGAAAAAATTGATTTGGGAAATCTGCTTACGAAAT	2102
Oy	2326	AGCATATGTGTGACGACAAAGTTTATGCTTATCTACACATGACTGTAGTCCAAAGATCAT	2385
Db	2103	TGCTCTAGGTGGGCGCCAAAGGCTTGTCTTATCTTCATCATATACGTAGCCCAAGGATATAT	2162
Oy	2386	TCACAGAACGTAAGTGTGTCMAACTTCTCTGGA CAAGACTTAAAGGCTGCTTGAAC	2445
Db	2163	ACACAGGGAATGTGAATCAAAAAATATATCTCTTGATTAAGATTTATGAGGCACATCTTAC	2222
Oy	2446	AGATTTTGAATAGCGAAAGCTTGTGTGTCTCAAACTCACATATTTCACTTACGTGAT	2505
Db	2223	AGACTTTGGCATTTGCTAAGAGTTTGTGTGTTCAAAAATCTCACAGTCTCACCTATGTGAT	2282
Oy	2506	GGGACGATAGTTATCATAGACCCCGAGTATGCTGCACTTCAAGGCTCACTGAAAAATC	2565
Db	2283	GGGAACATTTGGCTATATCGATCTCGAGTATGCTGCACTCTCCGCTCATGAAAAATC	2342
Oy	2566	CGATGTCTACAGTTATGGAATATGTCCTTCTGAAGTTGTTAAACCGAAGAAAGCCGTTGA	2625
Db	2343	TGATGTCTACAGCTATATGGCAATTTGTCTTGAAGTGTCTGACCGGAAAAAACCAAGTGA	2402
Oy	2626	TGACGAATTCATCTCCACCATCTGATATATGTCAAAAGACGGGAAACAATGAAATGATGA	2685
Db	2403	CACGAGTGCAATCTCCATCACTTGTATCTTGCAAAAGACGGCTAACATGCTGTCAATGA	2462
Oy	2686	AATGGCAATCCAGACATCACTGACGTGTAAAGATCTCGGTGTGTGAAGAAATTTT	2745

Db	2463	GACAGTGCACCCGGACATTGCACACCTTGCAGAGATCTTGGTGAAGTCAAGAAAGTGTT	2522
OY	2746	CCAACTGGCACTCCTTATGACCAAAAGACGCCGAATGATGCACCAATGACACAGT	2805
Db	2523	CCAGCTGGCGCTCCTTTTGCACCAAGAGACAAACCTCCGATCGCGCCGAATGACGAGGT	2582
OY	2806	GACTCGTGTTCGCGCAGTTTTATGCTATGGAAACAACAACCTGCTGC-----GAC	2856
Db	2583	TGTGCGGCTCTGTGACACTGCTAGTTCGTCCGACCCGCCCAAGCTCCGCACAGCACT	2642
OY	2857	TGACACGCTCAGCGACGCTGGCTGTTCTGTGCTACGTGATGATGATCAAAATCTCAAGAC	2916
Db	2643	GGCCATCCCGCAGGCGGCTGCTGTCCGACCTAATACAGAGATCTCAGCTTAACAGG	2702
OY	2917	TCCCTATTCTGTCATTTGCTC---TTCCATGAGGCTTGTGATGCTCAACTGTTTCTCG	2973
Db	2703	CACCAAGGTGCTCTCCCTGCGCAACTGTGTGTACTTCCGATGCTGACGTGTTTCTCA	2762
OY	2974	GTTTGAACAAGTATTTTCTCAGAAACAGTAGTAG	3007
Db	2763	GTTTGGCAGGTCATTTCTCAGAAACAAGATAG	2796

CC	AD132615	standard; DNA; 3000 BP.
XX	AD132615;	
XX	AD132615;	
XX	22-APR-2004	(first entry)
DE	Rice transpiration efficiency-related ERECTA DNA.	
XX	plant; transpiration efficiency; ERECTA; breeding; genetic engineering;	
KW	rice; ds; gene; chromosome 6.	
XX	Oryza sativa.	
XX	Key	Location/Qualifiers
FT	CDS	1..3000
FT	/*tag= a	
FT	/product= "Rice transpiration efficiency-related ERECTA	
FT	protein"	
XX	WO2004005555-A1.	
PN	15-JAN-2004.	
PD	02-JUL-2003; 2003WO-AU000854.	
PF	02-JUL-2002; 2002AU-00003339.	
PR	(AUSU ) UNIV AUSTRALIAN NAT.	
PA	Maele J, Farquhar GD, Gilmore SR;	
PI	WPI: 2004-091390/09.	
XX	P-PSDB; AD132616.	
DR	Selecting plant having enhanced transpiration efficiency, useful for	
XX	producing plants with enhanced transcription efficiency comprising	
PT	selecting plant expressing a genetic marker linked to the ERECTA locus in	
PT	the genome of the plant.	
XX	Claim 3; SEQ ID NO 3; 209pp; English.	
PS	The invention relates to a novel method for selecting a plant having	
XX	enhanced transpiration efficiency comprising detecting a genetic marker	
CC	for transpiration efficiency, where the marker comprises a nucleotide	
CC	sequence linked genetically to an ERECTA locus in the genome of the plant	
CC	and selecting a plant that comprises or expresses the genetic marker. The	
CC	method of the invention may be useful for selecting a plant having	
CC	enhanced transpiration efficiency. The isolated ERECTA gene or allelic	



CC variant or protein-encoding region may be useful in the preparation of a  
CC genetic construct for modulating the transcription efficiency of a plant.  
CC Furthermore, the ERBCTA genes may be useful for producing plants having  
CC enhanced transcription efficiency by both traditional plant breeding and  
CC genetic engineering approaches. The current sequence is that of the rice  
CC ERBCTA DNA of the invention which is located on chromosome 6.

XX Sequence 3000 BP; 796 A; 749 C; 724 G; 731 T; 0 U; 0 Other;

Query Match 32.6%; Score 1035.2; DB 12; Length 3000;  
Best Local Similarity 63.8%; Pred. No. 9.5e-293;  
Matches 1687; Conservative 0; Mismatches 888; Indels 69; Gaps 5;

```

QY 234 CGGATTTGTTGTCGAGAGGTGTGCTTGTGAAAAATGTCACCTTCATATGTTGTCCTC 293
DB 179 CCGACCACTGCGCGTGGCGCGGCTCACCTGCGAAGAGCTCTTGCGCGCTCTCCGCC 238
QY 294 TTAATTTGTCAGATTTGATCTTGATGAGAAATCTGACCTGCTATTGAGATCTCAAG 353
DB 239 TGAATCTTGTCAAACTTAACCTAGAGGTAGATCTGCGCGGCATCGAGAGCTCAAG 298
QY 354 GTCTCTTGTCAATGATCTGCGAGTATGCTTGTCTGCAAAATCCCTGATGATGTTG 413
DB 299 ATCTACAGTTCGTTGATCTCAAGGGGAAACAAGCTCACCTGCGCAATCCAGATGAGTTG 358
QY 414 GTGACGTGTTCTTCTTGCAAACTTAGACTTATCTTCAATGAAATTAGAGTGACATAC 473
DB 359 GGGACCTGCACTCTCTTAAATATTGATGATTTGTCGCAACTGCTTATGAGAGATCC 418
QY 474 CGTTTTCGATTTGCAAGTTGAAAGCACTTGAGAGCTGATTTCTGAAATATCAATTTGA 533
DB 419 CTTCTTCATCTCAAGCTCAAGAGCTTGAGAGCTGATTTTGAAGAACCAAGCTCA 478
QY 534 TAGAGCCGATCCCTTCAACCTTTACAGATTTCAAACTGAAATTTGAGCTTGAC 593
DB 479 CGGAGCCCACTCCCTTCCACATTTGCCAAATTCMAATCTCAAGACATTTGACCTGGAC 538
QY 594 AGAATTAACCTCAGTGTGAGATACCAAGACTTATTTTCTGGAATGAAATTTCTTCAATATC 653
DB 539 AGAACCAAGCTTAACAGGAGATCCCAAGCTCATATCTGGAATGAAATTTGCTGCAATAC 598
QY 654 TTGGGTTGCGAGGAAACAACTTAGTCGGTAACTTTCTCCAGATTTGTCTCAACTGACTG 713
DB 599 TAGGTTTGAAGGGTAACTCACTGACTGAGAACTTTGTCACTGACATGTGCAACTGACTG 658
QY 714 GTCTTTGATTTTGTGACGTAAAGAAACAAGCTTTGACTGTGATATACCTGAGACATAG 773
DB 659 GCGTGTGTGATCTTGTGATGTAAAGGGGAAACAATCTCAAGGGAGCAATTCAGAGAGCATAG 718
QY 774 GAAATTTGCACTGCTCCAGGTTTGTGACTTGTCTTCAATCAAGCTTAACTGTGAGATCC 833
DB 719 GGAATCTGACCAAGCTTTGAAATTTCTGGAATTTCTGTATTAACAAATCTCTGGGAAATAC 778
QY 834 CTTTTCGACATCGGCTTCTGCAAGTTGCAACATTATCATTTGCAAGGCAATCAACTCTCTG 893
DB 779 CTTACAACATAGGCTTTCTTCAAGTACCACTGTCACTTCAAGGAAATAGACTGACTG 838
QY 894 GGAAGATTCATCAGTATGTTGTCTCAATGCAAGCCCTTGCAAGCTTATGATCTAAGTGCA 953
DB 839 GGAATTTCTCAGATGTGATTTGCTGCTGATGCAAGCTCTTGTCTTATAGACTGAGTAGA 898
QY 954 ACTGTGTGAGTGTATCTTCTCCGATTTCTCGGAAATCTTATCTTTCACCGGAAATTTGT 1013
DB 899 ACAGCTGTGAGGCGCATTTCTTATACTGCGCAATCTATCTATCTGGAATATCTAT 958
QY 1014 ATTTCGACAGTAAACAAGTGAAGTGTTCATTTCACTGAGCTTGGAACATGTCAAAAC 1073
DB 959 ATTATCATGAGGAAACAATCTTACTGAGTCAATACGCGCGAGGCTTTGGGAATATAGTAAC 1018
QY 1074 TCCATTACTGGAACCTCAATGATATCATCTACGGGTCAATATACCAACAGAGCTTGGGA 1133
DB 1019 TTAGCTACCTTAACAATGATGATGAAATGTGTGGGCACAATTTCAAGAGAGCTTGGCA 1078
```

```

QY 1134 AGCTTACTGACTTGTGATCTGTAATGTGGCCAAACATGATCTGAGAGCACTATACCTG 1193
DB 1079 AACTTGAAGGCTTTTGAACCTAAATTTTCCAAACAACATCTTCAAGGCTCTTATTTCTG 1138
QY 1194 ATCATCTAGCTCTTGCAAAATCTTAAACAGCTTAAATGTTCAATGGGAACAAGTTTATG 1253
DB 1139 CAAACATCACTTCTGCACTGCTTAAACAATTTCAATGATTTTATGGCAATATAGCTAATG 1198
QY 1254 GCACATATCCCGAGCATTTTCAAAAGCTAGAAAGTATGATCTTATCTATCTGTCACGA 1313
DB 1199 GTTCTATTTCTGTGTGTTTCCAAAGTTGAGAGTGTGACTTGTGAACCTTATCTTCA 1258
QY 1314 ACAATATCAAGGATCCCAATCCCGATGAGCTATCTGATTCGGATTAATCTGATATCAATTTG 1373
DB 1259 ACAATTTCAAGGCAATTTCTTCTGAGCTTGTGATCATATCAACTTGTGAACAATTTG 1318
QY 1374 ATCTTTTCAACAAACAAGATTAATGGAATCTTCTTCTTCTGATTTGAGATC 1433
DB 1319 ATCTTTCTCAATGATTTCTGAGACCAATTCCTGCTACATTTGGTATCTAGACACC 1378
QY 1434 TTCTCAAGATGAACCTGAGTGAATCATATTAATCTGATGATTTCCAGGCACTTTGGA 1493
DB 1379 TTCTTGAACGAAATTTGATGAAGAACCATCTTGTAGGCGCAGTTCTGCTGAGATTTGGA 1438
QY 1494 ATCTAAGAGCATCATGGAATATGATCTTCAATATATGATCTGCGGCCAATTCAG 1553
DB 1439 ACTTGAAGAGCTCAAGATATGATATGTCAACAACAACCTTATCTGATGCTGCGCG 1498
QY 1554 AAGAGCTTAAACAATTAACAGAAATATTTGCTGAGACTGCAAAAATTAATACCTGACTG 1613
DB 1499 AGGAACCTGGAACAATTTCAAAACCTTGATAGCTGATTTCTTAACAACAATTTGTTG 1558
QY 1614 GTATATGTTTGTGATTAAGCAACTGTCTCACTCA-----CTGATTTGAAT 1660
DB 1559 GGGAGATCTCCCTGTCAATTTGGCCCACTGCTTCACTTAAATACCTGCAATTTCAAGAAAT 1618
QY 1661 GTATCTCATTAACAACCTCGAGTGAATCTCCCTTAAGAAACAATTAATCTTCAAGATTTTCA 1720
DB 1619 TTCTCATCAACAATTTATCTGAGCATGTCGCCAGATGCAAGAAATTTCTGAAATTTCCCA 1678
QY 1721 CCAGA-----CAGCTTCA 1733
DB 1679 ATGGAAGAGCATCTTCAATTTTCTGATTGCAACCAAGTAACTAATTAATGACAGCTTCT 1738
QY 1734 TTGGCAATCTCTGCTTTTGGCGGTAGTTGGCTAACTCACCGTGTCAATGATTTCTGCGAA 1793
DB 1739 TTGGTATCTCATTAATGATGATTTTACTGCGCAAGATTCAGAGCTGTGACACTCTCATGGA- 1797
QY 1794 CTGTAGAGGTCAATCTCTAGAGCAGCTATTCTTGAATAGCTATTGGGGGACTGTGA 1853
DB 1798 --CAAGAGTTAATATTTCAGAGACAGCAATGCTTGAATATCTTAAAGCTTTATCATATAT 1855
QY 1854 TCCCTTCAATGCTTAAATAGCAGCTTGCGGACCCGATATCTCTCTCTTTCTTGATG 1913
DB 1856 TGCTTGGCGTTTGTGCTGTGGCTATATATAAACAATTAACAACAGCAGCACTTGTCAAG 1915
QY 1914 GATCACTTAACAACAAGTAACTTATTTGACAACCGAAGCTCGTATCTTCAATGAACA 1973
DB 1916 GATCCGATTAAGCCAGTGAAGGAC-----CTCAAAAGCTAGTTGTTCTCCAGATGAGCA 1969
QY 1974 TTGGCACTCAAGCTTTTACGAGGATATGATGAGAAATGACAGAAATCTTAATGGAATATA 2033
DB 1970 TTGGCTATCAATCTTAAGAGGACATATAGGCTGACAGAAATTTGACGAGAAATATCA 2029
QY 2034 TCAATTTGGGACCGAGCATCAAGCACTGTATTAACAATGTTTGTGAGAAATTTGAAACCGG 2093
DB 2030 TCAATTTGGCTATGCGGCTCAAGACAGTGTCTAACAATGTAATCAAGACGCGAAGGCCA 2089
QY 2094 TTGGCATTAAGGCGCTTAACTCTCAACAACCAAGTCAATGAACAAGTTGAAACGAAC 2153
DB 2090 TTGCTGTCAAGGCGCTTTTACAGTCAATTAACCATAGCTCCGAGAGTTTGAACAGAAC 2149
QY 2154 TCGAGATGTAAATGATCATCAAGCAAGAAATCTTGTGAGCGCTAACAAGTTATTCCTCTCT 2213
```

```

Db      2150 TAGAGCAATTTGGAGATACGCGACAGAAATCTGTTAGCTTCATGGCTTCTCGCTAT 2209
QY      2214 CTACTTTGGGAGCTTCTGTTCTATATACATTTTGGAAAAATGGAGCTCTGGGANTTTC 2273
Db      2210 CTCACATGGAACCTTGCTCTTCTATATTAACATGAAAAATGGTTCTTGTGGATCTTC 2269
QY      2274 TTGATGGCCCTACGAGAAAAAGACTCTTGATTGGGACACAGCGCTTAAGATAGCATATG 2333
Db      2270 TCCACGCTCATTAAGAAAGTAGAGCTCAACTGGGACACAAAGACTAGATGCGGCTCG 2329
QY      2334 GTGACAGCAAGGTTTATAGCTTATCTACCACTGATGCTGTAGTCGAAGATCATTTACAGAG 2393
Db      2330 GAGCTGACAAAGGCTGCGCTATCTCCACATGACTGCACACCTCGCATATATCCACAGAG 2389
QY      2394 ACGTGAAGTGTCTCAACATTTCTTTGACAAAGACTTAGAGGCTGTTTACAGATTTTG 2453
Db      2390 ATGTCAAGTCTCTCAACATCTGCTCGACGAGAACTTGAAGCGCACCTTCAGATTTTCG 2449
QY      2454 GAATAGGAAAGGCTGTGTGTGTCAAAAGTCACATCTTCAACTTACGATGAGGACAGA 2513
Db      2450 GCATTAGCAAAATGTGTCCTCTGCGCAAGTCCATGCTCTCATCTTATGTCTAGAAACA 2509
QY      2514 TAGGTTACATAGACCCCGAGATGCTGCACTTCACGGCTTCAGAGAAATCCGATGCT 2573
Db      2510 TCGGCTACATTGATCCGAGATATGCGAGACTTCACAGGCTCAATGAGAAATCTGATGTG 2569
QY      2574 ACAGTTATGGAATGCTCTTCTGAGTTGTTTAAACCCGAAGAAACCGCTTGATGACGAT 2633
Db      2570 ACAGCTTCGGCATGCTCTTCTGGAATTTGTCACAGGAAAGGCGGTGCACAAAGAAAT 2629
QY      2634 CCATCTCCACATCTGATATATGTCAAAGACGGGGAACAATGAAGTATGAAATGCGAG 2693
Db      2630 CGAAGTTGCAATTAATTAATCTCTCCAAAGTGATGACACACAGTCAATGAGGCAATGG 2689
QY      2694 ATCCAGACATCACATGACGCTGTAAAGATCTCGGTGTGTGAAGAAATTTTCCAACTGG 2753
Db      2690 ACTCGAGGATGATGATGACGCGACGAGACATGGAAGTGTGACGAGAGGCTTCAGCTCG 2749
QY      2754 CACTCTCATGACCAAAAGACAGCCGAATGATGACCCCAACATGACACAGTGAATCTGTG 2813
Db      2750 CCCTTCTGTGACACCAAGAGGACCTTTCAGACCGGCGGACCATGACAGAGTTGCAAGGG 2809
QY      2814 TTCT 2817
Db      2810 TGCT 2813

```

RESULT 14  
ADX59740  
ID ADX59740 standard; cDNA; 2533 BP.

AC ADX59740;  
DT 21-APR-2005 (first entry)  
XX plant full length insert polynucleotide seqid 30583.  
XX plant protectant; plant growth regulant; gene therapy; plant;  
XX recombinant DNA construct; physical array; plant breeding marker;  
XX cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
XX extreme osmotic condition; pathogen tolerance; pest tolerance;  
XX growth rate; cell cycle pathway; disease resistance;  
XX galactomannan production; lignin production; plant growth regulator;  
XX yield; plant growth; plant development; seed oil; protein yield;  
XX protein content; gene; ss.  
XX Unidentified.  
XX OS  
XX US2004034888-A1.  
XX PN  
XX 19-FEB-2004.  
XX PD

```

PF      28-APR-2003; 2003US-00425114.
XX      06-MAY-1999; 99US-00304517.
PR      05-NOV-2001; 2001US-00985678.
XX      (LIU/) LIU J.
PA      (ZHOU/) ZHOU Y.
PA      (KOVA/) KOVALIC D K.
PA      (SCRE/) SCREEN S E.
PA      (TABAS/) TABASKA J E.
PA      (CAO/) CAO Y.
XX      Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX      WPI; 2004-180133/17.
XX      New recombinant DNA construct, useful for improving plant tolerance to
PT      cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT      pests, for conferring increased resistance to plant disease, or for
PT      improving yield.
XX      Claim 1; SEQ ID NO 30583; 15pp; English.
XX      The invention describes a recombinant DNA construct comprising a
CC      polynucleotide consisting of a sequence encoding an amino acid sequence
CC      available in electronic form from the US patent office at
CC      ftp.secdta.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
CC      of the invention are also useful in physical arrays of molecules and as
CC      plant breeding markers. The recombinant DNA construct is useful for
CC      improving plant tolerance to cold, heat, drought, herbicides, extreme
CC      osmotic conditions, pathogens or pests, for manipulating growth rate in
CC      plant cells by modification of the cell cycle pathway, for conferring
CC      increased resistance to plant disease, for producing galactomannan,
CC      lignin or plant growth regulators, for increasing the rate of homologous
CC      recombination in plants, for improving yield by modification of
CC      photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC      or by providing improved plant growth and development under at least one
CC      stress condition or for modifying seed oil or protein yield and/or
CC      content. This sequence represents a plant full length insert
CC      polynucleotide that can be used in the recombinant DNA construct of the
CC      invention.
XX      Sequence 2533 BP; 656 A; 630 C; 589 G; 658 T; 0 U; 0 Other;
SQ

```

Query Match 32.0%; Score 1015.4; DB 13; Length 2533;  
Best Local Similarity 68.7%; Pred. No. 5.7e-287;  
Matches 1413; Conservative 0; Mismatches 641; Indels 3; Gaps 1;

```

QY      794 GTTTGGACTTGTCTCAATCAATCACTGAGATCCCTTTGACATGCGCTTCCTG 853
Db      48 GTAGGATTTGTCTTCAACCGCTTTATCTGACCAATCCATTCAAATTTGGTTCTTA 107
QY      854 CAAAGTTCAACATTTATATTGCAAGGCAATCACTCTTGGGAAAGTTCCATAGATAT 913
Db      108 CAAAGTGTCACTATCTCTTGGCAAGGAAACAAATTCACGCGCCCAATCTTCAATAT 167
QY      914 GGTCTCATGCAAGCCCTTGAGCTTATGATCTAAGTGGCACTTGTGTAGTGTGATATT 973
Db      168 GGCTTATGCAAGGCTCTCGCTGCTTGAATCTAGATCTAGATCAACCAATTAATGTGCTATA 227
QY      974 CTTCGATTTGCGAAATCTTACTTTCACCGAAGATTTGATTGGACAGTAACAGCTG 1033
Db      228 CCATCTATATAGGCAACTTGACATACATGAAAGCTGTACATGCAAGCAACAGTTA 287
QY      1034 ACTGTTCAATTTCACTGAGCTTGGAAATATGCAAAATCCATTAACCTGGAAGTCAAT 1093
Db      288 ACTGATGATACACACGAGCTTAGAAATATGTCAACATCTTATTAACCTGAACTGAAT 347
QY      1094 GATATATCTCAACGGGTCAATATACACAGAGCTTGGGAAGTCTACTGACTTTGAT 1153
Db      348 GATATATCACTTATGAGGTCAATTTCCACGAGCTTGGAAAGGCTTAACAGGCTTTTGAC 407
QY      1154 CTGAATGTGGCCAAACAATGATCTGGAAGGACCTATATCTGATCATCTGAGCTTTGACA 1213

```

```
Db      408 CTGAACCTTGGAGTAACACCTTGAAGACCAATTCCTGACCAACTTAAGTCAATGTCGTG 467
Qy      1214 AATCTAAACAGCTTAAATGTCATGGAACAAGTTTAGTGCCACTATACCCGAGCATTT 1273
Db      468 AATCTCAATAGCTTCAATGCTTATGSCAACAAAGTTAATGGAAACATTCCTCGTTCCTG 527
Qy      1274 CAAAGGTAAAGAGTATGACTTACTTAATCTGCCAGCAACATATCAAAAGTCCATC 1333
Db      528 CGGAACCTTAAGACATGACCTATTAAATCTTCATCAAAATTTCAATAGTGCGCTAT 587
Qy      1334 CCGGTTAGGCTATCTCGTATCGGTAACTAGATACATTTGATCTTTCACAAACAAGATA 1393
Db      588 CTAATTGAGCTATCAAGATCAACAATTTGGACGCTTGAACCTTATCTGTAACATGATG 647
Qy      1394 AATGGAATCAATCTCTTCTCCCTTGTTGTAATGGAGCATCTTCAAGAATGAACCTT 1453
Db      648 ACGGATCAATTCATCATCATCTGGAACCTAGACATCTATTGAGGCTTAACTTGAGC 707
Qy      1454 AGAATCATATTAAGTGTAGTTCAGGCGACCTTGGAAAATCTAAGAAGCATGATGAA 1513
Db      708 AAGAATGATCTAGTGAATTCATCTCCGAGAGTTGTAATTTGAAGAAGTGCATGAG 767
Qy      1514 ATAGATCTTCAAAATATGATATCTGCGCCAAATCCAGAGAGCTTAAACAATTACAG 1573
Db      768 ATTGATTTATCTATATCAATCTTGTTGTCGATTCCTCAAGAACTTGGAAATGCTCAA 827
Qy      1574 AACATAATTTTGTGAGACTGGAAAATATATACCTGACTGTAATGTTGCTTATAGCC 1633
Db      828 AACCTGATGTTGGCTAAACCTGSAACACAAATTAATCTGGCGATGCTCTCTCTGATG 887
Qy      1634 AACTGTCTCAAGTCTCACTGATTTGAATGTAATCTCATAAACCTCGTAAGGATATCCCT 1693
Db      888 AACTGCTTCAGCTCAATATCTTAATGTCATACATATATTTGGCTGAGTCTCTCT 947
Qy      1694 AAGAACATATTAATCTTCAGAAATTTTCAACAGACAGCTTCAATGGCAATCCGTGCTT 1753
Db      948 ACTGACAAACAATCTCAACAGGTTTTCAATGACAGCTTTTAGTATCTCTGACCTCTGT 1007
Qy      1754 GGTAGTGGCTAAACCTCACGCTGTCATGATCTCTGTCGAACTGTACAGATGTCATCT 1813
Db      1008 GGATATTTGCTGTTCTTCTCATGTCGTTCCACTGGCACGSAACAAACGCGCAATCTCA 1067
Qy      1814 AGAGCAGCTATTTCTGGAATAGCTATTTGGGGAGCTTGTATCTCTCTCATGCTTATA 1873
Db      1068 AAGGCTGCCAAATATGTTGTTGCTGGGTGAGATTTGTATCTCCCTGATGATCTTATGA 1127
Qy      1874 GCAGCTTGGCGACCGCATATCTCTCTCTTTCTTATGATGATCACTTGAACAAACAGTA 1933
Db      1128 GCTGTATGACGGCCACACCACTCACTGCTTTTAAAGATGCCACTGTAAAGCAAGCCAGTG 1187
Qy      1934 ACTTATTCGACACCGAAGCTGCTATCTTCAATATGAACATGGCACTCAAGTTTACGAG 1993
Db      1188 AGCAATGTTCCACCCAAAGCTGTGATCTCTCATATGAACATGGCTCTTCATGTCCTTAT 1247
Qy      1994 GATATCATGAGATGACAGAGATCTTAAGTGAAGATATCAATTTGATTTGGGCAACGAGCATCA 2053
Db      1248 GATATATGAGATGATGAGAACTTGAAGTGAAGAAATCAATCATGTGATACGGGGCATCA 1307
Qy      2054 AGCAGTGTATACAAATGTTGTTTGAAGAAATTTGAACCGGTTGCGATTAAGCGGCTTAC 2113
Db      1308 AGTACAGTTTATTAATATGTTCTTAAGAAATTTGCAAAACCAATGGCAATAAAAAGCTGAT 1367
Qy      2114 TCTCACAACCCACAGTCATGAAGAACTTTGAAACAGAACTCGAATGCTAAGTACATC 2173
Db      1368 GCCCACTACCTCAGAGCCTTAAGATTTGAAACTGAGCTCAGACTGTTGGTAGCATC 1427
Qy      2174 AAGCAAGAAATCTGTGAGCCTTACAAAGCTATTCCTCTCTCACTGGGGAGTCTTCG 2233
Db      1428 AAACACCGGATCTAGTCAGCTTCAAGGGTACTCGTTGACCTGTTGGAACTCTCTC 1487
Qy      2234 TTCTATGACTATTTGGAAAAATGAGCTCTGGAGTCTTCTGAT--GGCCCTACGAG 2290
```

```
Db      1488 TTTTATGATTAATAGAGAGTGGACGCTTATGGGATTTTAACTAAGAGCTATCCAG 1547
Qy      2291 AAAAAGCTTTGATTTGGACACAGCGCTTAAGATACATATGTGTGACACAAAGTTTA 2350
Db      1548 AAGAACAAACTTGTACGTGGGTGACCTCGCTACGATCGCTCTTGTGTGACGCTCAAGGCTC 1607
Qy      2351 GCTTATGACACCATGACGTATGTCCAAGGATCATTCACAGAGACGTAAGTGTCCAA 2410
Db      1608 GCTTACCTTCAACATGACTGACGACGATATATTTACCGGAGCGTAAATCAAGAAAT 1667
Qy      2411 ATTCTCTTGACAAAGACTTAGAGGCTCGTTTGAACAGATTTTGAATAGCGAAAGCTTG 2470
Db      1668 ATACTCTGCAAAAGATTATAGAGCCCATCTTACAGACTTCGCGATTCGTAAGACTT 1727
Qy      2471 TGTGTCAAAAGTCATCACTTCACTTACGTATGATGGGCAAGATAGTTACATAGACCC 2530
Db      1728 TGTGTCTGAAAGCTCACAGCTCAACCTTACGTATGGGCACTTATGTTACATTTGATCCC 1787
Qy      2531 GAGTATGCTGCACTTACAGGCTCACTGAGAAATCCGATGCTTACAGTTATGGAATAGTC 2590
Db      1788 GAGTACGCGCCGACCTCCGCTTACAGAGAGTGTGATCTTACAGCTACGGGATGTT 1847
Qy      2591 CTTCTTGAGTTGTTAACCCGAAAGAAAGCCGTGATGACGAATCCAATCTCAACATCTG 2650
Db      1848 CTGCTGAGCTGCTGACCGGCAAGAGCCAGTGAACAACAGATGCAATCTCAATCACTTG 1907
Qy      2651 ATATGTCAAAAGACGGGGAACAATGAATGATGAAATGGCAATCCAGATCAATCATCG 2710
Db      1908 ATCTTATCGAAGACGGGACCAACAGATGATGAGACCGGTGACCCGACGTTGGAGAC 1967
Qy      2711 ACGGTAAAGATCTCGGTGTGTGGAAGAAAGTTTCCAATGGCACTCCATAGCACAAA 2770
Db      1968 AACTGCAAGACCTGGGCGAGTGAAGAGCTGTTCAGCTGGCGCTCTGACCAAG 2027
Qy      2771 AGACAGCCGATGATGACCCACAATGACCAAGTGACTGTGTTCTGGCACTTTATG 2830
Db      2028 CGGCAAGCTTCGGACCGGCGAGATGACAGATGGTGGGCTCTTGAATCCTGCTGTG 2087
Qy      2831 CTATCGGAACACCAACC 2847
Db      2088 AACCCGAGCGCGCC 2104

RESULT 15
ADX27817
ID ADX27817 standard; cDNA; 1872 BP.
XX
AC ADX27817;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polynucleotide seqid 10637.
XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomanan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; se.
XX
OS Unidentified.
XX
XX US2004034888-A1.
XX
PN 19-FEB-2004.
PD
PE 28-APR-2003; 2003US-00425114.
PF
XX 06-MAY-1999; 99US-00304517.
XX
PR 05-NOV-2001; 2001US-00985678.
XX
```



QY 2836 -----GGAACACCACTGCTGAGACTGACACGTCAGCGACGCTGCTGCTGCTGCTAC 2890  
 Db 1562 CCAAGCAACTAGCTGCACTACCACTGCTTCAATCCATCTGCCAAAGTCCATGCTAC 1621  
 QY 2891 GTGATGAGTATGCAAACTCAAGACTCTCATTTCTGTCATTGCTTTCATGAGTCT 2950  
 Db 1622 GTGATGAGTATGCAAACTCAAGACTCCACACTTGTGAAGTCCCTCATGAGCACC 1681  
 QY 2951 TCTGATGCTCACTGTTTCTTCGTTTGAACAAGTATTCTCAGAACAGTGAGT 3005  
 Db 1682 TCAGATGCTCAACTTCTTCAAGTTTGAGAAAGTATCTCTCAAAACAGTGAGT 1736

Search completed: September 5, 2006, 17:48:38  
 Job time : 1902 secs

**THIS PAGE IS BLANK**



GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 3, 2006, 18:07:16 ; Search time 14319 Seconds  
(without alignments)  
12403.087 Million cell updates/sec

Title: US-10-519-135-1  
Perfect score: 3176  
Sequence: 1 gttctctctcatgagact.....actctctatagttcttgc 3176

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 2795965780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
EST:\*  
1: gb\_est1:\*  
2: gb\_est3:\*  
3: gb\_est4:\*  
4: gb\_est5:\*  
5: gb\_est6:\*  
6: gb\_hic:\*  
7: gb\_est2:\*  
8: gb\_est7:\*  
9: gb\_est8:\*  
10: gb\_est9:\*  
11: gb\_gsa1:\*  
12: gb\_gsa2:\*  
13: gb\_gsa3:\*  
14: gb\_gsa4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	915.4	28.8	2895	13	CL963372 OaIFCC009
2	638	20.1	639	7	AV827602 AV827602
3	621.2	19.6	626	1	AV523662 AV523662
4	604.4	19.0	974	9	CX675276 CX675276
5	548.6	17.3	948	10	DR929080 DR929080
6	535	16.8	535	1	AV528628 AV528628
7	532.2	16.7	1273	8	CX043849 CX043849
8	530.8	16.7	1273	6	AY106598 AY106598
9	519.8	16.4	889	10	DR938199 DR938199
10	519.6	16.4	841	9	DR069662 DR069662
11	517.6	16.3	841	10	DV137758 DV137758
12	506.2	15.9	511	1	AI992763 AI992763
13	505.6	15.9	823	10	DV129724 DV129724
14	501	15.8	501	1	AV529789 AV529789
15	495.4	15.6	868	10	DT756599 DT756599
16	486.2	15.3	859	10	DT730942 DT730942
17	482.8	15.2	805	11	BZ508185 BZ508185
18	482.4	15.2	907	10	DT763952 DT763952
19					

20	473.4	14.9	857	11	BZ508175 BZ508175
21	470.6	14.8	791	8	CO104679 CO104679
22	452.8	14.3	705	8	CV705151 CV705151
23	451.8	14.2	816	10	DT599409 DT599409
24	448	14.1	990	10	DR929079 DR929079
25	447.8	14.1	816	5	CF438419 CF438419
26	441.8	13.9	870	10	DT728959 DT728959
27	441.2	13.9	446	10	DR63249 DR63249
28	437.4	13.6	939	10	DT763951 DT763951
29	433.2	13.6	710	3	BQ69038 BQ69038
30	427.4	13.5	429	7	AV798760 AV798760
31	424	13.4	679	1	AI937984 AI937984
32	419.4	13.2	769	8	CV566963 CV566963
33	416	13.1	416	3	BP612895 BP612895
34	415	13.1	720	2	BG125328 BG125328
35	415	13.1	687	10	DT751244 DT751244
36	410.4	12.9	799	10	DM130381 DM130381
37	410.4	12.9	881	8	CV292292 CV292292
38	409.6	12.9	745	8	CV567734 CV567734
39	408.8	12.9	873	10	DR938198 DR938198
40	408.6	12.9	751	8	CO531771 CO531771
41	408.6	12.9	854	9	CX675277 CX675277
42	408	12.8	641	8	CV003016 CV003016
43	406.4	12.8	871	10	DR805250 DR805250
44	404.8	12.7	740	8	CO092850 CO092850
45	402.2	12.7	407	3	BP831239 BP831239

## ALIGNMENTS

RESULT 1  
CL963372 2895 bp DNA linear GSS 21-SEP-2004  
DEFINITION OaIFCC009320 Oryza sativa Expressed Library Oryza sativa (indica  
CL963372  
CL963372.1 GI:52381472  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa (indica cultivar-group)  
Oryza sativa (indica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP  
clade; Euharoidae; Oryzaceae; Oryza.

1 (bases 1 to 2895)

Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,  
Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,  
Wong, G. K. S., Deng, X. W. and Wang, J.

An analysis of transcriptional regulation of the rice genome and  
its comparison to Arabidopsis  
Unpublished (2004)

## JOURNAL

COMMENT  
Contact: Chen Chen  
Department of Bioinformatics  
Beijing Institute of Genomics  
Chinese Academy of Sciences, Beijing 101300, China  
Tel: 86-10-80481559  
Fax: 86-10-80486876  
Email: chenchen@genomics.org.cn  
Rice genomic sequence.  
Class: exon-trapped.  
Location/Qualifiers  
1..2895  
/organism="Oryza sativa (indica cultivar-group)"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:39946"  
/clone\_lib="Oryza sativa Expressed Library"  
/note="Oryza sativa exon trapped genomic sequences"

## FEATURES

source  
ORIGIN  
Query Match 28.8%; Score 915.4; DB 13; Length 2895;  
Best Local Similarity 62.9%; Pred. No. 3.3e-247;  
Matches 1529; Conservative 0; Mismatches 816; Indels 84; Gaps 4;

OY	392	GGACAATCCCTGATGAGATTGGTACGTGTTCTTCTTTGCAAAACCTTAGCTTAATCTCTC	451
Db	349	GGTAGATCTCGCGGCATCGGAGAGCTCAAGAACTACAGTTCCGTGGATTTGTCTGGC	408
OY	452	AATGAAATTAAGTGGGACATACCGTTTTCATTTCCAAAGTTGAAGCAACTGAGACCTG	511
Db	409	AACCTTCTGTATGGAGACATCCCTCTTCCATCTCCAGCTCCAGACCTTGAAGACCTG	468
OY	512	ATTCTGAAGAAATTAACCAATTGATAGGACCGATCCCTTCACACCTTTCACAGATTTCAAC	571
Db	469	ATTTGAAGAACACACAGCTCACGGGACCCATCCCTTCACATGTGCCAAATTCCAAT	528
OY	572	CTGAATAATTCCTGACTTGGCAGAAATTAATCTAGTGGTGAATACCAAGACTATTAC	631
Db	529	CTCAAGACATTGGACCTGGCACAGAACCAAGCTTACAGCCGATATCCAAAGGCTCATATAC	588
OY	632	TGGAATGAAGTCTTACGATCTTGGGTGGGAGGAAACAATTAGTCGGTAACATTTCT	691
Db	589	TGGAATGAAGTCTGCAATACCTAGGTTGAGGGTAATCTCAGTACTGGAACTTTGTCA	648
OY	692	CCAGATTTGTGTCACTGACTGTCCTTTGGTATTTTGAAGTAAGAAACAAGTTGACT	751
Db	649	CCTGACATGTCCCACTGACCTGCGCTGTGTACTTTGATGTAAAGGGAATCAATCTCACA	708
OY	752	GGTAGTATACCTGAGACGATAGAAATTCACCTGCTTCCAGTGTGAGACTTGCTTAC	811
Db	709	GGGACCATTTCCAGAGAGCATAGGGAACCTGCACAGCTTTGAGATTCGAGACATTTGGTAT	768
OY	812	AATCAGCTAACTGGTGAATCCCTTTTGAATGGCTTCCGCAAGTTGCAACATTAATCA	871
Db	769	AACCAAACTCTGGAGAAATACCTTACCAACATAGGCTTTTTCAAAGTAGCCACACTGCA	828
OY	872	TTGCAAGCAATCAACTCTCTGGGAAAGTCCATCAGATGTTGGTCTCATGCAAGCCTT	931
Db	829	CTTCAAGAAATAGACTGACTGAGGAAATTCAGAATGTGATTTGGCTGATGCAAGCTT	888
OY	932	GCAGTCTTAGATCTAAGTGCCAATTGTTGAGTGATCTATTTCTCGGATTTCCGAAAT	991
Db	889	GCTGTTCTA-----	897
OY	992	CTTACTTTCACCGAATAATGATTTTGGACAGTAAACAAGTACGTGTAATTCACCT	1051
Db	898	-----TATTTAATGGGAAACAATTAATCTGAGTCAACCGCG	936
OY	1052	GAGCTTGGAAACATGTCAAAACTCCATTAACCTGGAACCTCAATGATTAATCATCTCACGGGT	1111
Db	937	GAGCTTGGGAACATAGTAATTAATTAAGTACCTACCTACCAATGATTAATGATTTGTGGCG	996
OY	1112	CATATACCAACAGACTTGGGAAGCTTACTGACTTGTGATCTGAATGTGGCCAAACAT	1171
Db	997	ACAATTTCCAGACGAGACTTGGCCAACTTGAAGAGCTTTTGAATCAATTTCTGCCAACAC	1056
OY	1172	GATCTGGAAAGCCATACCTGATCATCTGAGCTCTTGGCAACAATCTTAACAGCTTAAT	1231
Db	1057	AATCTTCAAGGCTCAATCTCTGCAAAACATCAAGTTCTTGACCTGCTTAACAAATTCAT	1116
OY	1232	GTTCAATGGGAACAAGTTTAGTGGCACTTAACCCGAGACTTTCAAAAAGCTGGAAGATAG	1291
Db	1117	GTTTATGGCAATTAAGCTAAATGTGTTCTAATCTCTGCTGTTTCCAGAGTTGGAGAGCTG	1176
OY	1292	ACTTAACCTTAATCTGTCCAGCAACAATATCAAAAGGTCCAAATCCCGGTGAGCTATCTGCT	1351
Db	1177	ACTTACTTGAACCTTAATCTTCAAAACAATTTCAAAAGGCATTAATCTTGAAGCTTGTGTAC	1236
OY	1352	ATCGGTAACCTTAGATACATTTGATCTTTCCAAACAAGAATTAATGGAATCATTTCTTCT	1411
Db	1237	ATCATCAACTTGGACACATTTGATCTTTCTTAACAATGAATTCCTGAGCAAGTTCCTGCT	1296
OY	1412	TCCCTGGGATTTGGAGCATTTCTCAAGATGAAGCTTGAGTAAGAAATCATATACTGCT	1471
Db	1297	ACCAATTTGGATCTAGAGCACTTCTTGAACCTGAATTTGATGAAGACCAATCTTGAATGGG	1356
OY	1472	GTAGTTCAGGCACTTTGGAATCTAAGAACATCATGAAATAGATCTTTCAATTAAT	1531

Db	1357	CCAGTTCCTGCTGATGTTTGGAACTTGGAAAGCGTCAAGTAAATGATATGTCACAAAC	1416
OY	1532	GATATCTGTGGCCCAATTCGAAAGAGCTTAAACAATTACAGAACATAATTTGCTGAGA	1591
Db	1417	AACCTATCTGTAGTCTGCCCGGAGAACTTGGACAACCTTCAAAACCTTGATAGCCTGATTT	1476
OY	1592	CTGGAAAAATTAACCTGACTGGTAAATG---TGGTCAATTAAGCAACGTGCTCAAGTGC	1648
Db	1477	CTTAACAACAACAATTTGGTTGGGGAGATCCCTGCTCAATTTGGCCACTGCTTCAGCTTA	1536
OY	1649	ACTGATTTGAATGATATCTCATACAAACCTGTAGGTGATATCCCTAAGAACATAATTC	1708
Db	1537	AATTAACCTGAATTTGTTCATACAACAATTTATCTGGACATGATCCGATGGCAAAAGAACTTC	1596
OY	1709	TCAAATTTTACACCAAGAGCTTCAATGGCAATCCTGGTCTTTGGGGTAAAGTTGGCTAAAC	1768
Db	1597	TCGAAATTCCTCAATGGAAAGCTTCTGGGTAAATCAATTAACGATGTTTACCTGCAAAAT	1656
OY	1769	TCACCGGTGATGATTTCTGTGCAACTGTAGAGAGTGCATATCTTAGAGAGCTTATGTT	1828
Db	1657	TCCAGCTGTGAGAACTCTCATGGA---CAAAAGTTAAATTTCAAAGACAGCAATTCCT	1713
OY	1829	GGAATAGCTTATTTGGGGGAACTGTGATCCTTCTCATGTGCTTAAATAGCAGCTTCGACCG	1888
Db	1714	TGCATTATCTTAGGCTTTATTCATATATGTGCTGTGCTGTCTGTTGGCTAATATATAAACA	1773
OY	1889	CATTAATCTCTCTCTCTTTCTGTATGGAATCACTTGAACAAACCGATTAATTTGACACCG	1948
Db	1774	AATCAACCAAGCACTGTCTCAAAAGGATCCGATAGCCAGTGCAG---GACCTTCA	1827
OY	1949	AAGCTCGTCAATCCCTTCATATGAAACATGAGCACTCAAGTTTACAGAGATATCATGAAATG	2008
Db	1828	AAGTATGTTGTTCTCCAGATGAGCATGGCTATTCATTAACGAGACATCATGAGCGTG	1887
OY	2009	ACAGAGATTAATAGTGAAGATTTATCATATTTGGGACAGAGCATCAAGCATGTATATACAA	2068
Db	1888	ACAGAGAAATTTGACGAGAAATTCATCATATGGCTATAGGGCTCAAGCACTGTCTAACAA	1947
OY	2069	TGATTTTGAAGATTTGAAAACGGGTGGGATTAAGCGGCTTACTCTCACAAACCACAG	2128
Db	1948	TGTBACTCAAGACGGCGAAGGCAATGGCTGTCAAGCGGCTTTACAGTCAGATAACAT	2007
OY	2129	TCAATGAACAGTTTGAACAGAACTGAGATGCTAATGATCAAGACAGAAATCTT	2188
Db	2008	AGCTCCGAGAGTTTGAACAGAACTAGAGACAAATGGAGCATAGGACAGGAATCTT	2067
OY	2189	GTGAGCTTAACACCTAATTCCTCTCTCACTTGGGGAGTCTCTGTCTATGACTAATTTG	2248
Db	2068	GTTAGCTTCATAGCTTCTGCTATCTCCACATGAAATTTGCTCTTCTAATATTAATCATG	2127
OY	2249	GAAAAATGTAAGCTCTGGGATCTTCTTCAATGGCCCTACGAGAAAAAGACTTTGATTTGG	2308
Db	2128	GAAAAATGTTCTTGTGGGATCTTCTCCACGGTCCATCAAAAGAAAGTAGAAGCTCAACTGG	2187
OY	2309	GACACACGGCTTAAATAGATATGTGTGACGACAAAGTTTAGCTTAATCTAACCATGAC	2368
Db	2188	GACACAAAGATGTAGATCGGGGTGGAGCTGCAAAAGGGCTGCTATCTCCACATGAC	2247
OY	2369	TGTAGTCCAAGGATTCATTCACAGAGAGTGAAGTCTGCCAATTTCTTTGGACAAAGAC	2428
Db	2248	TGCAACCTTGCAATTCACACAGATGTCAAGTCTCCAAATCTGCTGTGACAGAAAC	2307
OY	2429	TTAGAGGCTGCTTGAACAGATTTTGAATAGCGAAAAAGCTTGTGTGTCAAAATGCAT	2488
Db	2308	TTTCGAAACCGCACTCTTCAGATTTCCGCAATAGCCAAATGTGTCCCTCTGCCAAAGTCCAT	2367
OY	2489	ACTTCACTTAAGTATGGGCAAGATAGGTTATATAGACCCCGAGATGCTGCACTTCA	2548
Db	2368	GCTTCCATTATGTCTAGAACCAATCGGCTACATTAATTCGAGATATCCAGAACTTCC	2427
OY	2549	CGGCTCACTAGAAATCCGATGTCTACAGTTATGAATAGTCTTCTTGGATTTGTTAAC	2608

Db 2428 AGGCTCAATGAGAAATCTGATGTGTACAGCTTCGGATCGTCTCTTGGAATTGCTCACA 2487  
QY 2609 CGAAGGAAGCCGTGTGATGACGATCCATCTCCACATCTGATTAATGCAAGAGGGG 2668  
Db 2488 GGGAGGAAGCCGTCGACACGAATCGAATCTTGATTAATGATCTCTCAAGCTGAT 2547  
QY 2669 AACATGAACTGATGGAATATGAGATCCAGATCATCATGACGTGTAAAGATCTCGT 2728  
Db 2548 GACACACATCTCATGAGGAGGAGTGGACTCGAGGTGTCACTGACGTGACAGGACATGGGA 2607  
QY 2729 GTGGTGAAGAAAGTTTCCAACTGGCAGCTCCATGACCAAAAGACGCCGAATGATCGA 2788  
Db 2608 CTGGTAGGAAGGCTTCACGCTCGCCCTTCTGTGACCAAGAGGACCCCTTGACACCGG 2667  
QY 2789 CCCACATGACGACGAGTGGTCTGTTCT 2817  
Db 2668 CCGACCATGACGAGGTTGCAAGGTTCT 2696

RESULT 2  
AV827602 639 bp mRNA linear EST 01-APR-2002  
LOCUS AV827602 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-17-H05 5'  
DEFINITION AV827602.1 GI:19869662  
ACCESSION AV827602  
VERSION AV827602.1  
KEYWORDS EST  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
1 (bases 1 to 639)  
Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,  
Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,  
Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.  
and Shinozaki,K.  
Large scale analysis of Arabidopsis full-length cDNA (2002b)  
Unpublished (2002)  
Contact: Motoaki Seki  
Plant Functional Genomics Research Group  
RIKEN Genomic Sciences Center  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: 81-298-36-4359  
Fax: 81-298-36-9060  
Email: mseki@rc.riken.go.jp  
An Arabidopsis full-length cDNA library was constructed essentially  
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI  
and XhoI was ligated to modified Lambda FIC-1 vector (Carninci et  
al., submitted for publication) digested with BamHI and SalI. This  
clone is in a modified plasmid vector. Please visit our web  
site (http://www.gsc.riken.go.jp/e/Plant/index\_e.html) for further  
details.

FEATURES  
source  
1. 639  
/organism="Arabidopsis thaliana"  
/mol\_type="mRNA"  
/db\_xref="taxon:3702"  
/clone="RAFL09-17-H05"  
/dev\_stage="Plants at various developmental stages from  
germination to mature seeds"  
/lab\_host="DH10B"  
/clone\_lib="RAFL9"  
/note="Site 1: BamHI, Site 2: SalI, subjected to  
dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24  
hr) treatments"

ORIGIN  
Query Match 20.1%; Score 638; DB 7; Length 639;  
Best Local Similarity 100.0%; Pred. No. 8.9e-169;  
Matches 638; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTTCTTCTTCATGAGACTTGAAGCTTTAAAGTATATCTAAAAACGACGCTGTTTA 60

Db 2 GTTCTTCTTCATGAGACTTGAAGCTTTAAAGTATATCTAAAAACGACGCTGTTTA 61  
QY 61 AGACTGTGTGAGAAATAGCTCTGTTTAGAGATATGTTCTTCTGGTTTCTCTTCG 120  
Db 62 AGACTGTGTGAGAAATAGCTCTGTTTAGAGATATGTTCTTCTGGTTTCTCTTCG 121  
QY 121 CTGAGCTTAGTACTGACTGTGACTTCAGAGGAGGAGCAAGTCTGAGATTAAAG 180  
Db 122 CTGAGCTTAGTACTGACTGTGACTTCAGAGGAGGAGCAAGTCTGAGATTAAAG 181  
QY 181 GTCAATCAAGATGTGAACATGTTCTTATGATCTGAGCAACTTCACTTCCGATTA 240  
Db 182 GTCAATCAAGATGTGAACATGTTCTTATGATCTGAGCAACTTCACTTCCGATTA 241  
QY 241 TTGTGTCTGAGAGGTGTCTTGTGAAATGTCACTTCAATGTTGCTTAAATT 300  
Db 242 TTGTGTCTGAGAGGTGTCTTGTGAAATGTCACTTCAATGTTGCTTAAATT 301  
QY 301 GTCAATTTGAATCTTGATGAGAAATCTCACTGCTATGAGATCTCAAGATCTCTT 360  
Db 302 GTCAATTTGAATCTTGATGAGAAATCTCACTGCTATGAGATCTCAAGATCTCTT 361  
QY 361 GTCAATTTGATCTGCGAGGTATCGCTTGTCTGACAAATCCCTGATGAGATTGTA 420  
Db 362 GTCAATTTGATCTGCGAGGTATCGCTTGTCTGACAAATCCCTGATGAGATTGTA 421  
QY 421 TTCTTCTTTGCAAAACTTGACATTATCTTCAATGAATTAAGTGTGACATACCGTTTC 480  
Db 422 TTCTTCTTTGCAAAACTTGACATTATCTTCAATGAATTAAGTGTGACATACCGTTTC 481  
QY 481 GATTGGAAGTTGAACCACTTGAGCAGCTGATTCGAAATTAACCAATTGATAGACC 540  
Db 482 GATTGGAAGTTGAACCACTTGAGCAGCTGATTCGAAATTAACCAATTGATAGACC 541  
QY 541 GATCCCTTCAACACTTTCACAGATTCCAACCTGAAATTTCTGACTTGGACAGATTA 600  
Db 542 GATCCCTTCAACACTTTCACAGATTCCAACCTGAAATTTCTGACTTGGACAGATTA 601  
QY 601 ACTCAGTGTGAGATTCGAAGCTTATTTACTGGATG 638  
Db 602 ACTCAGTGTGAGATTCGAAGCTTATTTACTGGATG 639

RESULT 3  
AV523662/c  
LOCUS AV523662 626 bp mRNA linear EST 18-FEB-2004  
DEFINITION AV523662 Arabidopsis thaliana aboveground organs two to six-week  
old Arabidopsis thaliana cDNA clone APZL5f03F 3', mRNA sequence.  
ACCESSION AV523662  
VERSION AV523662.1 GI:8683190  
KEYWORDS EST.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
1 (bases 1 to 626)  
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.  
A large scale analysis of cDNA in Arabidopsis thaliana: Generation  
of 12,028 non-redundant expressed sequence tags from normalized and  
size-selected cDNA libraries  
DNA Res. 7 (3), 175-180 (2000)  
JOURNAL PUBLISHED  
10907847  
COMMENT Contact: Erika Asamizu  
The First Laboratory for Plant Gene Research  
Kazusa DNA Research Institute  
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan  
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.  
Location/Qualifiers  
1. 626  
/organism="Arabidopsis thaliana"  
/mol\_type="mRNA"



Db 121 AGACTGGACTACATAATTTATTCAGGGAGTAAATGTGCTGATCAATGCTCAGTCTT 180  
 Qy 1649 ACTGATATGATATGATCTATTAACACCTGCTAGTATATCCCTAAGAAATTAATTC 1708  
 Db 181 TCTGTCTTAAACCTATCTTATTAACACCTGCTAGTATATCCCTAAGAAATTAATTC 240  
 Qy 1709 TCAAGATTTTACCAGACAGCTTCAATGCGAATCTGCTTTGCGGTAGTGGCTAAAC 1768  
 Db 241 TCAAGATTTTACCAGACAGCTTCAATGCGAATCTGCTTTGCGGTAGTGGCTCAAT 300  
 Qy 1769 TCACCGTGTATGATTTCTGCTGACATGTAAGATGTCAATCTCTAAGACAGCTATTCTT 1828  
 Db 301 TCTGACATGCGGTGATCTCAATCCAAAGGAAAGATTTCTAAGACAGCTATTCTC 360  
 Qy 1829 GGAATGACTATTTGGGGGACTTGTGATCTCTCTCTCTCTTAAATAGAGAGCTTGGCCGAC 1888  
 Db 361 GGAATGCTCTCGGTGACCTTGAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420  
 Qy 1889 CATATATCT 1948  
 Db 421 CACATATCT 480  
 Qy 1949 AAGCTGTCTATCT 2008  
 Db 481 AAGTATGATCT 540  
 Qy 2009 ACAGAGATCTATGATGAGATATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2068  
 Db 541 ACCGAGATTTGATGAGATATATCT 600  
 Qy 2069 TGTGTTTGAAGAATTTGAACCGGTGCGATTTAAGCGGCTTCTCTCTCTCTCTCTCTCTCTCTCT 2128  
 Db 601 TGTGTTTGAAGAATTTGAACCGGTGCGATTTAAGCGGCTTCTCTCTCTCTCTCTCTCTCTCTCT 660  
 Qy 2129 TCAATGAACAGTTTGAACAGAACTCGAGATGCTAATGATGATCAAGCAAGAAATCTT 2188  
 Db 661 TGTGTTGAAGAATTTGAGACAGAGCTTGAACAGGCTTGGAGACATCAAGCAAGAAATCTG 720  
 Qy 2189 GTAGAGCTAAGCTTATCT 2248  
 Db 721 GTAGAGCTTCAAGAGATATCTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780  
 Qy 2249 GAAATATGATGCTCTGAGATCT 2308  
 Db 781 GAAATATGATGCTCTGAGATCT 840  
 Qy 2309 GACACACGCTTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2368  
 Db 841 GACACTGCTGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
 Qy 2369 TGTATGTCAGAGATCTATTCACAGAGAGTGAAGTCTGCAACATCTCTCTGAGCAAGAC 2428  
 Db 901 TGTATGTCCTGAAATCAACCGGATGATGATGATGATGATGATGATGATGATGATGATGATG 960  
 Qy 2429 TTAGAGGCTGCTT 2442  
 Db 961 TTGGAAGCCATCT 974

RESULT 5  
 DR929080 948 bp mRNA linear EST 02-AUG-2005  
 LOCUS EST1120619 Aquilegia cDNA library Aquilegia formosa x Aquilegia  
 DEFINITION pubescens cDNA clone COINU40, mRNA sequence.  
 ACCESSION DR929080 GI:71698443  
 VERSION DR929080.1  
 KEYWORDS EST.  
 ORGANISM Aquilegia formosa x Aquilegia pubescens  
 SOURCE Aquilegia formosa x Aquilegia pubescens  
 Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;  
 Ranunculaceae; Aquilegia.  
 REFERENCE 1 (bases 1 to 948)

AUTHORS Hodges, S.A., Rensink, W., Buehl, C.R., Borevitz, J., Kramer, E.,  
 Nordborg, M., and Tomkins, J.  
 TITLE Generation of ESTs from Aquilegia  
 JOURNAL Unpublished (2005)  
 COMMENT Other ESTs: EST1120618  
 Contact: Scott Hodges  
 Department of Ecology, Evolution and Marine Biology  
 University of California, Santa Barbara  
 Santa Barbara, CA 93106, USA  
 Tel: 805 893 7813  
 Fax: 805 893 4724  
 Email: hodges@lifesci.ucsb.edu  
 Seq primer: M13 Reverse.  
 Location/Qualifiers  
 FEATURES  
 source  
 1.948  
 /organism="Aquilegia formosa x Aquilegia pubescens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:338618"  
 /clone="COINU40"  
 /tissue\_type="mixed shoot and floral apical meristems,  
 flower buds, leaves and roots"  
 /lab\_host="DH10B 11 (11 and 15 phage resistance)"  
 /clone\_lib="Aquilegia cDNA library"  
 /note="Vector: PCMV SPORT6.1; Site 1: EcorI; Site 2: NotI;  
 F2, F3, and F4 lines of Aquilegia formosa x A. pubescens  
 were grown from seed in greenhouses at UC Santa Barbara.  
 From these plants three sets of tissue were collected: 1)  
 Small flower buds (<10 mm) and very young inflorescences  
 (71 & 29% by weight respectively), 2) Medium (7-20 mm) and  
 large (at or near anthesis) flower buds (65 & 35% by  
 weight respectively) and 3) Shoot apical meristems. A  
 fourth set of tissue was collected from plants of A.  
 formosa. These plants were grown from seed in sand and at  
 approximately 1 month root tissue and leaf tissue of  
 various developmental stages were collected (84 & 16% by  
 weight respectively). Total RNA was extracted from each  
 set of tissue and pooled in the following proportions:  
 1.5X from sets 1 & 2, 1X from sets 3 & 4. From the pooled  
 total RNA, mRNA was extracted and enriched for full-length  
 messages and then normalized with proprietary methods by  
 Invitrogen."

ORIGIN  
 Query Match 17.3%; Score 548.6; DB 10; Length 948;  
 Best Local Similarity 74.5%; Pred. No. 2.2e-143;  
 Matches 704; Conservative 0; Mismatches 239; Indels 2; Gaps 1;

Qy 1759 TTGGCTAAATCTCACCGTGCATGATTTCTGCGAAGTGTACAGTCTCATCTCTAGAGC 1818  
 Db 1 TTGGATGATGATTCACCTTGTACAGTTCCACCTAAGAAAGAGCTCCAAATATCTAAAGC 60  
 Qy 1819 AGCTATTTCTGGAATGCTATTTGGGGAGCTTGTGATCTCTTCATGCTTAAATAGCAGC 1878  
 Db 61 GGCTATTTCTGGAATGCTATTTGGGGAGCTTGTGATCTCTTCATGCTTAAATAGCAGT 120  
 Qy 1879 TTGGCGACGCGAATATCT 1938  
 Db 121 ATGCAAGCGCGAATATCT 180  
 Qy 1939 TTGCAACGCGAAGCTGTCATCTCTCATATGACATGAGCACTCCAGTTTACAGAGATAT 1998  
 Db 181 TATCTCACCAAGCTGTGATCTCTCATATGAAATGAGGCTTCAATGATAGCAAGACAT 240  
 Qy 1999 CATGAGATGACAGAGATCTAATGATGAGATGATGATGATGATGATGATGATGATGATG 2058  
 Db 241 CATGAGATGACAGAGATTTTGTGAGAAATATATATATTTGTTATGAGGACATCTGACAC 300  
 Qy 2059 TGTATCAATGCTGTTTGAAGATTTGTAACCGGTGCGATTTAAGCGGCTTAACTCTCA 2118  
 Db 301 TGTCTTAAATGCTCTGTAAGACTGCAAGACCATTAAGAGCTTAACTCTCA 360  
 Qy 2119 CAACCGACGTCATGAAACAGTTTGAACAGAACTCGAGATGCTAAGTACATCAAGCA 2178

Db 361 TTACCTCAGAGCCTGAGAGGTTTGAGACAGAGCTTGAGGATTCAGACA 420  
QY 2179 CAGAAAATTCTGTAGCCTACAGGCTTATTCCTCTCTACCTGGGAGGCTTCTGTCTA 2238  
Db 421 TCGGAATCTTTGTTTCTCCAGGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480  
QY 2239 TGACTATTTGGAAAATGTAGCCTCTGGGATCTTCTTCATGGCCCTCAGAAAAAGAC 2298  
Db 481 TGACTACATGAGATGTAGCCTTGGGATCTCTCTCATGGCCCTCAAAAAACAGAA 540  
QY 2299 TCTTGATTTGGACACAGCCTTAAGATAGCATATGTGACACACAGTTTACTTATCT 2358  
Db 541 ACTGAGCTGGGAATCTGCTCAAAATAGCTCTTGAGCTGCGAGGGGCTAGCTTATCT 600  
QY 2359 ACACATGACTGTAGTCCAGAGATCATTCACAGAGAGTGAAGTGCACCAATCTCTT 2418  
Db 601 TCATCATGATTTGATGTCGGCTATAGTCCACAGAGAGCTGAATCATCAATCTCTCT 660  
QY 2419 GGACAAAGACTTAGAGGCTGTTTGACAGATTTTGAAATAGCGAAAAGCTTGTGTGTC 2478  
Db 661 AGACAAAGATTTTGAAGCCATCTCACAGATTTTGGAAATGCGAAGAGCTTGTGCACTTC 720  
QY 2479 AAAGTCACATCTTCAACTTACGTATGGGACGATAGCTTACTTACATCCCGAGATGTC 2538  
Db 721 CAAGTTGTACACCTCGACCTATGTTATGGGACCATAGGCTACATAGACCTTGATATGC 780  
QY 2539 TCGCACTTCAAGGCTCCTAGAAATCCGATGCTACATGTTAGGAATAGCTTCTCTTGA 2598  
Db 781 TCGCACTTCTGCGCTTACTGAGAACTTGATGTTTACGCTATGGAATGATCTCTCTTGA 840  
QY 2599 GTTGTTAACCGAAGAAAGCGCTTGATGACGAATCCATCTCCACCATCTGATATGTC 2658  
Db 841 GCTGTTCACGGGAAGAAAGCGGTGGAATGATGATGCAATCTTCATCATCTGATATA--TGT 898  
QY 2659 AAAGACCGGGCAACATGATGATGGAATGGGACGATCCACACT 2703  
Db 899 CTGAGCTGCCAACATGCCGTATGAGAGACTGTTGATCTGACAT 943

RESULT 6  
LOCUS AV528628/c 535 bp mRNA linear EST 19-FEB-2004  
DEFINITION AV528628 Arabidopsis thaliana aboveground organs two to six-week old Arabidopsis thaliana cDNA clone APZL1410R 5', mRNA sequence.  
ACCESSION AV528628  
VERSION AV528628.1 GI:8688911  
KEYWORDS EST.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE 1 (bases 1 to 535)  
AUTHORS Aasamizu, E., Nakamura, Y., Sato, S. and Tabata, S.  
TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries  
JOURNAL DNA Res. 7 (3), 175-180 (2000)  
PUBMED 10907847  
COMMENT Contact: Erika Asamizu  
The First Laboratory for Plant Gene Research  
Kazusa DNA Research Institute  
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan  
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/planc/.  
Location/Qualifiers  
1. .535  
/organism="Arabidopsis thaliana"  
/mol\_type="mRNA"  
/ecotype="Columbia"  
/db\_xref="taxon:3702"  
/clone="APZL1410R"  
/tissue\_type="aboveground organs"  
/dev\_stage="two to six-week old"

ORIGIN  
Query Match 16.8%; Score 535; DB 1; Length 535;  
Best Local Similarity 100.0%; Pred. No. 1.3e-139;  
Matches 535; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XhoI

/clone\_1ib="Arabidopsis thaliana aboveground organs two to six-week old"  
/note="Vector: pBluescriptII SK-; Site\_1: EcoRI; Site\_2: XhoI"

QY 2597 GAGTGTAAACCCGAGGAAGACCGTGTAGAGAAATCCAAATCCACCATCTGATTAAG 2656  
Db 535 GAGTGTAAACCCGAGGAAGACCGTGTAGAGAAATCCAAATCCACCATCTGATTAAG 476  
QY 2657 TCAAGACGGGGAACAATGATGATAATGGAGATCCAGATCCATCATGAGCTGT 2716  
Db 475 TCAAGACGGGGAACAATGATGATAATGGAGATCCAGATCCATCATGAGCTGT 416  
QY 2717 AAGATCTCGTGTGTGAAGAAAGTTTCCAACTGGCACTCTTATGACCAAAAGACAG 2776  
Db 415 AAGATCTCGTGTGTGAAGAAAGTTTCCAACTGGCACTCTTATGACCAAAAGACAG 356  
QY 2777 CCGAATGATGACCCCAATGACACAGGATCTGCTGCGCACTTTATGCTATG 2836  
Db 355 CCGAATGATGACCCCAATGACACAGGATCTGCTGCGCACTTTATGCTATG 296  
QY 2837 GAACAACACACTCTGCTGACATGACAGCTGACAGCCTGCTGCTGCTGCTGCTGCTGCT 2896  
Db 295 GAACAACACACTCTGCTGACATGACAGCTGACAGCCTGCTGCTGCTGCTGCTGCTGCT 296  
QY 2897 GAGTATGCAAAATCTCAAGACTCTCATCTGTGCAATGCTCTTCCATGATGCTTGTGAT 2956  
Db 235 GAGTATGCAAAATCTCAAGACTCTCATCTGTGCAATGCTCTTCCATGATGCTTGTGAT 176  
QY 2957 GCTCACTGTTCTTCTGCTTGGTGGACAGATATTTCTCAGAACAGTGAAGTCTTTCGTT 3016  
Db 175 GCTCACTGTTCTTCTGCTTGGTGGACAGATATTTCTCAGAACAGTGAAGTCTTTCGTT 116  
QY 3017 AGGAGGGAATCTTTAAACGGTATCTTTTCTGCTGAAGCTGTAGAAAAATTAATG 3076  
Db 115 AGGAGGGAATCTTTAAACGGTATCTTTTCTGCTGAAGCTGTAGAAAAATTAATG 56  
QY 3077 TCTCATGTAAAGTATTAATGACATGCTTATTTATTTAGCAAGTGTGTGTGTG 3131  
Db 55 TCTCATGTAAAGTATTAATGACATGCTTATTTATTTAGCAAGTGTGTGTGTG 1

RESULT 7  
LOCUS AV529393 535 bp mRNA linear EST 19-FEB-2004  
DEFINITION AV529393 Arabidopsis thaliana aboveground organs two to six-week old Arabidopsis thaliana cDNA clone APZL35f03R 5', mRNA sequence.  
ACCESSION AV529393  
VERSION AV529393.1 GI:8688916  
KEYWORDS EST.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE 1 (bases 1 to 535)  
AUTHORS Aasamizu, E., Nakamura, Y., Sato, S. and Tabata, S.  
TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries  
JOURNAL DNA Res. 7 (3), 175-180 (2000)  
PUBMED 10907847  
COMMENT Contact: Erika Asamizu  
The First Laboratory for Plant Gene Research  
Kazusa DNA Research Institute  
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan  
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/planc/.  
Location/Qualifiers



```

source
1. 535
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
/clone="APL35f03R"
/tissue_type="aboveground organs"
/dev_stage="two to six-week old"
/clone_id="Arabidopsis thaliana aboveground organs two to
six-week old"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"

ORIGIN

Query Match      16.8%; Score 535; DB 1; Length 535;
Best Local Similarity 100.0%; Pred. No. 1.3e-139;
Matches 535; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      30  TTAAGATATCTAAAAACGACGCTTTTAAAGCTGTGTGAGAAAGCTCTGTTT 89
Db      1  TTAAGATATCTAAAAACGACGCTTTTAAAGCTGTGTGAGAAAGCTCTGTTT 60

QY      90  GAGATATGTTCTTCTGTTCTCTTCTGCTTGTAGCTTAGTGTGACTTCTGAG 149
Db      61  GAGATATGTTCTTCTGTTCTCTTCTGCTTGTAGCTTAGTGTGACTTCTGAG 120

QY      150  AGAGAGGAGCAAGCTTCTGTGAGATTAAAGATCAAAAGATGTGAACAATGTTCTT 209
Db      121  AGAGAGGAGCAAGCTTCTGTGAGATTAAAGATCAAAAGATGTGAACAATGTTCTT 180

QY      210  ATGACTGACACACTTCACTTCTCGGATTAATGTGCTGAGAGGCTGCTTGTGAAA 269
Db      181  ATGACTGACACACTTCACTTCTCGGATTAATGTGCTGAGAGGCTGCTTGTGAAA 240

QY      270  ATGTCACTTCAATGTTGTGCTCTTAAATTTGTGCAATTTGAATCTTGATGAGAAATCT 329
Db      241  ATGTCACTTCAATGTTGTGCTCTTAAATTTGTGCAATTTGAATCTTGATGAGAAATCT 300

QY      330  CACCTGCTATGAGATCTTCAAGAGTCTTCTTCAATTTGATCTGCGAGTAAATCGCTTGT 389
Db      301  CACCTGCTATGAGATCTTCAAGAGTCTTCTTCAATTTGATCTGCGAGTAAATCGCTTGT 360

QY      390  CTGGACAAATCCCTGTGATGTGATGCTGCTTCTTCTTGGCAAACTTGAACCTTATCTT 449
Db      361  CTGGACAAATCCCTGTGATGTGATGCTGCTTCTTCTTGGCAAACTTGAACCTTATCTT 420

QY      450  TCAATGAATTAAGTGTGATACCGTTTTCGATTTGCAATTTGAAGTGAACAATTGAGCAGC 509
Db      421  TCAATGAATTAAGTGTGATACCGTTTTCGATTTGCAATTTGAAGTGAACAATTGAGCAGC 480

QY      510  TGATTTCTGAAGATTAACAATTGATGAGACCGATCCCTTGAACACTTTTCAAGAT 564
Db      481  TGATTTCTGAAGATTAACAATTGATGAGACCGATCCCTTGAACACTTTTCAAGAT 535

RESULT 8
CX043849      810 bp      CRNA      linear      EST 09-DEC-2004
LOCUS      CX043849
DEFINITION      UCRCS07.13G10.g Parent Washington Navel Orange Thrip-Challenged
                  Flavado CDNA Library UCRCS07 Citrus sinensis cDNA clone
ACCESSION      UCRCS07.13G10-N19-1-7.g, mRNA sequence.
VERSION      CX043849
KEYWORDS      CX043849.1 GI:56528140
SOURCE      EST.
ORGANISM      Citrus sinensis
              Citrus sinensis
              Citrus sinensis
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
              rosids; eurosids II; Sapindales; Rutaceae; Citrus.
REFERENCE      1 (bases 1 to 810)
AUTHORS      Close,T.J., Roose,M.L., Federici,C.F., Fenton,R.D., Watkins,P.,
              Morse,J., Wamamaker,S., Lyon,M., Ye,X.R., Jang,C., Quintilio,C.,
              Ikeda,J., Collin,M., Kacar,Y., Landry,B., Hubert,N., Laforest,M.,

```

```

TITLE      Landry,J. and Ligonde,A.
JOURNAL      Development of EST Resources and New Genetic Markers for California
COMMENT      Citrus - Parent Washington Navel Orange Thrip-Challenged Flavado
              CDNA Library UCRCS07
              Unpublished (2004)
              Contact: Timothy J. Close
              Department of Botany & Plant Sciences
              University of California
              Riverside, CA 92521-0124, USA
              Tel: 909-787-3318
              Fax: 909-787-4437
              Email: timothy.close@ucr.edu
              Seq primer: T3

FEATURES
source
1. 810
/organism="Citrus sinensis"
/mol_type="mRNA"
/cultivar="Parent Washington Navel"
/db_xref="taxon:2711"
/clone="UCRCS07.13G10-N19-1-7.g"
/tissue_type="Flavado"
/dev_stage="11 year old trees"
/lab_host="E. coli TJC121"
/clone_id="Parent Washington Navel Orange
Thrip-Challenged Flavado CDNA Library UCRCS07"
/note="Vector: lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Trees were grown in the field
at University of California, Riverside using standard
horticultural practices. Young fruits were placed in a
cage with thrips (Scirtothrips citri). Infestations were
conducted by Watkins (Morse lab) and flavado collected by
Federici (Roose lab) from May-June 2003. The thrips were
collected from naturally infested Rus plants by sucking
into a tube. A flexible hose was attached to a tube that
extended into a covered vial, and another tube stuck out
of the vial at a right angle. The bent tube was held above
the thrips, sucking on the flexible tube created a vacuum,
pulling the thrips into the vial. Thrips were knocked off
the Rus plant onto a manila folder, then only second
instars were captured. This was done repeatedly until
enough were obtained. Approximately 7-10 thrips were caged
on each fruit within a plastic vial made of a 8 cm long by
5 cm diameter tube that had a very fine mesh organdy
fabric glued to the bottom. The plastic cap was slit from
the edge to the center so it could be slipped over the
stem of the fruit. It was put in place, the thrips were
knocked into the vial and it was fastened onto the cap
then all gaps were closed with masking tape. The thrips
naturally move up to the fruit. The cages were left in
place for two days, then removed. The fruit were checked
to be sure the thrips had stayed on, and then brought to
the lab to cut off the flavado using a razor blade. Only
the flavado from the stem 1/3 to 1/2 of the fruit was
used. For controls an equal number of comparable sized
fruit were caged without thrips, and the peel collected
from them in the same manner. Tissues were frozen in
liquid nitrogen, then stored at -80C until further
processing. Fenton (Close lab) purified RNA by the phenol
method described in J. Japanese Soc. Hort. Sci. 1996. 64
(4): 809-814, purified poly(A) mRNA using an Oligotex mRNA
Kit (Qiagen), produced a primary cDNA library using a
lambda ZAP XR CDNA Synthesis Kit (Stratagene), then
mass-excised 0.77 million plu from the primary library to
produce a phagemid population. The library was made from
equal portions of RNA from each of the two treatments.
Phagemids were plated, plasmid DNA purified, cDNA clones
archived, and DNA sequences determined bi-directionally
using an ABI3730 at DNA landmarks (Landry, Hubert,
Laforest, Landry, Ligonde). Chromatogram files were
downloaded by FTP by Close, then processed by Wamamaker
(Close lab) using the Harvest pipeline
(http://harvest.ucr.edu) to remove vector and cloning
oligo sequences and various contaminants, and to trim to a

```

high quality region. Sequences that retained a phred 17 region of at least 100 bases were assembled, then chimeras were removed following manual inspection of assemblies (Close, Roose, Federici, Wamaker, Lyon, Ye, Yang, Collin, Kacar, Ikeda, Quintilio). Sequences that survived all removal steps were submitted to GenBank."

## ORIGIN

```

Query Match      16.8%; Score 532.2; DB 8; Length 810;
Best Local Similarity 78.6%; Pred. No. 9.5e-139;
Matches 636; Conservative 0; Mismatches 173; Indels 0; Gaps 0;

QY 464 GGTGACATACCGTTTCGATTTCGAAGTGAAGCACTTGAGCAGCATTTCTGAAGAT 523
Db 1 GGAGACATACCTTTCTCAATTTCTAAAGTGAACAACTGGAATTTCTAATTTGAAAAAC 60

QY 524 AACCAATTTGATAGACGCGATCCCTTCAACATTTACAGATTCGAAACCTGAAATTCG 583
Db 61 AATCAGTTGATTTGACCAATTCCTTCTAATTTGTCTCAGCTTCTTAATTTAAAGTTT 120

QY 584 GACTTGACAGAAATTAATCTCAGTGAGATACCAAGACTATTTTCTGGAATGAAGT 643
Db 121 GACCTGGCTCTAAATTAATCTCAGTGAGAAATACCAAGCTTTAATCTGGAATGAAGT 180

QY 644 CTTCAGTATCTTGCGGTTGCGAGAAACAATTAAGTTCGGAATTTCTGAGATTTGT 703
Db 181 TTACAAATCTTGTTGCGAGGGAACAACTGTTGTTACATTTCTCCAGATATGT 240

QY 704 CAACTGATCTGCTTTGGTATTTTGAAGTAAACAAGTTGACTGTGATATACCT 763
Db 241 CAGCTTTCTGGGTTGTGTGATCTTGAATGTGAATTAACAGTTGACAGGAGCATTCCT 300

QY 764 GAGACGATAGAAATTCGACGCTTCAGGTTTGAATTTGCTTCCTCAATCAGCTACT 823
Db 301 CAGAAATTTGCAATTCGACTTCTTCAGGCTTGAATTTCTCAACCAAGCTAAGT 360

QY 824 GGTGAGATCCCTTTTGAATCGGCTTCCTGCAATTCGCAATATATGCAAGCAAT 883
Db 361 GGAGAGATTCATTCATCAATTTGGGTTTGTGAATATCTATATATCTTGCAAGAAAT 420

QY 884 CAACTCTTGGAAGATTCATCAAGTATGTGTCTCATGCAAGCCCTTGCACTTTAGAT 943
Db 421 CAGCTGACAGGGAAGATTCATCAATGTGTCTTAATGCAAGGCTTGCAAGTATGAT 480

QY 944 CTAGTGGCACTTGTTGAGTGTATCTATTCCTCGAATTCGGAATCTTACTTGACC 1003
Db 481 TTGAGTGCACATGTATGAGTGAACCAATTCCTCCATTTAGSAAATTTGAGTTACACA 540

QY 1004 GAGAAATTTGATTTGACAGTAAACAGTGAAGTGTCAATTCGACCTGAGCTTGAAC 1063
Db 541 GAGAAATTTGATTTTACAGTAAACAGTGAAGTGTCAATTCGACCTGAGCTTGAAC 600

QY 1064 ATGTCAAAATCTCCCTTACCTGGAACCTCAATGATATATCTCAGGGCTATATACCA 1123
Db 601 ATGCAAAAGCTTCACTCTGGAATTAATGATATATCAGCTCAAGGCAATATTCCTCCA 660

QY 1124 GAGCTTGGGAAGCTTACTGACTTGTGATGATGGAATGAGGCAATGATCTGGAAGA 1183
Db 661 GCGCTTGGGAAGCTTCACTGATTTTATGACTTAATGAGCAACCAACCACTTGAAGG 720

QY 1184 CCTATACCTGATCATCTGAGCTCTTGCACAAAATTAACAGCTTAAATGTTTCATGGAAC 1243
Db 721 CCTATACCTGATCATCTTAAATGATGCACAAAATCTCAACAGCTGGAATGTCATGGAAT 780

QY 1244 AAGTTTATGTCGACTATATCCCGAGCAT 1272
Db 781 AAGTTTAAACGAAACATTCGCGCAGCAT 809

RESULT 9
LOCUS AY106598 1273 bp mRNA linear HTC 22-FEB-2005
DEFINITION Zea mays PC0069596 mRNA sequence.

```

```

ACCESSION AY106598
VERSION AY106598.1 GI:21209676
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 1273)
Gardiner,J., Schroeder,S., Polacco,M.L., Sanchez-Villada,H.,
Fang,Z., Morgante,M., Landewe,T., Fenger,K., Uesche,F.,
Hanafey,M., Tingey,S., Chou,H., Wing,R., Soderlund,C. and Coe,E.H.
Jr.
Anchoring 9,371 maize expressed sequence tagged unigenes to the
bacterial artificial chromosome contig map by two-dimensional
overgo hybridization
Plant Physiol. 134 (4), 1317-1326 (2004)
2 (bases 1 to 1273)
15020742
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitesitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/Dupont Consensus Sequences for Design of
Overgo Probes
Unpublished (2002)
3 (bases 1 to 1273)
Coe,E.H.
Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones,
these are publicly available from ZMDB and may be found by BLAST
searching at MSL, maizegap.org; ZMDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
maize cDNA sequences is either Virginia Walbot, Stanford or Pat
Schnable, Iowa State, then clones may be requested from ZMDB:
www.zmdb.iastate.edu.
Location/Qualifiers
1. 1273
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="maizeGDB:633781"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/Dupont Cornsensus
Library"
/notes="this sequence is part of a project of EST
assemblies resulting from the application of public
contigs to seed Dupont contigs; this resource was
assembled by Dupont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
Mapping Project"

ORIGIN

Query Match      16.7%; Score 530.8; DB 6; Length 1273;
Best Local Similarity 69.2%; Pred. No. 2.7e-138;
Matches 769; Conservative 0; Mismatches 337; Indels 6; Gaps 3;

QY 1742 CTTGTCCTTGGCGTATGTTGGTAACTCAACGCTGATGATTTCTGCGAAGTGAACA 1801
Db 1 CTTGGAAGCTGTGGATATTTGGCTTGTCTTCAATGCTGCTCCAGCTGGCAACGACAA 60

QY 1802 GTGTCAATCTCTAGACGACTATTTCTGGAATGCTATTTGGGGAAGTGTGATCTTCTC 1861
Db 61 CCGCAATCTCAAAAGGCTGCATTAATTTGGTGTGTGAGGAGCACTTGTATCTCTCTG 120

QY 1862 ATGTCTTATACAGCTTGCCGACCGCAATATCCCTCTTTCTTGATGATGACTT 1921
Db 121 ATGATCTTATACCTGTATGCAAGGCAACACATTCACCTGCTTTTAAAGTGCACATGTA 180

QY 1922 GACAAACAGTAACTTATTTGACACGGAAGCTGTCATCTTCTATATGAACATGCACTC 1981
Db 181 AGCAAGCAGTATGACATGTCACCAACAGCTGTATCTTCTATATGAACAGGCTCTT 240

QY 1982 CAGCTTTACGAGATATCATGAGATGACAGAGAACTTAAGTAGAAGATATATCTTGGG 2041

```

```

Db      241 CATGCTTTGATGATATATGAGGATGACCTGAGAACTTGAGTGAATATCATTTGGA 300
QY      2042 CAGGAGACATCAAGACACTGTATATACAAATGTGTTTGAAGAAATGTAAACCGGTTCGATT 2101
Db      301 TAGGGGGCATCAAGTATACAGTTTATTAATGTGTTCTTAAAGAAATGGCAAAACGAGTGGCAATA 360
QY      2102 AAGCGGCTTACCTCTCAACACCC-ACAGTCAATGAACAGTTTGAACACAGAACTCGAGAT 2160
Db      361 AAAAAGCTGATATGCCCATCTACCTCGCAGAGCTTTAAGAAATTTGAATCTAGCTCGAGAC 420
QY      2161 GCTAAGTAGCATAGACACAGCAAAATCTTGTAGAGCTT-ACAGCTTATTCCTCTCTCAC 2218
Db      421 TGTGTGATAGATCAAAACCGGAACTTAGTCAAGCTTGCCAAAGGATACGTTGTGTACCT 480
QY      2219 TTGGGAGACTTTCTGTTCTATGACTATTTGAAAAATGTATGCTTGGGATCTTCTTCAT 2278
Db      481 GTTGGGAACCTCCTCTTTTATGATATATATGAGAGTGGCAGCTTATGGAATGTTTATCAT 540
QY      2279 ---GGCCCTACGAAGAAAAAGACTTGATTGGGACACAGGCTTATAGATATAGT 2335
Db      541 GAAGGCTCATCAAGAAAGAAACAACTTGACTGGGTGACTGCTTACGAGATCGCTCTTGT 600
QY      2336 GCAGCAAAAGTTAGCTTATCTACACCATGACTGTAGTCCAAAGATCATTTCAACAGAC 2395
Db      601 GCAGCTCAAGGCTCGCTTACCTTACCATGACTGACGCCCAAGAAATTCACCGGGAC 660
QY      2396 GTGAAGTCTGCAACATTTCTTTGAGACAAAGTACAGGCTCGTTGACAGATTTTGA 2455
Db      661 GTTAAATCAAAAGATATATCTCTCGACAAAGATATAGGCCCATCTTACAGACTTCGGC 720
QY      2456 ATAGCGAAAGCTTGTGTGTGTAAGTCAATCTTCACTTACGTTACGTAAGGGCAGATATA 2515
Db      721 ATGCTTAAGGCTTATGTGTCTCGAAGACTCAACGTAACCTTACGTCATGGGACTATT 780
QY      2516 GGTACATAGACCCCGAGATAGTCTCGCACTTCAACGCTCACTAGAAATCCGATGTCTAC 2575
Db      781 GGTACATTTGATCCCGAGTACGCCCGCACTCCCGCTCAACGAAAGTCTGATGTCTAC 840
QY      2576 AGTTATGAATAGTCTCTTCTTGAAGTTGTAACCGAAGAAAGCCGTTGATGACGAATCC 2635
Db      841 AGCTACGGGCACTCTTCTGCTGAGCTGCTGACCGGCAAGCAAGTGAACAACGAGTGC 900
QY      2636 AATCTCCACATCTGATATGTCAAAGACGGGGAACAATAGTGAATGGAATGGCGAT 2695
Db      901 AATCTCCATCTTGTATCTATGAAACGCGCAGCAACAGGTCATGAGAGCGTGTGAC 960
QY      2696 CCAGACATCAATCGACGTGTAAAGATCTCGGTGTGTGAAGAAAGTTTCCAACTGGCA 2755
Db      961 CCGGACGTGGGACACACTGCAAGACTGGGCGAGGTGAAGAGCTGTTCAGACTGGCG 1020
QY      2756 CTCCTATGACCAAAAAGACGCGGAATATGCAACCAATGCAACGAGTACTCGTGT 2815
Db      1021 CTCCTCTGACCAAGGCGGAGCCCTCGGACCGGCGGACGATGACGAGGTGTGGCGT 1080
QY      2816 CTCGGAGTTTATGCTATGCGAAACAACCC 2847
Db      1081 CTGACTGCTGTGTGAACCGGAGCGCGCC 1112

```

```

RESULT 10
DR938199      889 bp      mRNA      linear      EST 02-AUG-2005
LOCUS      EST1129738 Aquilegia cDNA library Aquilegia formosa x Aquilegia
DEFINITION      pubescens cDNA clone COLPM01, mRNA sequence.
ACCESSION      DR938199
VERSION      DR938199.1 GI:71707562
KEYWORDS      EST.
SOURCE      Aquilegia formosa x Aquilegia pubescens
ORGANISM      Aquilegia formosa x Aquilegia pubescens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
Ranunculaceae; Aquilegia.

```

```

REFERENCE      1 (bases 1 to 889)
AUTHORS      Hodges,S.A., Rensink W., Buell,C.R., Borevitz,J., Kramer,E.,
              Nordborg,M. and Tomkins,J.
TITLE      Generation of ESTs from Aquilegia
JOURNAL      Unpublished (2005)
COMMENT      Other ESTs: EST1129737
              Contact: Scott Hodges
              Department of Ecology, Evolution and Marine Biology
              University of California, Santa Barbara
              Santa Barbara, CA 93106, USA
              Tel: 805 893 7813
              Fax: 805 893 4724
              Email: hodges@lifesci.ucsb.edu
              Seq primer: M13 Reverse.
FEATURES
  source
    1..889
    /organism="Aquilegia formosa x Aquilegia pubescens"
    /mol_type="mRNA"
    /db_xref="taxon:338618"
    /clone="COLPM01"
    /tissue_type="mixed shoot and floral apical meristems,
    flower buds, leaves and roots"
    /lab_host="DH10B T1 (T1 and T5 phage resistance)"
    /clone_lib="Aquilegia cDNA library"
    /note="Vector: pCMV SPORT6.1; Site 1: EcorI; Site 2: NotI;
    F2, F3, and F4 lines of Aquilegia formosa X A. pubescens
    were grown from seed in greenhouses at UC Santa Barbara.
    From these plants three sets of tissue were collected: 1)
    Small flower buds (<10 mm) and very young inflorescences
    (T1 & T9 by weight respectively), 2) Medium (7-20 mm) and
    large (at or near anthesis) flower buds (65 & 35% by
    weight respectively) and 3) Shoot apical meristems. A
    fourth set of tissue was collected from plants of A.
    formosa. These plants were grown from seed in sand and at
    approximately 1 month root tissue and leaf tissue of
    various developmental stages were collected (84 & 16% by
    weight respectively). Total RNA was extracted from each
    set of tissue and pooled in the following proportions:
    1.5X from sets 1 & 2, 1X from sets 3 & 4. From the pooled
    total RNA, mRNA was extracted and enriched for full-length
    messages and then normalized with proprietary methods by
    Invitrogen."

```

## ORIGIN

```

Query Match      16.4%; Score 519.8; DB 10; Length 889;
Best Local Similarity 75.4%; Pred. No. 3.2e-135;
Matches 672; Conservative 0; Mismatches 217; Indels 2; Gaps 2;

QY      1726 CAGCTTCATTTGGCAATCCGTGTTGGCGGTAGTGGCTAAACTCACCGTGCATGATTC 1785
Db      1 CAGCTTCATTTGGGAACCTTATCTGTGTGTAATGATGATTCACATGTGTACAGTTC 60
QY      1786 TCCTCGAAGTATGAGTGTCAATCTTAGAGCAGCTATTTGGAATAGCTTATGGGGG 1845
Db      61 CCACTCAACAAGACGAGCTCAATATCTAAAGCGGCTATTTCTTAGAATGTGTTGGGGGG 120
QY      1846 ACTTGATGCTCTTCATAGTCTTAAATAGACGCTTCCGACCGCATTAATCTCTCTTT 1905
Db      121 ACTTGTATCTCTTCTATATGATCTTAGTGACAGATATGACGCGCAATATCCACTCTCTT 180
QY      1906 TCTTGATGATCACTTGACAAACCAAGTACTTATGACACCGAAGCTGTCTACTCTCA 1965
Db      181 TTCAGAAGTACTCTTGACAAACCAATAGTCTATATCTCAACAAAGCTGTATCTTCCA 240
QY      1966 TATGAACATGCACTCACGTTTACGAGATATCATGAGATATGACAGAAATCTAAAGTA 2025
Db      241 TATGAACATGCGCTCTTCAATGATATGCAAAACATCAATGACGAGAAATTTGAGTGA 300
QY      2026 GAAGTATATCATTTGGGACGAGCATCAAGCACTGTATCAAAATGTGTTTGAAGATTG 2085
Db      301 GAAATATTAATATTTGTTAAGAGCACTGTCTTAATATGTGTCTTAAGAAATCG 360
QY      2086 TAAACGGTTGGATTAAGCGGCTTACTCTCAACCAACGATCAATGAACAGTTTGA 2145

```

Db 361 CAGACCGAGTACCAATAAGAGGCTATCTCTCATATACCTCAGAGCCTGAAGAGTTGA 420  
Qy 2146 AAGAGAACTGAGATGTAGTAGCATCAAGCAGAAATCTGTGAGCCTACAGCTTA 2205  
Db 421 GACAGAGCTGAGAGCTGTGGAGTATCAAGCAGAAATCTGTGAGCCTCAGGATA 480  
Qy 2206 TTCCCTCTCTCACTGGGAGTCTTCTGTCTATAGTATTTGGAAATGGTAGCCTTG 2265  
Db 481 CTCTTGTCTCTCTTCTGGAACCTCTCTTTATAGTACATGAGATGGTAGCCTTG 540  
Qy 2266 GGATCTTCTTCAATGAGCCCTTACGAAAGAAAGACTCTTGATTGGGACACAGGCTTAAGAT 2325  
Db 541 GGATCTCTCAATGAGCCCTTCAAAAAACAGAACTGGAGGATCTGCGCTCAAAAT 600  
Qy 2326 AGCATATGCGCAGCACAAGGTTTATAGTTATCTACACATGAGCTGTGCTCAAGATCAT 2385  
Db 601 AGCTTTGGAGCTGCGAGAGGGCTTATCTTATCTTATCATATGATGATGATGCTGCTATAGT 660  
Qy 2386 TCACAGAGAGCTGAGATGCTCCAACTTCTTGGACAAAGACTTAGAGGCTGCTTGAC 2445  
Db 661 CCACAGAGAGCTGAAATCATCTCAATCTCTAGACAAAGATTTGAAGCCATCTCAC 720  
Qy 2446 AGATTTGGATAGCGAAAGCTTGTGTGTCTCAAGTCACTACTTCAACTTATGAT 2505  
Db 721 AGATTTGGATAGCGAAAGCTTGTGTGTCTCAAGTCACTACTTATGAT 780  
Qy 2506 GGGAGCATATGATGATACATGAGCCCGAGTATGCTGAGCTTCAAGGCTCAGGAAATC 2565  
Db 781 GGGAGCATATGATGATACATGAGCCCGAGTATGCTGAGCTTCAAGGCTCAGGAAATC 839  
Qy 2566 CGATGCTACAGTATGATGATGATGCTTCTTGTGATTTGAACCGGAGGAA 2616  
Db 840 TGATGT-TACAGCATAGGATGCTCTCTGAGCTGTTGACGGGAGGAA 889

RESULT 11  
LOCUS DR066962 841 bp mRNA linear EST 07-JUN-2005  
DEFINITION she01-10ms1-a04 She01 Saruma henryi cDNA clone she01-10ms1-a04 5',  
mRNA sequence.  
ACCESSION DR066962  
VERSION DR066962.1 GI:67006033  
SOURCE EST.  
ORGANISM Saruma henryi  
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; magnolids; Piperales;  
Aristolochiaceae; Saruma.  
1 (bases 1 to 841)  
dePamphilis, C., Carlson, J., Ma, H., Soltis, D., Soltis, P.,  
Oppenheimer, D., Frohlich, M., Doyle, J., Tanksley, S., Webb, M.,  
Leebens-Mack, J., Landherr, L., Ilut, D. and Mall, K.  
Generation of ESTs from early flower buds of Saruma henryi  
Unpublished (2004)  
Contact: Claude dePamphilis or James Leebens-Mack  
Muller Laboratory  
Penn State University  
208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn  
State University, University Park, PA 16802, USA  
Tel: 814 863 6413  
Fax: 814 865 9131  
Email: cwd3@psu.edu or jh110@psu.edu  
The sequence provided is trimmed of vector and low quality regions.  
Full sequence and original trace file are available from the Plant  
Genome Network website (http://psn.cornell.edu)  
Plate: she01-10ms1 row: a column: 04  
Seq primer: M13F.  
Location/Qualifiers  
1..841  
/organism="Saruma henryi"  
/mol\_type="mRNA"  
/db\_xref="Pn:She01-10ms1-a04"

FEATURES  
source

/db\_xref="taxon:13258"  
/clone="she01-10ms1-a04"  
/issue\_type="flower buds"  
/dev\_stage="2.5mm buds"  
/lab\_host="SOLR"  
/clone\_lib="She01"  
/note="Vector: pBluescript SK (+/-); Site\_1: EcoRI;  
Site\_2: XhoI; This is a directionally cloned,  
non-normalized library. This library has been generated by  
the Floral Genome Project (FGP). The Floral Genome Project  
is funded by NSF's Plant Genome Research Program  
(DBI-0115684). More information about the project can be  
obtained at http://fgp.bio.psu.edu"

ORIGIN  
Query Match 16.4%; Score 519.6; DB 9; Length 841;  
Best Local Similarity 76.3%; Pred. No. 3.6e-135;  
Matches 639; Conservative 0; Mismatches 199; Indels 0; Gaps 0;  
Qy 278 TTCAATGTTGCTCTCTTAATTTGTGAGATTTGATTTGATGAGAAATCTGACTGCT 337  
Db 4 TTGATGTTGTTGCGCTTAATCTGTGAGGCTCATCTAGATGAGAAATATCTCCCTGCA 63  
Qy 338 ATTGAGATCTCAAGAGTCTTGTCAATGATCTGGAGATAATGCTTGTCTGACAA 397  
Db 64 ATTGAGGCTTTAAAGGCTTGTCTCTCATGATCTAAGGGGAATCATCTGTCGGGAG 123  
Qy 398 ATCCCTGATGAGATTTGGTGAAGTCTTCTTCTTCAAACTTAGACTTATCTTCAATGAA 457  
Db 124 ATTCTGATGATGATTTGGTGAAGTCTTCTTCTTCAAACTTAGACTTATCTTCAATGAA 457  
Qy 458 TTAAGTGTGATACATCCGTTTGTGATTTGATTTGATTTGATTTGATTTGATTTGAT 517  
Db 184 ATTACGGGAGCATTTCAATCTCAATTTCAAAATTTGAAGCACTAGAAACCTTGTGTTG 243  
Qy 518 AAGATTAACCAATTTGATAGAGCCGATCCCTTCAACCTTCAAGATTTCAAACTGAA 577  
Db 244 AAGAACCAACAGTATACAGAGCCATCCCTTCAACCTTCTCAAGATTTCAAACTGAA 303  
Qy 578 ATTCTGATTTGGCACAAGATTAATCACTGATGATGATGATGATGATGATGATGATGAT 637  
Db 304 ATTTTGAAGCTGCTCAAAATTAATCACTGATGATGATGATGATGATGATGATGATGAT 363  
Qy 638 GAAATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 697  
Db 364 GAAATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 423  
Qy 698 TTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 757  
Db 424 ATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 483  
Qy 758 ATACCTGAGAGATGAGAAATTTGACATGCTTCCAGGTTTGGATGCTTCAATCAG 817  
Db 484 ATTCTCAAAATTTGACATGCTTCCAGGTTTGGATGCTTCAATCAG 543  
Qy 818 CTATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 877  
Db 544 CTATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 603  
Qy 878 GGCATTAATCTTCTGGAAGATTTCAATGATGATGATGATGATGATGATGATGATGAT 937  
Db 604 GGCATTAATCTTCTGGAAGATTTCAATGATGATGATGATGATGATGATGATGATGAT 663  
Qy 938 TTGATATTAAGTGAAGTCTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 997  
Db 664 CTAGATTTTGAAGTGAAGTCTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 723  
Qy 998 TTCAACGAAATTTGATTTTGAACATGATGATGATGATGATGATGATGATGATGATGAT 1057  
Db 724 TACATGAGAAATTTGATTTGCAAGCAATGATGATGATGATGATGATGATGATGATGAT 783  
Qy 1058 GGAACATGTCAAATCTCCATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1115







Db 181 CCAAGTGGCTATCAAGAGGCTCTACTCTCACTATCCCAAGTGTAAAGAAATCGAACA 240  
QY 2150 GAACCTGAGATGCTAAGTAGCATCAAGCACAAGAAATCTTGAGCCCTACAGGCTTAATCC 2209  
Db 241 GAACCTGCGACATTTGAGACATCAACATCGGAAATGTGTCAGCTCCAGAGATCTCC 300  
QY 2210 CTCTCTCACTTGGGAGGCTCTTCTGTCTATGACTATTTGAAAAATGTAGCCTCTGGGAT 2269  
Db 301 CTCTCCCTTTGGGGAACCTTCTTTCTACGATTAATGAAAATGGAACCTGTGGGAT 360  
QY 2270 CTCTCTCACTTGGGAGGCTCTTCTGTCTATGACTATTTGAAAAATGTAGCCTCTGGGAT 2229  
Db 361 CAACCTTCACGGCTCTCAAGAAAGAAAGAAAGCTGGAAGAGCCGGGTGCAAGATAGCT 420  
QY 2330 TATGTGACGACACAAGGTTAGCTTAATCTACACATGACTGTAGTCCAGAGATCTTAC 2389  
Db 421 CTGAGAGCAGCTCAAGGGCTAGACATCTTACACATGACTGTAGTCCGAGATGATTCAC 480  
QY 2390 AGAGACGTGAAGTGTCTCAACATCTCTTGGACAAAGACTTAGAGGCTCGTTGACAGAT 2449  
Db 481 CAGAGATGTGAAGTCAATCGAATATCTATTGGAACAAGATTTGAGAGGCTCATCTACGAT 540  
QY 2450 TTTGGAATAGCGAAAGCTGTGTGTGTCTCAAGTCAATACCTTCACTTACGATGAGC 2509  
Db 541 TTTGGGATTTGCAAAAGCTTTGTGTATCAAAATCTCACACTCCACTCATTAATAGGA 600  
QY 2510 ACATATGTTTACATATACACCCGAGTATGCTCGCATTCAGGCTCACTGAGAAATCCGAT 2569  
Db 601 ACCATTGGTTATATTAACCCAGAGTATGACGCACTTCCGACTCACTGAAAGATCCGAT 660  
QY 2570 GTCTACAGTTATGAGATAGTCTCTTGTGAGTTGTAACCCGAGAAAGCTTGTATGAC 2629  
Db 661 GTATACAGTTTGGGATCGTTCTCTCGAGTTCTGTAAGTGGANNMNGCTAGACAAT 720  
QY 2630 GAATCCAAATCTCCACCATCTGATTAATGTCAAGACGGGGAACAATGAATGAGGAATG 2689  
Db 721 GAATGCAATCTTCATCATCTGATCTTGTCTC-CAGACGGCCAAACGGGANNMAGGGAACA 779  
QY 2690 GCGATCCGACATCTCATGAGTGTAAAGATCTCGTGTGTGT 2733  
Db 780 GTAGATCCGAGATTAACGGCTACATGTAAGATCTCGGGGAGCT 823

RESULT 15  
AV529789 501 bp mRNA linear EST 19-FEB-2004  
DEFINITION AV529789 Arabidopsis thaliana aboveground organs two to six-week  
ACCESSION AV529789 old Arabidopsis thaliana cDNA clone APZL48a03R 5', mRNA sequence.  
VERSION AV529789.1 GI:8690072  
KEYWORDS EST.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE 1 (bases 1 to 501)  
Asamizu, E., Nakamura, Y., Sato, S., and Tabata, S.  
A large scale analysis of cDNA in Arabidopsis thaliana: Generation  
of 12,028 non-redundant expressed sequence tags from normalized and  
size-selected cDNA libraries  
DNA Res. 7 (3), 175-180 (2000)  
JOURNAL PUBMED 10907847  
COMMENT Contact: Erika Asamizu  
The First Laboratory for Plant Gene Research  
Kazusa DNA Research Institute  
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan  
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.  
FEATURES  
source  
1..501  
/organism="Arabidopsis thaliana"  
/mol\_type="mRNA"  
/ecotype="Columbia"

/db\_xref="taxon:3702"  
/clone="APZL48a03R"  
/issue\_type="aboveground organs"  
/dev\_stage="two to six-week old"  
/clone\_lib="Arabidopsis thaliana aboveground organs two to six-week old"  
/note="Vector: pBluescriptII SK-; Site\_1: EcoRI; Site\_2: XhoI"  
ORIGIN  
Query Match 15.8%; Score 501; DB 1; Length 501;  
Best Local Similarity 100.0%; Pred. No. 5.7e-130;  
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 CTCTTCAGAGGACCTGAAGCTTTAAAGTATCTATCTAAAAAGCAGTCTTTAAGAC 64  
Db 1 CTCTTCAGAGGACCTGAAGCTTTAAAGTATCTATCTAAAAAGCAGTCTTTAAGAC 60  
QY 65 TGTGTGAGAAATGGCTCTGTTAGAGATATTGTTCTTTGGGTTTCTCTTCTGCTTG 124  
Db 61 TGTGTGAGAAATGGCTCTGTTAGAGATATTGTTCTTTGGGTTTCTCTTCTGCTTG 120  
QY 125 AGCTTAGTACTTACTGACTTCAAGAGAGGAGCAACGTTGCTGAGATTAAAGATCA 184  
Db 121 AGCTTAGTACTTACTGACTTCAAGAGAGGAGCAACGTTGCTGAGATTAAAGATCA 180  
QY 185 TTCAAAGATGTAACAATGTTCTTTATGACTGGAACAATTCACCTTCCGATTAATGTG 244  
Db 181 TTCAAAGATGTAACAATGTTCTTTATGACTGGAACAATTCACCTTCCGATTAATGTG 240  
QY 245 GTCTGAGAGTGTGCTTGTGAAATGTCAACCTTCAATGTTGTTCTTAATTTGTCA 304  
Db 241 GTCTGAGAGTGTGCTTGTGAAATGTCAACCTTCAATGTTGTTCTTAATTTGTCA 300  
QY 305 GATTTGAATCTTGATGAGAAATCTCACTGCTATTGAGATCTCAAGACTCTTGTCTCA 364  
Db 301 GATTTGAATCTTGATGAGAAATCTCACTGCTATTGAGATCTCAAGACTCTTGTCTCA 360  
QY 365 ATTTGATCTGAGTAAATGGCTTGTCTGACAAATCCCGATGAGATTGTTGATCTGTC 424  
Db 361 ATTTGATCTGAGTAAATGGCTTGTCTGACAAATCCCGATGAGATTGTTGATCTGTC 420  
QY 425 TCTTTCGAAAACCTTAGACTTATCTCAATGAATTAAGTGTGACATACCGTTTTCGATT 484  
Db 421 TCTTTCGAAAACCTTAGACTTATCTCAATGAATTAAGTGTGACATACCGTTTTCGATT 480  
QY 485 TCGAAGTTGAAGCAACTTGAG 505  
Db 481 TCGAAGTTGAAGCAACTTGAG 501

Search completed: September 3, 2006, 22:06:09  
Job time : 14326 secs

**THIS PAGE IS BLANK**

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 3, 2006, 18:06:38 ; Search time 17318 Seconds  
(without alignments)  
11727.509 Million cell updates/sec

Title: US-10-519-135-1

Perfect score: 3176

Sequence: 1 gttctctctcatgagagact.....acttctataagttcttgc 3176

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Genbankl:\*

1: gb env:\*

2: gb pat:\*

3: gb ph:\*

4: gb pl:\*

5: gb pr:\*

6: gb ro:\*

7: gb sts:\*

8: gb sy:\*

9: gb un:\*

10: gb vi:\*

11: gb ov:\*

12: gb hcg:\*

13: gb in:\*

14: gb om:\*

15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3174.4	99.9	3192	4	AY035110 Arabidops
2	3136.2	98.7	3176	2	E12705 Arabidops
3	3136.2	98.7	3176	2	AT047029 Arabidops
4	2930	92.3	2930	2	AX651657 Sequence
5	1495.4	47.1	1508	4	AK221886 Arabidops
6	1343.8	42.3	3673	4	AK073793 Oryza sat
7	1161.8	35.0	3089	4	AY244746 Arabidops
8	1112.8	35.0	3100	4	AY244745 Arabidops
9	1102	34.7	9295	2	E12706 Arabidops
10	1102	34.7	9295	4	AT047029 Arabidops
11	1102	34.7	9295	4	AC004484 Arabidops
12	1044.4	32.9	2796	4	AX654471 Arabidops
13	1035.2	32.6	3184	4	AY332474 Oryza sat
14	915.4	28.8	2895	2	AX654770 Sequence
15	800.6	25.2	2450	4	AX654770 Sequence
16	552.4	17.4	1888	4	AY182166 Elaeis gu
17	533.8	16.8	4356	2	BD267395 Compositi
18	533.8	16.8	4356	2	ARS66916 Sequence

19	467.8	14.7	1881	4	AK064052 Oryza sat
20	422.6	13.3	1202	4	AK118052 Arabidops
21	284.2	8.9	549	4	AY069973 Camelina
22	275	8.7	11000	4	AP008212_016
23	275	8.7	14313	4	AP000559 Oryza sat
24	275	8.7	155643	4	AP000391 Oryza sat
25	269.4	8.5	81736	4	AB019235 Arabidops
26	267.4	8.4	4686	2	AX654735 Sequence
27	263.4	8.3	104607	4	AT178014 Arabidops
28	248.4	7.8	3375	2	AX505972 Sequence
29	241.6	7.6	3330	2	AX654255 Sequence
30	234.4	7.4	110000	4	AP008210_252
31	234.4	7.4	130779	4	OSJ000283 Oryza sat
32	234.4	7.4	143582	4	OSJ000271 Oryza sat
33	232	7.3	83232	4	AP004503 Lotus cor
34	225.4	7.1	3222	2	BD267346 Compositi
35	225.4	7.1	3222	2	ARS66867 Sequence
36	224.8	7.1	4017	2	BD267387 Compositi
37	224.8	7.1	4017	2	ARS66908 Sequence
38	224.8	7.1	4056	2	BD267340 Compositi
39	224.8	7.1	4056	2	ARS66861 Sequence
40	221.2	7.0	130527	12	AC151806 Medicago
41	220.2	6.9	3562	4	AY793347 Lycopersi
42	220.2	6.9	3562	4	AY793348 Lycopersi
43	220.2	6.9	3562	4	AY793349 Lycopersi
44	220.2	6.9	3573	2	AS7133 Sequence 4
45	220.2	6.9	3573	2	AR168711 Sequence

#### ALIGNMENTS

RESULT 1  
LOCUS AY035110 3192 bp mRNA linear PLN 18-SEP-2002  
DEFINITION Arabidopsis thaliana putative receptor protein kinase, ERECTA  
(At2g26330) mRNA, complete cds.

ACCESSION AY035110.1 GI:14334873  
VERSION FL1\_CDNA.  
KEYWORDS Arabidopsis thaliana (thale cress)  
SOURCE Arabidopsis thaliana  
ORGANISM Arabidopsis thaliana

REFERENCE  
Auker, R.W., Ecker, J.R. and Theologis, A.  
1 (bases 1 to 3192)  
Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K.,  
Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bower, L.,  
Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,  
Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,  
Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T.,  
Satou, M., Seki, M., Shim, P., Southwick, A., Shinzaki, K.,  
Davis, R.W., Ecker, J.R. and Theologis, A.  
Arabidopsis Full Length cDNA Clones

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K.,  
Goldsmith, A.D., Lee, J.M., Quach, H.L., Tang, C.C., Toriumi, M., Yu, G.,  
Bower, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y.,  
Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J.,  
Kim, C., Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M.,  
Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M.,  
Shim, P., Southwick, A., Shinzaki, K., Davis, R.W., Ecker, J.R. and  
Theologis, A.  
Direct Submission  
Submitted (07-MAY-2001) Plant Gene Expression Center, 800 Buchanan  
Street, Albany, CA 94710, USA

TITLE  
JOURNAL  
COMMENT  
Riken Genomic Sciences Center (GSC) members carried out the  
collection and clustering of RFLP cDNAs (RFLP cDNA: "RIKEN  
Arabidopsis Full-Length cDNA": Seki, M., Narusaka, M., Ishida, J.,  
Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,  
Hayashizaki, Y. and Shinzaki, K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada, K., Liu, S. X., Sakano, H., Pham, P. K., Banh, J., Chung, M. K., Goldsmith, A. D., Lee, J. M., Quach, H. L., Tang, C. C., Tortum, M., Yu, G., Bower, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Koesema, E., Lam, B., Lin, J., Meyer, M. C., Miranda, M., Nguyen, M., Palm, C. J., Shim, P., Southwick, A., Davis, R. W., Ecker, J. R. and Theologis, A.

Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

## FEATURES

## source

1. 3192  
/organism="Arabidopsis thaliana"  
/mol\_type="mRNA"  
/db\_xref="taxon:3702"  
/chromosome="2"  
/clone="RAFL09-17-H05 (R09457)"  
/ecotype="Columbia"  
/note="This clone is in a modified pBlueScript vector (pUC-1) as a BamHI/XhoI insert."

## gene

1. 76  
/gene="At2g26330"

## 5'UTR

77. 3007  
/gene="At2g26330"

## CDS

/gene="At2g26330"  
/experiment="experimental evidence, no additional details recorded"  
/codon\_start=1  
/product="putative receptor protein kinase, ERECTA"  
/protein\_id="AK59615.1"  
/db\_xref="GI:14334874"

/translation="MALFRDVLVGLFCLSVATVTSERATLLEIKSKFKDNNVLYDTTSPSDYCVWRGVSCENVNVALNLSIDNLDEGLSPAGDLSKLSIDLRNRLSGQIDPEIDCSLONLDSFNLGSDIPFSISKQLEQLIKNNOIGIPSTLSOIPNLKILDAONKLSGEIPRIYVNEVLOYGLRNNLVGNSTPLCOLGTGWYDVRNNSLTGSIPTGNCCTAFQVLDVSNOLGEPIDPIGLQVATSLDQNOISKP SVICGMQALAVLDLSENLGSLPPIIGNLITTEKYLHNSKLTGSIPEELGNKSKHYLELNDNLHGLHPEELGKLTDLFDLVANNDDLEGP1PDHLSCTNLNLSVHGKNSGT1PRAQKLESMTYLMSSNNIKGPIPELSRIGNLDTLDLSNNKINGIIPSLGDL EHLKNNLSRNHITGVDPDFGNLRSIMEIDLSNNDISGPIPEELNQLQI1LLRLSN NNLTVNGVSLANCLSTVLNVSHNVLGDI PKNNFSPSPSPISGNGLCSMLNLP CHNSRTVRVSIISRAIIGIAGIIVLLAVLILAACRPHNPPPLDGLSKPVTYSPR KUYILHNNMALSIVEDIIMRTENISEKTIIGHGASSYVYKCVAKNCPVAIKRLYSN PDSKOPETELEMJLSIKHRLVSLQVYSLSHLSLPIYDLENGSLMDLHGTKKK TLMDWTRLKIAYGAQGLAYLHDCSPRI1HRDVSNNILDLKDLERLDFGLAKSL CVSKSHSTYVMGTIGYIDEPYATSRSLTEKSDVSYGIVLELLETRKXVDENSLH HLMSKTNNEVMEMADPDITSCKDGLVKKVFOALDLCTKRQPNDRPTMHQVTRVL GSFMSIQPRAADTTSATLTAAGSCYVDEVANLKTPHSVCSMSMSADQLFLRQVVIS QNSB"

## misc\_difference

2803

/gene="At2g26330"  
/note="compared to genomic sequence"  
/replace="g"  
3008. 3192  
/gene="At2g26330"

## ORIGIN

Query Match 99.9%; Score 3174.4; DB 4; Length 3192;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 3175; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTCTCTTCATGAGACTTGAAGCTTTAAAGTATCTAAAGACGAGTGGTTTA 60  
DB 1 GTTCTCTTCATGAGACTTGAAGCTTTAAAGTATCTAAAGACGAGTGGTTTA 60  
QY 61 AGACTGTGTGAGAAATGGCTCTGTTAGAGATATGTTCTTGGGTTTCTCTCTG 120  
DB 61 AGACTGTGTGAGAAATGGCTCTGTTAGAGATATGTTCTTGGGTTTCTCTCTG 120

QY 121 CTGAGCTTAGTAGCTACTGTGACTTCAGAGAGAGGAGCAACCTTGCTGAGATTAGAA 180  
DB 121 CTGAGCTTAGTAGCTACTGTGACTTCAGAGAGAGGAGCAACCTTGCTGAGATTAGAA 180  
QY 181 GTCATTCAAGATGTGAACAATGTTCTTTATGACTGACCACTTCACCTTTCGGATTA 240  
DB 181 GTCATTCAAGATGTGAACAATGTTCTTTATGACTGACCACTTCACCTTTCGGATTA 240  
QY 241 TTGAGTGTGAGAGAGGTGTGCTTGTAATAATGACCTTCAATGTTGTTCTTAATT 300  
DB 241 TTGAGTGTGAGAGAGGTGTGCTTGTAATAATGACCTTCAATGTTGTTCTTAATT 300  
QY 301 GTCAGATTTGAATCTTGATGAGAGAAATCTGACCTGCTATTGAGATCTCAAGTCTCT 360  
DB 301 GTCAGATTTGAATCTTGATGAGAGAAATCTGACCTGCTATTGAGATCTCAAGTCTCT 360  
QY 361 GTCATTGATCTGAGAGATTAATGCTTGTGAGCAAAATCCCTGATGAGATTGGTACTG 420  
DB 361 GTCATTGATCTGAGAGATTAATGCTTGTGAGCAAAATCCCTGATGAGATTGGTACTG 420  
QY 421 TTCTCTTTGCAAAACTTAGACTTATCCCTCAATGAAATTAAGTGTGACATACCGTTTC 480  
DB 421 TTCTCTTTGCAAAACTTAGACTTATCCCTCAATGAAATTAAGTGTGACATACCGTTTC 480  
QY 481 GATTTCGAAGTTGAGCACTTGAGCAGCTGATTTGCAAGATTAACCAATTGATAGACC 540  
DB 481 GATTTCGAAGTTGAGCACTTGAGCAGCTGATTTGCAAGATTAACCAATTGATAGACC 540  
QY 541 GATTCCTTCAACACTTTCACAGATTCCAAACTGAAATTTCTGACTTGGCACAAGATTA 600  
DB 541 GATTCCTTCAACACTTTCACAGATTCCAAACTGAAATTTCTGACTTGGCACAAGATTA 600  
QY 601 ACTCAGTGTGAGATACCAAGACTTATTTACTGGAATGAAGTCTTCAGATCTTGGGTT 660  
DB 601 ACTCAGTGTGAGATACCAAGACTTATTTACTGGAATGAAGTCTTCAGATCTTGGGTT 660  
QY 661 GCGAGGAACAACCTTAGTCGGTAACTTTCTCCAGATTGTGCAACTGACTGCTCTTG 720  
DB 661 GCGAGGAACAACCTTAGTCGGTAACTTTCTCCAGATTGTGCAACTGACTGCTCTTG 720  
QY 721 GTATTGTTGAGTGAAGAAACAAGTTGACTGCTGATGATTCCTGAGACGATTAAGAAATTG 780  
DB 721 GTATTGTTGAGTGAAGAAACAAGTTGACTGCTGATGATTCCTGAGACGATTAAGAAATTG 780  
QY 781 CACTGCTTCAGGTTTGGACTTGTCTCTCAATCACTAAGTGTGAGATCCCTTTTGA 840  
DB 781 CACTGCTTCAGGTTTGGACTTGTCTCTCAATCACTAAGTGTGAGATCCCTTTTGA 840  
QY 841 CATCGCTTCCTGCAAGTTGCAACATTATCATTTGCAAGGCAATCAACTCTTGGGAAGAT 900  
DB 841 CATCGCTTCCTGCAAGTTGCAACATTATCATTTGCAAGGCAATCAACTCTTGGGAAGAT 900  
QY 901 TCCATCAGATGATGCTGCTCATGCAAGCCCTTGGAGCTTATGATCTAAGTGGCAACTTGT 960  
DB 901 TCCATCAGATGATGCTGCTCATGCAAGCCCTTGGAGCTTATGATCTAAGTGGCAACTTGT 960  
QY 961 GAGTGAATCTAATCTCTCCGATTCCTGGAATCTTACCTTCAACCGAAGAAATTTGATTTGCA 1020  
DB 961 GAGTGAATCTAATCTCTCCGATTCCTGGAATCTTACCTTCAACCGAAGAAATTTGATTTGCA 1020  
QY 1021 CAGTAAACAGCTGAGTTCATTCACCTGAGCTTGAAGACATGTCAAACTCCATTA 1080  
DB 1021 CAGTAAACAGCTGAGTTCATTCACCTGAGCTTGAAGACATGTCAAACTCCATTA 1080  
QY 1081 CCTGGAACCTAATGATATATCTCACGGGTCTATTAACCAACGAGAGCTTGGGAAGCTTAC 1140  
DB 1081 CCTGGAACCTAATGATATATCTCACGGGTCTATTAACCAACGAGAGCTTGGGAAGCTTAC 1140  
QY 1141 TGACTGTTGATCTGAATGTGGCAACAAATGATCTGGAAGAGACTTACCTGATCATCT 1200  
DB 1141 TGACTGTTGATCTGAATGTGGCAACAAATGATCTGGAAGAGACTTACCTGATCATCT 1200

QY 1201 GAGCTCTTGCAAAATCTAAACAGCTTAAATGTTTCATGGGACAAAGTTAGTGCACTAT 1260  
|  
|  
|  
Db 1201 GAGCTCTTGCAAAATCTAAACAGCTTAAATGTTTCATGGGACAAAGTTAGTGCACTAT 1260  
|  
|  
|  
QY 1261 ACCCCGAGCATTTCAAAAGCTAGAAAGTATGACTTACCTTAATCTGTCCAGCAACATAT 1320  
|  
|  
|  
Db 1261 ACCCCGAGCATTTCAAAAGCTAGAAAGTATGACTTACCTTAATCTGTCCAGCAACATAT 1320  
|  
|  
|  
QY 1321 CAAGAGTCGAATCCGGTTAGCTATCTCGATCGGTAACCTAGATCATTTGATCTTTCC 1380  
|  
|  
|  
Db 1321 CAAGAGTCGAATCCGGTTAGCTATCTCGATCGGTAACCTAGATCATTTGATCTTTCC 1380  
|  
|  
|  
QY 1381 CAACCAACAGATTAATGGAATCAATCCCTTCCCTGTGATTTGGAGCATCTTCTCAA 1440  
|  
|  
|  
Db 1381 CAACCAACAGATTAATGGAATCAATCCCTTCCCTGTGATTTGGAGCATCTTCTCAA 1440  
|  
|  
|  
QY 1441 GATGAATTTGATGAATCATATATCTGTGTATGTTCCAGGCGCATTTGGAAATCTTAAG 1500  
|  
|  
|  
Db 1441 GATGAATTTGATGAATCATATATCTGTGTATGTTCCAGGCGCATTTGGAAATCTTAAG 1500  
|  
|  
|  
QY 1501 AAGCATATGGAATAGATCTTTCAATTAATGATATCTGGGCCAATTCAGAAAGCT 1560  
|  
|  
|  
Db 1501 AAGCATATGGAATAGATCTTTCAATTAATGATATCTGGGCCAATTCAGAAAGCT 1560  
|  
|  
|  
QY 1561 TAAACAATTCAGAACATATTTTGTGAGACTGGAAATATATACCTGACTGGTAATGT 1620  
|  
|  
|  
Db 1561 TAAACAATTCAGAACATATTTTGTGAGACTGGAAATATATACCTGACTGGTAATGT 1620  
|  
|  
|  
QY 1621 TGGTTCATTAGCCAACTGTCTCACTCTCACTGTATTTGAATGTATCTGATTAACAACCTCGT 1680  
|  
|  
|  
Db 1621 TGGTTCATTAGCCAACTGTCTCACTCTCACTGTATTTGAATGTATCTGATTAACAACCTCGT 1680  
|  
|  
|  
QY 1681 AGGTGATATCCCTTAAGAACATATCTTCAAGATTTTCCACAGACGCTTCATTTGGCAA 1740  
|  
|  
|  
Db 1681 AGGTGATATCCCTTAAGAACATATCTTCAAGATTTTCCACAGACGCTTCATTTGGCAA 1740  
|  
|  
|  
QY 1741 TCCGTGCTTTGGCGATAGTGGCTAACTCAACGCTGCATGATTTCTGTGCGAATCTGACG 1800  
|  
|  
|  
Db 1741 TCCGTGCTTTGGCGATAGTGGCTAACTCAACGCTGCATGATTTCTGTGCGAATCTGACG 1800  
|  
|  
|  
QY 1801 AGTGTCAATCTCTAGAGACAGCTATCTTGGAAATGCTAATTTGGGGGACTTGTGATCTTCT 1860  
|  
|  
|  
Db 1801 AGTGTCAATCTCTAGAGACAGCTATCTTGGAAATGCTAATTTGGGGGACTTGTGATCTTCT 1860  
|  
|  
|  
QY 1861 CATGTGCTTAATAGACAGCTTGGCGACCGCATTAATCCCTCTCTTTTCTTATGATGATCT 1920  
|  
|  
|  
Db 1861 CATGTGCTTAATAGACAGCTTGGCGACCGCATTAATCCCTCTCTTTTCTTATGATGATCT 1920  
|  
|  
|  
QY 1921 TGACAAACAGTAATCTTATCGACACCGAAGCTCGTATCTTCATATGAAATGCGACT 1980  
|  
|  
|  
Db 1921 TGACAAACAGTAATCTTATCGACACCGAAGCTCGTATCTTCATATGAAATGCGACT 1980  
|  
|  
|  
QY 1981 CCAAGTTTACGAGATATCATGAGATGACAGAAATCTAAGTGAAGATATCATTTGG 2040  
|  
|  
|  
Db 1981 CCAAGTTTACGAGATATCATGAGATGACAGAAATCTAAGTGAAGATATCATTTGG 2040  
|  
|  
|  
QY 2041 GCAACGAGATCAAGCACTGTATCAAAATGTGTTTGAAGATTTTGAACCGGTGGCAT 2100  
|  
|  
|  
Db 2041 GCAACGAGATCAAGCACTGTATCAAAATGTGTTTGAAGATTTTGAACCGGTGGCAT 2100  
|  
|  
|  
QY 2101 TAAAGCGGCTTACTCTCACAACCAAGCATATGAAACAGTTTGAACAGAACTCGAGAT 2160  
|  
|  
|  
Db 2101 TAAAGCGGCTTACTCTCACAACCAAGCATATGAAACAGTTTGAACAGAACTCGAGAT 2160  
|  
|  
|  
QY 2161 GCTAAGTATGATCAAGACAGAAATCTTGTGAGCTTCAAGCTTATTCCTCTCTCACTT 2220  
|  
|  
|  
Db 2161 GCTAAGTATGATCAAGACAGAAATCTTGTGAGCTTCAAGCTTATTCCTCTCTCACTT 2220  
|  
|  
|  
QY 2221 GGGGAGCTTCTGTCTTATGATATTTTGAAGATGTAAGCTCTGGGATCTTCTTCAATGG 2280  
|  
|  
|  
Db 2221 GGGGAGCTTCTGTCTTATGATATTTTGAAGATGTAAGCTCTGGGATCTTCTTCAATGG 2280  
|  
|  
|  
QY 2281 CCTACGAAGAAAAAGACTCTTATTTGGGACACACGCGCTTAAAGTATAGTGTGACG 2340  
|  
|  
|

Db 2281 CCTACGAAGAAAAAGACTCTTATTTGGGACACACGCGTTAAATATAGATATGTGTGACG 2340  
|  
|  
|  
QY 2341 ACAAGTTTATGCTTATCTACACCATGATCTGTATCCAAAGATATTTCAAGAACGTTGA 2400  
|  
|  
|  
Db 2341 ACAAGTTTATGCTTATCTACACCATGATCTGTATCCAAAGATATTTCAAGAACGTTGA 2400  
|  
|  
|  
QY 2401 GTGCTCCAACTCTCTTGGACAAAGACTTAGAGGCTCGTTTGAAGATTTTGAATAGC 2460  
|  
|  
|  
Db 2401 GTGCTCCAACTCTCTTGGACAAAGACTTAGAGGCTCGTTTGAAGATTTTGAATAGC 2460  
|  
|  
|  
QY 2461 GAAAAGCTGTGTGTCTCAAAAGTCAATATCTTCACTTAAGTATGAGGACGATAGCTTA 2520  
|  
|  
|  
Db 2461 GAAAAGCTGTGTGTCTCAAAAGTCAATATCTTCACTTAAGTATGAGGACGATAGCTTA 2520  
|  
|  
|  
QY 2521 CATAGACCCCGAGATATGCTGCGACTTACAGGCTCACTGAGAAATCCGATGCTACATTA 2580  
|  
|  
|  
Db 2521 CATAGACCCCGAGATATGCTGCGACTTACAGGCTCACTGAGAAATCCGATGCTACATTA 2580  
|  
|  
|  
QY 2581 TGGATATGCTCTTGAATGTTAAACCGAAGAAAGCGTTGATGACGAATCCAACT 2640  
|  
|  
|  
Db 2581 TGGATATGCTCTTGAATGTTAAACCGAAGAAAGCGTTGATGACGAATCCAACT 2640  
|  
|  
|  
QY 2641 CCAACATCTGATATGTCAAAGACGCGGAAACAATGAAGTATGAAATGGCAGATCCAGA 2700  
|  
|  
|  
Db 2641 CCAACATCTGATATGTCAAAGACGCGGAAACAATGAAGTATGAAATGGCAGATCCAGA 2700  
|  
|  
|  
QY 2701 CATCATGATGACCTGTAAAGATCTCGGTGTGTGAAGAAAGTTTCCAACTGCGACTCT 2760  
|  
|  
|  
Db 2701 CATCATGATGACCTGTAAAGATCTCGGTGTGTGAAGAAAGTTTCCAACTGCGACTCT 2760  
|  
|  
|  
QY 2761 ATGCACCAAAAGACACCGCAATGATGACCCCAAGCAACAGAGTACTGTGTTCCGG 2820  
|  
|  
|  
Db 2761 ATGCACCAAAAGACACCGCAATGATGACCCCAAGCAACAGAGTACTGTGTTCCGG 2820  
|  
|  
|  
QY 2821 CAGTTTATATGCTATTCGAAACAACCACTGCTGCGACTGACACGCTGCTGCTG 2880  
|  
|  
|  
Db 2821 CAGTTTATATGCTATTCGAAACAACCACTGCTGCGACTGACACGCTGCTGCTG 2880  
|  
|  
|  
QY 2881 TTGCTGCTATGCTGATGATGATCAAAATCTCAAGACTCTCATTTCTGTCAATGCTCTTC 2940  
|  
|  
|  
Db 2881 TTGCTGCTATGCTGATGATGATCAAAATCTCAAGACTCTCATTTCTGTCAATGCTCTTC 2940  
|  
|  
|  
QY 2941 CATGAGCTCTGAGCTCAACTGTTCTTGGGTTTGGCAAGTATTTCCAGAACAG 3000  
|  
|  
|  
Db 2941 CATGAGCTCTGAGCTCAACTGTTCTTGGGTTTGGCAAGTATTTCCAGAACAG 3000  
|  
|  
|  
QY 3001 TGAGTAGTTTTCGTTAGGAGAGAACTTTAAACGCTATCTTTTCTGTCGTTAAGCT 3060  
|  
|  
|  
Db 3001 TGAGTAGTTTTCGTTAGGAGAGAACTTTAAACGCTATCTTTTCTGTCGTTAAGCT 3060  
|  
|  
|  
QY 3061 GTTAGAAAAATTAATGCTCATGATAAAGTATTAATGCACTGCTTATTAATTAAGCAAG 3120  
|  
|  
|  
Db 3061 GTTAGAAAAATTAATGCTCATGATAAAGTATTAATGCACTGCTTATTAATTAAGCAAG 3120  
|  
|  
|  
QY 3121 TGTGTGTGTGAATATGCTCTTACAGCTGGCACTTACATTCCTAATAGTTCCTGCC 3176  
|  
|  
|  
Db 3121 TGTGTGTGTGAATATGCTCTTACAGCTGGCACTTACATTCCTAATAGTTCCTGCC 3176  
|  
|  
|

## RESULT 2

E12705 3176 bp DNA linear PAT 27-APR-1998  
LOCUS E12705  
DEFINITION Arabidopsis thaliana cDNA encoding a protein involved in morphogenesis.  
ACCESSION E12705  
VERSION E12705.1 GI:3251537  
KEYWORDS JP 1997056382-A/1.  
SOURCE unclassified  
ORGANISM unclassified  
REFERENCE 1 (bases 1 to 3176)  
AUTHORS Mitsuoka,N. and Robaato,E.U.

TITLE GENE CODING FOR PROTEIN CONTROLLING MORPHOGENESIS OF PLANT  
JOURNAL Patent: JP 1997056382-A 1 04-MAR-1997;  
CHIKU KANKYO SANGYO GIJUTSU KENKYU KINO, MITSUI GYOSAI SHOKUBUTSU  
BIO KENKYUSHO:KK  
COMMENT OS Arabidopsis thaliana (thale cress)  
PN JP 1997056382-A/1  
PD 04-MAR-1997  
PF 24-AUG-1995 JP 1995216187  
PI MITSUKAWA NORIHIRO, ROBAATO EFU UITSUTSURA  
PC C12N15/09,A01H5/00,C12N5/10,  
CC strandedness: Double;  
CC topology: Linear;  
FH Key Location/Qualifiers  
FT source 1..3176 /organism='Arabidopsis thaliana' FT  
FT /strain='colombia' 51..2981  
FT CDS /product='a protein involved in FT  
morphogenesis'.  
LOCATION/Qualifiers  
1..3176  
/organism='unidentified'  
/mol\_type='genomic DNA'  
/db\_xref='taxon:32644'

ORIGIN

Query Match 98.7%; Score 3136.2; DB 2; Length 3176;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3138; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

27 CTTTAAAGTATCTAAAAACGACGTCGTTTAAAGCTGTGTGAGAAATGCTGT 86  
1 CTTTAAAGTATCTAAAAACGACGTCGTTTAAAGCTGTGTGAGAAATGCTGT 60  
87 TTAGAGATTTGTTCTTCTGGGTTTCTCTTCTGCTGAGCTTAGTACTAGTACT 146  
61 TTAGAGATTTGTTCTTCTGGGTTTCTCTTCTGCTGAGCTTAGTACTAGTACT 120  
147 CAGAGGAGGAGCAACGTTGCTGAGATTAAGAGTCAATCAAGATGTAACAATGTC 206  
121 CAGAGGAGGAGCAACGTTGCTGAGATTAAGAGTCAATCAAGATGTAACAATGTC 180  
207 TTATGACTGAGCAACTTCACTTCTCGATTAATGTTGCTGAGAGAGTGTCTGTG 266  
181 TTATGACTGAGCAACTTCACTTCTCGATTAATGTTGCTGAGAGAGTGTCTGTG 240  
267 AAAATGTCACCTTCAATGTTGTTGCTCTTAAATTTGTCAGATTTGAATCTTGATGAGAAA 326  
241 AAAATGTCACCTTCAATGTTGTTGCTCTTAAATTTGTCAGATTTGAATCTTGATGAGAAA 300  
327 TCTGACCTGCTATGAGATCTCAAGAGTCTTGTCAATGATCTGAGAGTAAATGCT 386  
301 TCTGACCTGCTATGAGATCTCAAGAGTCTTGTCAATGATCTGAGAGTAAATGCT 360  
387 TGTCTGAGCAAAATCCCTGATGAGATGAGTGTGACTGTTCTTTTCAAAACTTAGACTTAT 446  
361 TGTCTGAGCAAAATCCCTGATGAGATGAGTGTGACTGTTCTTTTCAAAACTTAGACTTAT 420  
447 CTTTCAATGAATTAAGTGTGACATACCGTTTGTGATTTGCAAGTTGAAGCACTTGAAC 506  
421 CTTTCAATGAATTAAGTGTGACATACCGTTTGTGATTTGCAAGTTGAAGCACTTGAAC 480  
507 AGCGATTTCTGAAATTAACAATGATGATAGGACCGATCCCTTCAACCTTACAGATTC 566  
481 AGCGATTTCTGAAATTAACAATGATGATAGGACCGATCCCTTCAACCTTACAGATTC 540  
567 CAAACCTGAAATTTCTGACTTGGCACAAGATTAACCTGAGTGTGAGTACCAAGACTTA 626  
541 CAAACCTGAAATTTCTGACTTGGCACAAGATTAACCTGAGTGTGAGTACCAAGACTTA 600  
627 TTAACTGGAATGAAGTTCTTCAATCTTGGGTTGCGAGAAACAATTAAGTGTGATA 686

601 TTAACTGGAATGAAGTTCTTCAATCTTGGGTTGCGAGAAACAATTAAGTGTGATA 660  
687 TTCTCCAGATTTGTGTCACACTGACTGCTTGTGATTTTGAAGTAAAGAACAGT 746  
661 TTCTCCAGATTTGTGTCACACTGACTGCTTGTGATTTTGAAGTAAAGAACAGT 720  
747 TGACTGTGATTAATCTGAGACGATAGGAATGCACTGCTTCCAGTTTGTGACTTGT 806  
721 TGACTGTGATTAATCTGAGACGATAGGAATGCACTGCTTCCAGTTTGTGACTTGT 780  
807 CTTAATCAATCACTTAATCTGAGATCCCTTTTGAATCGCTTCTGCAAGTTGCAAT 866  
781 CTTAATCAATCACTTAATCTGAGATCCCTTTTGAATCGCTTCTGCAAGTTGCAAT 840  
867 TATCATTCGAAGCAATCAATCTCTGAGAAAGATTCATGATGATGCTCATGCAAG 926  
841 TATCATTCGAAGCAATCAATCTCTGAGAAAGATTCATGATGATGCTCATGCAAG 900  
927 CCCTTGACGCTTAAATCTTAAGTGGCAACTGTGAGTGTATCTTCCGATTTCTCG 986  
901 CCCTTGACGCTTAAATCTTAAGTGGCAACTGTGAGTGTATCTTCCGATTTCTCG 960  
987 GAAATCTTACTTTCAACGAGAAATGATTTGCAACGTAACAAGCTGACTGTTCAATTC 1046  
961 GAAATCTTACTTTCAACGAGAAATGATTTGCAACGTAACAAGCTGACTGTTCAATTC 1020  
1047 CACCTGAGCTTGGAAACATGTCAAAACCTCATTAAGTGAATCAATGATTAATCATCTCA 1106  
1021 CACCTGAGCTTGGAAACATGTCAAAACCTCATTAAGTGAATCAATGATTAATCATCTCA 1080  
1107 CCGGTCTAATACCAACGAGCTTGGAAAGCTTAATGATTTGATCTGAATGTGGCCA 1166  
1081 CCGGTCTAATACCAACGAGCTTGGAAAGCTTAATGATTTGATCTGAATGTGGCCA 1140  
1167 ACAATGATCTGGAAGACCTTAATCTGATATCTGAGCTTTTCAAACTTAACAGCT 1226  
1141 ACAATGATCTGGAAGACCTTAATCTGATATCTGAGCTTTTCAAACTTAACAGCT 1200  
1227 TAAATGTTCAATGGGAAACAAATTAAGTGGCACTTAATCCCGAGATTTCAAAAGCTAGAA 1286  
1201 TAAATGTTCAATGGGAAACAAATTAAGTGGCACTTAATCCCGAGATTTCAAAAGCTAGAA 1260  
1287 GTATGACTTAACCTTAATCTGTCCAGCAACAATTAAGTGGCACTTAATCCCGAGATTT 1346  
1261 GTATGACTTAACCTTAATCTGTCCAGCAACAATTAAGTGGCACTTAATCCCGAGATTT 1320  
1347 CTGTATCGGTAATCTTAATGATGATCTTTTCAACCAACAAGATTAATGAATCATTC 1406  
1321 CTGTATCGGTAATCTTAATGATGATCTTTTCAACCAACAAGATTAATGAATCATTC 1380  
1407 CTTCTTCCCTTGGATTTTGAAGCATCTTCAAGATGAATGAGTGAATCATTA 1466  
1381 CTTCTTCCCTTGGATTTTGAAGCATCTTCAAGATGAATGAGTGAATCATTA 1440  
1467 CTGTGATGTTCCAGGCGACTTTGGAATCTTAAGAGCATCATGGAATGATCTTCA 1526  
1441 CTGTGATGTTCCAGGCGACTTTGGAATCTTAAGAGCATCATGGAATGATCTTCA 1500  
1527 ATTAATGATATCTGTGCGCCAAATCCAGAGAGCTTAACCAATTAAGAGAAATATTTG 1586  
1501 ATTAATGATATCTGTGCGCCAAATCCAGAGAGCTTAACCAATTAAGAGAAATATTTG 1560  
1587 TGAGACTGGAATAATTAATCACTGATGATGATGATGATGATGATGATGATGATGATG 1646  
1561 TGAGACTGGAATAATTAATCACTGATGATGATGATGATGATGATGATGATGATGATG 1620  
1647 TCACTGATTAATGATTAATCACTGATGATGATGATGATGATGATGATGATGATGATG 1706  
1621 TCACTGATTAATGATTAATCACTGATGATGATGATGATGATGATGATGATGATGATG 1680  
1707 TCTCAAGATTTTCAACGAGAGCTTCAATGAGCAATCTGATCTTTTGGGATGATGATG 1766  
1681 TCTCAAGATTTTCAACGAGAGCTTCAATGAGCAATCTGATCTTTTGGGATGATGATG 1740



QY 1767 ACTCACCCTGTCATGATTTCTCGTGAACGTGATGAGTGCATCTCTAGACAGCTATTC 1826  
 Db 1741 ACTCACCCTGTCATGATTTCTCGTGAACGTGATGAGTGCATCTCTAGACAGCTATTC 1800  
 QY 1827 TTGGAAATGCTATTGGGGGAGCTGTGATCCCTTCATGATGCTTAAATAGACAGCTTGCCGAC 1886  
 Db 1801 TTGGAAATGCTATTGGGGGAGCTGTGATCCCTTCATGATGCTTAAATAGACAGCTTGCCGAC 1860  
 QY 1887 CGGATATCTCTCCCTCTTTCTTGAATGATCATCTTGACAAACAGTAACTTATTCGACAC 1946  
 Db 1861 CGGATATCTCTCCCTCTTTCTTGAATGATCATCTTGACAAACAGTAACTTATTCGACAC 1920  
 QY 1947 CGAAGCTGTCATCTCTCATATGACATGAGCATCCAGCTTTACGAGATATCATGAGAA 2006  
 Db 1921 CGAAGCTGTCATCTCTCATATGACATGAGCATCCAGCTTTACGAGATATCATGAGAA 1980  
 QY 2007 TGAACAGAAATCTAAGTGAAGATATCATTTGGGACGAGCATCAAGCACTGTATACA 2066  
 Db 1981 TGAACAGAAATCTAAGTGAAGATATCATTTGGGACGAGCATCAAGCACTGTATACA 2040  
 QY 2067 AATGTTTGAAGAAATGTTAAACCGGTTCGATTAAGCGGCTTTACTTCACAAACCAC 2126  
 Db 2041 AATGTTTGAAGAAATGTTAAACCGGTTCGATTAAGCGGCTTTACTTCACAAACCAC 2100  
 QY 2127 AGTCATGAAACAGTTTGAACAGAACTCGAGATGCTAAGTACATCAAGCAGCAAAATC 2186  
 Db 2101 AGTCATGAAACAGTTTGAACAGAACTCGAGATGCTAAGTACATCAAGCAGCAAAATC 2160  
 QY 2187 TTGTGAGCCTCAAGCTTATTCCTCTCTCACTTGGGAGCTCTTGTGTATGACTATT 2246  
 Db 2161 TTGTGAGCCTCAAGCTTATTCCTCTCTCACTTGGGAGCTCTTGTGTATGACTATT 2220  
 QY 2247 TGGAAATGCTACCTCTTGGGATCTTCTTATGAGCCCTTACGAAAGAAACATCTTGATT 2306  
 Db 2221 TGGAAATGCTACCTCTTGGGATCTTCTTATGAGCCCTTACGAAAGAAACATCTTGATT 2280  
 QY 2307 GGGACACACGGCTTAAGATAGCATGATGATGTCAGACAAAGGTTTAGCTTATCTACCATG 2366  
 Db 2281 GGGACACACGGCTTAAATAGCATGATGATGTCAGACAAAGGTTTAGCTTATCTACCATG 2340  
 QY 2367 ACTGATGCTCAAGATCATTCACAGACAGTGAAGTGTCTCAACATCTCTTGGACAAAG 2426  
 Db 2341 ACTGATGCTCAAGATCATTCACAGACAGTGAAGTGTCTCAACATCTCTTGGACAAAG 2400  
 QY 2427 ACTTAAGGCTGCTTGAACAGATTTTGGAAATGAGAAAGCTTGTGTCTCAAGTCTAC 2486  
 Db 2401 ACTTAAGGCTGCTTGAACAGATTTTGGAAATGAGAAAGCTTGTGTCTCAAGTCTAC 2460  
 QY 2487 ATACTTCAACTTACGATGAGGACAGATGATGATTAACATGACCCCGAGTATGCTCGACTT 2546  
 Db 2461 ATACTTCAACTTACGATGAGGACAGATGATGATTAACATGACCCCGAGTATGCTCGACTT 2520  
 QY 2547 CACGGCTCACTGGAATCCGATGTCTACAGTATGGAATAGTCTTCTTGAAGTGTAA 2606  
 Db 2521 CACGGCTCACTGGAATCCGATGTCTACAGTATGGAATAGTCTTCTTGAAGTGTAA 2580  
 QY 2607 CCCGAGGAAAGCCGTTGATGACGAATCCAAATCTCAACATCTGATATGTCAAAGCG 2666  
 Db 2581 CCCGAGGAAAGCCGTTGATGACGAATCCAAATCTCAACATCTGATATGTCAAAGCG 2640  
 QY 2667 GGAACATGAAAGTGAAGTGAAGTGGAGATCCAGACATCAATGAGAGTGAAGTCTG 2726  
 Db 2641 GGAACATGAAAGTGAAGTGAAGTGGAGATCCAGACATCAATGAGAGTGAAGTCTG 2700  
 QY 2727 GTGTGTTGAAGAAAGTTTCTCAACTGCACTCTATGACCAAAAGACAGCCGATGATC 2786  
 Db 2701 GTGTGTTGAAGAAAGTTTCTCAACTGCACTCTATGACCAAAAGACAGCCGATGATC 2760  
 QY 2787 GACCCGATGACACAGGTGATCTGTTCTTGGCAGTTTATGCTATGGAACAAACAC 2846  
 Db 2761 GACCCGATGACACAGGTGATCTGTTCTTGGCAGTTTATGCTATGGAACAAACAC 2820

QY 2847 CTGCTGCACTGACACGTGACGACGCTGCTGTTCTGCTCACTGATGATGATGCA 2906  
 Db 2821 CTGCTGCACTGACACGTGACGACGCTGCTGTTCTGCTCACTGATGATGATGCA 2880  
 QY 2907 ATCTCAGACTCTCTCATTTCTGTCATTTGCTTCCATGAGTCTTCTGATGCTCACTGT 2966  
 Db 2881 ATCTCAGACTCTCTCATTTCTGTCATTTGCTTCCATGAGTCTTCTGATGCTCACTGT 2940  
 QY 2967 TTCTTGGTTTGAACAAGTATTTCTCAGAACGTAGATGTTTCTGTTAGAGAGAGA 3026  
 Db 2941 TTCTTGGTTTGAACAAGTATTTCTCAGAACGTAGATGTTTCTGTTAGAGAGAGA 3000  
 QY 3027 TCTTTAAACGAGTATCTTTCTGTTGCTTAAGCTGTTAGAAATTAATGTCATGTA 3086  
 Db 3001 TCTTTAAACGAGTATCTTTCTGTTGCTTAAGCTGTTAGAAATTAATGTCATGTA 3060  
 QY 3087 AGTATTATGACACTGCTTATTTATTTAGACAAGTGTGTGTGAATATGCTTCAGAC 3146  
 Db 3061 AGTATTATGACACTGCTTATTTATTTATTTAGACAAGTGTGTGTGAATATGCTTCAGAC 3120  
 QY 3147 TGGCACTTACACTTCTCTATA 3167  
 Db 3121 TGGCACTTACACTTCCAAAA 3141

RESULT 3  
 ATTU47029  
 LOCUS Arabidopsis thaliana ERECTA mRNA, complete cds.  
 DEFINITION Arabidopsis thaliana ERECTA mRNA, complete cds.  
 ACCESSION U47029  
 VERSION U47029.1 GI:1345131  
 KEYWORDS  
 SOURCE ORGANISM Arabidopsis thaliana (thale cress)  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 3176)  
 Torii,K.U., Mitsuoka,N., Oosumi,T., Matsuura,Y., Yokoyama,R.,  
 Whittier,R.F. and Komeda,Y.  
 The Arabidopsis ERECTA gene encodes a putative receptor protein  
 kinase with extracellular leucine-rich repeats  
 Plant Cell 8 (4), 735-746 (1996)  
 862444  
 2 (bases 1 to 3176)  
 Torii,K.U., Mitsuoka,N., Whittier,R.F., Komeda,Y. and Oosumi,T.  
 Direct Submision  
 Submitted (23-JAN-1996) Keiko U. Torii, Biology, ONL 301, Yale  
 University, 165 Prospect Street, New Haven, CT 06510, USA  
 Location/Qualifiers  
 1..3176  
 /organism="Arabidopsis thaliana"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3702"  
 /chromosome="2"  
 /ecotype="Columbia"  
 1..3176  
 /gene="ERECTA"  
 51..2981  
 /gene="ERECTA"  
 /note="extracellular ligand binding domain has  
 leucine-rich repeat motif; functions in regulation of  
 organ shape; putative receptor protein kinase"  
 /codon\_start=1  
 /product="ERECTA"  
 /protein\_id="AAC49302.1"  
 /db\_xref="GI:1345132"  
 /translation="MALPRDYLGLPCLSLVATVTSPEGATLLEIKSPKDVNVNL  
 YDWTTPSSSDYCVNMGVSCENVTRVVALNSDLNLDGRIAPADGLSLISIDRGN  
 RUSGQIPDEIGDSSLQNDLSEFNLSDIPISIKLQLEQLILKNNQLIGIPSTL  
 SOIPNLKILDLQNTLSGEIPRLIYNWEVLQYLGRNNLVGNISIPDLQNLGTLWFD  
 VVNNLSITGSIPTETIGCTAFVLDLSYNQLTSEIPFDIGFLQVATLSLQNLGSKIP  
 SVIGMQALAVLDLSGNLISGISIPILGNLFTREKLVLHNSKLTGSIPELGNMEXKH

YLEINDNHLTGH1PEELGKLTDLFNVANNDEGP1PDHLSCTTINSINLVHGNKFS  
GTTIPRAFOKLESMITVYLNLSNNIKPIPELISRGINDTLDSLNKNGIIPSLGDL  
EHLKKNLSRHITGVVSGPNNLRISMEIDLSNNDISGPIPELINDLOMILRLBN  
NNLTGNSLANCLSLTVLNSHNHVLGDI.PKXNNRFRSPDSIGRPG.OGSMNLR  
CHSRRTVRVSRISRAILGLAIGSLVLLNVLNLIACRPNRPDPDSLDLKPWTYSR  
KLVTYLNHMLDHVEDIMRNTENISEKTIIGHGASVTVKVLNCKPVAIKRYSBN  
POSUKOPELEMLSSI.KHRNLSLQVYLSHLSLL.PYULENGS.LMDLHGRTKK  
TLMDWTRKLIAYGAOGLAYLHDSPRI.IHRDVKSNNILDXLEARLDPGLAKSL  
CVSKSHTSYVMGTIGYIDPEYARSLRKSVDVYSYGIYILELTLTRKKAVIDESNLH  
HLMSKTGNNEVMEMADPDITSTCKDGLGVKVFOLALLCTKRPNRPIMHOVTRVL  
GSPFLSEQPPAIDTSTATLHAGSCVDEYANLKTPHSVNCSMSASDQLFLRBOQVLS  
QNSE"

## ORIGIN

Query Match 98.7%; Score 3136.2; DB 4; Length 3176;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3138; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 27 CTTTAAAGTATATCTAAAAACGAGTCGTTTAAAGCTGTGTGAGAAATGGCTCTGT 86  
Db 1 CTTTAAAGTATATCTAAAAACGAGTCGTTTAAAGCTGTGTGAGAAATGGCTCTGT 60  
QY 87 TTAGAGTATTTGTTCTTCTGGGTTTCTCTCTGCTTGAGCTTGTAGCTACCTGTACTT 146  
Db 61 TTAGAGTATTTGTTCTTCTGGGTTTCTCTCTGCTTGAGCTTGTAGCTACCTGTACTT 120  
QY 147 CAGAGAGGAGCAGAGCTTGAGAGATTAGAAGCTTCAAGAGTGAACATGTTT 206  
Db 121 CAGAGAGGAGCAGAGCTTGAGAGATTAGAAGCTTCAAGAGTGAACATGTTT 180  
QY 207 TTATGACTGAGCAACTTCACTTTCGGATTAATGTGTCTGAGAGAGTGTCTTGTG 266  
Db 181 TTATGACTGAGCAACTTCACTTTCGGATTAATGTGTCTGAGAGAGTGTCTTGTG 240  
QY 267 AAAATGTCACTTGAAGTGTGCTCTTAATTTGTCAAGTTGAATCTTGAAGAAA 326  
Db 241 AAAATGTCACTTGAAGTGTGCTCTTAATTTGTCAAGTTGAATCTTGAAGAAA 300  
QY 327 TCTCAGCTGTATTTGAGAGATCTCAAGAGTCTTGTCAATGTATCTGAGAGTAACTGCT 386  
Db 301 TCTCAGCTGTATTTGAGAGATCTCAAGAGTCTTGTCAATGTATCTGAGAGTAACTGCT 360  
QY 387 TGTCTGAGCAAAATCCCTGATGAGATGTGTGACTGTTCTTTTGCAAAACTTGAATCTTAT 446  
Db 361 TGTCTGAGCAAAATCCCTGATGAGATGTGTGACTGTTCTTTTGCAAAACTTGAATCTTAT 420  
QY 447 CCTTCATGAAATTAAAGTGTGACATACCGTTTGTGATTTGCAATGTGAAGCACTTGAAGC 506  
Db 421 CCTTCATGAAATTAAAGTGTGACATACCGTTTGTGATTTGCAATGTGAAGCACTTGAAGC 480  
QY 507 AGCTGATTTCTGAAGATTAACCAATTGATAGGACCGATCCCTTCAACATTTCAAGATTC 566  
Db 481 AGCTGATTTCTGAAGATTAACCAATTGATAGGACCGATCCCTTCAACATTTCAAGATTC 540  
QY 567 CAAACCTGAAAAATCTGGACTTGGCAAGAAATAAATCAGTGTGAGATACCAAGACTTA 626  
Db 541 CAAACCTGAAAAATCTGGACTTGGCAAGAAATAAATCAGTGTGAGATACCAAGACTTA 600  
QY 627 TTTTACGTGAATGAAAGTTCTTCAATATCTTGGGTTGCGAGAAACAACCTTATCGGTAA 686  
Db 601 TTTTACGTGAATGAAAGTTCTTCAATATCTTGGGTTGCGAGAAACAACCTTATCGGTAA 660  
QY 687 TTTTCTCAGATTTTGTCTCAACTGA CTGGTCTTTGGTATTTTGAAGTAAGAAACAAGTT 746  
Db 661 TTTTCTCAGATTTTGTCTCAACTGA CTGGTCTTTGGTATTTTGAAGTAAGAAACAAGTT 720  
QY 747 TGACTGTGATGATACTGAGACGATAGGAAATTGCACTGCTTCCAGGTTTGGACTTGT 806  
Db 721 TGACTGTGATGATACTGAGACGATAGGAAATTGCACTGCTTCCAGGTTTGGACTTGT 780  
QY 807 CCTCAATCTAGCTAACTGAGTGAATCCCTTTTGA CA TGGGCTTCTGCAATGCAACAT 866  
Db 781 CCTCAATCTAGCTAACTGAGTGAATCCCTTTTGA CA TGGGCTTCTGCAATGCAACAT 840

QY 867 TATCATTTGCAAGGCAATCAACTCTCTGGGAGATTCCATCAGTATGTGTCTCATGCAAG 926  
Db 841 TATCATTTGCAAGGCAATCAACTCTCTGGGAGATTCCATCAGTATGTGTCTCATGCAAG 900  
QY 927 CCTTGCAGCTTTAGATCTTAAGTGGCACTTTGTTGATGGAATCTATCTCCGATTTCTG 966  
Db 901 CCTTGCAGCTTTAGATCTTAAGTGGCACTTTGTTGATGGAATCTATCTCCGATTTCTG 960  
QY 987 GAAATCTTACTTTCAACCGAAGAAATGATTTGCAAGTAACAAGCTGACTGTTCATATTC 1046  
Db 961 GAAATCTTACTTTCAACCGAAGAAATGATTTGCAAGTAACAAGCTGACTGTTCATATTC 1020  
QY 1047 CACCTGAGCTTGGAAAATGATCAAAATCTCCATTAACCTGAACTCAATGATTAATCATCTCA 1106  
Db 1021 CACCTGAGCTTGGAAAATGATCAAAATCTCCATTAACCTGAACTCAATGATTAATCATCTCA 1080  
QY 1107 CGGATCATATCAACCAAGAGCTTGGAAAGCTTACTGACTTTGTTGATCTGAATGTGGCCA 1166  
Db 1081 CGGATCATATCAACCAAGAGCTTGGAAAGCTTACTGACTTTGTTGATCTGAATGTGGCCA 1140  
QY 1167 ACAATGATCTGGAAGGACTATACCTGATCATGAGCTTGGCACAAAATCTTAAACAGCT 1226  
Db 1141 ACAATGATCTGGAAGGACTATACCTGATCATGAGCTTGGCACAAAATCTTAAACAGCT 1200  
QY 1227 TAAATGTTCAATGGGAAACAAAGTTTAAAGTGACTATA CCCCAGAGATTTCAAAAGCTGAAA 1286  
Db 1201 TAAATGTTCAATGGGAAACAAAGTTTAAAGTGACTATA CCCCAGAGATTTCAAAAGCTGAAA 1260  
QY 1287 GTATGACTTACCTTAATCTGTCCAGCAACAAATCAAAAGTCCAAATCCCGTGAAGCTAT 1346  
Db 1261 GTATGACTTACCTTAATCTGTCCAGCAACAAATCAAAAGTCCAAATCCCGTGAAGCTAT 1320  
QY 1347 CTCGTATCGGTAACCTTAATGATTAATGGAATCTTTCACAAACAAGATTAATGGAATCAATTC 1406  
Db 1321 CTCGTATCGGTAACCTTAATGATTAATGGAATCTTTCACAAACAAGATTAATGGAATCAATTC 1380  
QY 1407 CTTCTTCCCTTGGTGAATTTGGAAGATCTTCAAGATGAACCTTGAAGTAATCATATAA 1466  
Db 1381 CTTCTTCCCTTGGTGAATTTGGAAGATCTTCAAGATGAACCTTGAAGTAATCATATAA 1440  
QY 1467 CTGATGATGTTCCAGGAGACTTTTGGAAATCTTAAGAACATCAATGGAATCTTTCACAA 1526  
Db 1441 CTGATGATGTTCCAGGAGACTTTTGGAAATCTTAAGAACATCAATGGAATCTTTCACAA 1500  
QY 1527 ATATGATATCTGTGCGCAATTCAGAAAGCTTAAACAATTAACAGATTAATTTTGC 1586  
Db 1501 ATATGATATCTGTGCGCAATTCAGAAAGCTTAAACAATTAACAGATTAATTTTGC 1560  
QY 1587 TGAGACTGAAAAATTAATACCTGA CTGTGATATGTGTTGATTAGCCAACTGTCTCAGTC 1646  
Db 1561 TGAGACTGAAAAATTAATACCTGA CTGTGATATGTGTTGATTAGCCAACTGTCTCAGTC 1620  
QY 1647 TCACTGATATGATGATATCTCATATAACAACCTCGAGTGAATATCCCTTAAGAAACAATAACT 1706  
Db 1621 TCACTGATATGATGATATCTCATATAACAACCTCGAGTGAATATCCCTTAAGAAACAATAACT 1680  
QY 1707 TCTCAAGATTTTCAACGAGACTTCAATGGAACAATCTGTGCTTTTGGGAGTGTGCTTAA 1766  
Db 1681 TCTCAAGATTTTCAACGAGACTTCAATGGAACAATCTGTGCTTTTGGGAGTGTGCTTAA 1740  
QY 1767 ACTCAGCGTGTATGATTTCTGTGAACTGTACGAGTGAATCTCTTAAGACAGCTATTC 1826  
Db 1741 ACTCAGCGTGTATGATTTCTGTGAACTGTACGAGTGAATCTCTTAAGACAGCTATTC 1800  
QY 1827 TTGGAATAGCTATTTGGGGGACTTGTGATCTTCTCATAGTCTTAAATAGAGCTTTGCCGAC 1886  
Db 1801 TTGGAATAGCTATTTGGGGGACTTGTGATCTTCTCATAGTCTTAAATAGAGCTTTGCCGAC 1860  
QY 1887 CGCATTAATCTCTCTCTCTTTCTTGAATGATCACTTGAACAACAGTAATCTTATTCGACAC 1946  
Db 1861 CGCATTAATCTCTCTCTCTTTCTTGAATGATCACTTGAACAACAGTAATCTTATTCGACAC 1920

QY 1947 CGAAGCTCGTCATCTTCATATGACATGCGACCTCCAGCTTTACGAGATATCATGAA 2006  
 |||||  
 Db 1921 CGAAGCTCGTCATCTTCATATGACATGCGACCTCCAGCTTTACGAGATATCATGAA 1980  
 QY 2007 TGAACAGAACTCTAAGTGAAGATATTCATTTGGGACGAGACATCAAGCATCTGTATACA 2066  
 |||||  
 Db 1981 TGACAGAGATCTAAGTGAAGATATTCATTTGGGACGAGACATCAAGCATCTGTATACA 2040  
 QY 2067 AATGTGTTTGAAGATTTGAACCCGGTTGCGATTAAGCGGCTTTACTCTCAACACCCAC 2126  
 |||||  
 Db 2041 AATGTGTTTGAAGATTTGAACCCGGTTGCGATTAAGCGGCTTTACTCTCAACACCCAC 2100  
 QY 2127 AGTCAATGAAACAGTTTGAACAGAACTCGAGATGCTAATAGCATCAACAGAAATC 2186  
 |||||  
 Db 2101 AGTCAATGAAACAGTTTGAACAGAACTCGAGATGCTAATAGCATCAACAGAAATC 2160  
 QY 2187 TTGTGAGCTTACAGCTTATTCCTCTCTCTACCTTGGGAGCTTTGTGTATGACTATT 2246  
 |||||  
 Db 2161 TTGTGAGCTTACAGCTTATTCCTCTCTCTACCTTGGGAGCTTTGTGTATGACTATT 2220  
 QY 2247 TGGAAATATGCTAGCTCTGGGATCTTCTTATGATGGCCCTAGAGAAACAACTCTTGATT 2306  
 |||||  
 Db 2221 TGGAAATATGCTAGCTCTGGGATCTTCTTATGATGGCCCTAGAGAAACAACTCTTGATT 2280  
 QY 2307 GGGACACACGCTTAAAGATAGCATATGCTGACACACAGGTTTATCTACACCATG 2366  
 |||||  
 Db 2281 GGGACACACGCTTAAAGATAGCATATGCTGACACACAGGTTTATCTATCTACACCATG 2340  
 QY 2367 ACTGTATCCAGAGATCTTACACAGACGCTGAAGTGTCCAACTTCTTGGACAAAG 2426  
 |||||  
 Db 2341 ACTGTATCCAGAGATCTTACACAGACGCTGAAGTGTCCAACTTCTTGGACAAAG 2400  
 QY 2427 ACTTAAGGCTCTTTGACAGATTTTGGAAATAGCGAAACCTGTGTCTCAAGTCTC 2486  
 |||||  
 Db 2401 ACTTAAGGCTCTTTGACAGATTTTGGAAATAGCGAAACCTGTGTCTCAAGTCTC 2460  
 QY 2487 ATACTTCAACTTACGTGATGGGACGATAGTATACATAGACCCGAGTATGCTCGCACTT 2546  
 |||||  
 Db 2461 ATACTTCAACTTACGTGATGGGACGATAGTATACATAGACCCGAGTATGCTCGCACTT 2520  
 QY 2547 CACGGCTCACTGAGAAATCCGATGTCTACAGTTATGGAATAGTCTTCTTGAAGTTTAA 2606  
 |||||  
 Db 2521 CACGGCTCACTGAGAAATCCGATGTCTACAGTTATGGAATAGTCTTCTTGAAGTTTAA 2580  
 QY 2607 CCGAAGGAAAGCCGTTGATGAGAAATCCAACTTCCACCATCTGATTAATGTCAAAGACG 2666  
 |||||  
 Db 2581 CCGAAGGAAAGCCGTTGATGAGAAATCCAACTTCCACCATCTGATTAATGTCAAAGACG 2640  
 QY 2667 GGAACATGAAAGTGAAGAAATGGCAGATCCAGACATCACATCGAGTGTAAAGATCTCG 2726  
 |||||  
 Db 2641 GGAACATGAAAGTGAAGAAATGGCAGATCCAGACATCACATCGAGTGTAAAGATCTCG 2700  
 QY 2727 GTGTGTTGAAGAAAGTTTTCACACTGCGACTCTATGACCAAAAGACAGCCGAAATGATC 2786  
 |||||  
 Db 2701 GTGTGTTGAAGAAAGTTTTCACACTGCGACTCTATGACCAAAAGACAGCCGAAATGATC 2760  
 QY 2787 GACCCCAATGACACAGGTGACTCGGTGTTTGGGCACTTTTATGCTATGCGAAACAACAC 2846  
 |||||  
 Db 2761 GACCCCAATGACACAGGTGACTCGGTGTTTGGGCACTTTTATGCTATGCGAAACAACAC 2820  
 QY 2847 CTGCTCGACTGACAGTCAAGCAGCCTGGCTGGTCTGCTACGTCGATGAGTATGCA 2906  
 |||||  
 Db 2821 CTGCTCGACTGACAGTCAAGCAGCCTGGCTGGTCTGCTACGTCGATGAGTATGCA 2880  
 QY 2907 ATCTCAAGACTCTCTCAATCTGTCAATGCTCTTTCATGAGTCTTGTATGCTCAACTGT 2966  
 |||||  
 Db 2881 ATCTCAAGACTCTCTCAATCTGTCAATGCTCTTTCATGAGTCTTGTATGCTCAACTGT 2940  
 QY 2967 TTCTTGCTTTGGAACAAGTATTTCTCAAGAACAGTATGTTTCTGTTAGAGAGAGAA 3026  
 |||||  
 Db 2941 TTCTTGCTTTGGAACAAGTATTTCTCAAGAACAGTATGTTTCTGTTAGAGAGAGAA 3000  
 QY 3027 TCTTTAAACGATATCTTTTCTGTTGCTTAAAGCTGTTAGAAATTAATGTCTCATGTA 3086

Db 3001 TCTTTAAACGATATCTTTTCGTTGCGTTAAGCTGTTAGAAATTAATGTCTCATGTA 3060  
 |||||  
 QY 3087 AGTATATGACATGCTCTTATTTATTTATTAGACAAGTGTGTGTGAATATGTCTTACAG 3146  
 |||||  
 Db 3061 AGTATATGACATGCTCTTATTTATTTATTAGACAAGTGTGTGTGAATATGTCTTACAG 3120  
 QY 3147 TGGCACTTAGACTTCTCTATTA 3167  
 |||||  
 Db 3121 TGGCACTTAGACTTCTCTATTA 3141  
 |||||

RESULT 4  
 AX651657  
 LOCUS  
 DEFINITION  
 AX651657  
 ACCESSION  
 VERSION  
 AX651657.1 GI:29154475  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Arabidopsis thaliana (thale cress)  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE  
 AUTHORS  
 Chang, H. S., Chen, W., Cooper, B., Glazebrook, J., Goff, S. A., Hou, Y. M.,  
 Katagiri, F., Quan, S., Tao, Y., Whitcham, S., Xie, Z., Zhu, T. and Zou, G.  
 TITLE  
 JOURNAL  
 Patent: WO 03000898-A 480 03-JAN-2003;  
 Syngenta Participations AG (CH)  
 FEATURES  
 source  
 1..2930  
 /organism="Arabidopsis thaliana"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:3702"

ORIGIN  
 Query Match 92.3%; Score 2930; DB 2; Length 2930;  
 Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;  
 Matches 2930; Conservative 0;

QY 77 ATGGCTCTGTTAGAGATATTTGTTCTTCTTGGGTTTCTTCTGCTGAGCTTAGTACT 136  
 |||||  
 Db 1 ATGGCTCTGTTAGAGATATTTGTTCTTCTTGGGTTTCTTCTGCTGAGCTTAGTACT 60  
 QY 137 ACTGTACTTCAGAGAGGAGCAACGTTGCTGAGATTTAAGAGTCAATCAAGATGTG 196  
 |||||  
 Db 61 ACTGTACTTCAGAGAGGAGCAACGTTGCTGAGATTTAAGAGTCAATCAAGATGTG 120  
 QY 197 AACCAATGCTTTTATGACATGAGCAACTTCACTTCTTGGATTTATGCTGAGAGGT 256  
 |||||  
 Db 121 AACCAATGCTTTTATGACATGAGCAACTTCACTTCTTGGATTTATGCTGAGAGGT 180  
 QY 257 GTGTCTTGAAGAAATGTCACCTTCAATGTTGTGCTCTTAATTTGACATTTGAATCTT 316  
 |||||  
 Db 181 GTGTCTTGAAGAAATGTCACCTTCAATGTTGTGCTCTTAATTTGACATTTGAATCTT 240  
 QY 317 GATGAGAAATCTCACCTGCTATTTGAGATCTCAAGAGTCTCTTGCAATTTGATCTGCA 376  
 |||||  
 Db 241 GATGAGAAATCTCACCTGCTATTTGAGATCTCAAGAGTCTCTTGCAATTTGATCTGCA 300  
 QY 377 GGTAAATGCTGTGTCGAGCAAAATCCCTGATGAGATTGGTGAAGTCTCTTGGCAAAAC 436  
 |||||  
 Db 301 GGTAAATGCTGTGTCGAGCAAAATCCCTGATGAGATTGGTGAAGTCTCTTGGCAAAAC 360  
 QY 437 TTAGACTTATCTTCAATGAATTAAGTGTGACATACCGTTTTCGATTTGGAAGTTGAAG 496  
 |||||  
 Db 361 TTAGACTTATCTTCAATGAATTAAGTGTGACATACCGTTTTCGATTTGGAAGTTGAAG 420  
 QY 497 CAACCTTGACAGCTGATTTGGAAGATTAACAATGATAGACCGATTCCTTCAACACTT 556  
 |||||  
 Db 421 CAACCTTGACAGCTGATTTGGAAGATTAACAATGATAGACCGATTCCTTCAACACTT 480

QY 557 TCACAGATTCGAACTGAAATTCGAGCTTGCGACAGATAAACTCAGTGTGAGATA 616  
| | | | |  
Db 481 TCACAGATTCGAACTGAAATTCGAGCTTGCGACAGATAAACTCAGTGTGAGATA 540  
| | | | |  
QY 617 CCAAGACTTTATTTAGTGAATGAAGTTCTTCAGATATCTTGGGTGCGAGGAAACAATT 676  
| | | | |  
Db 541 CCAAGACTTTATTTAGTGAATGAAGTTCTTCAGATATCTTGGGTGCGAGGAAACAATT 600  
| | | | |  
QY 677 GTGGTAAACATTTCTCCAGATTTGTGCACTGACTGGTCTTTGGTATTTTGAAGTAA 736  
| | | | |  
Db 601 GTGGTAAACATTTCTCCAGATTTGTGCACTGACTGGTCTTTGGTATTTTGAAGTAA 660  
| | | | |  
QY 737 AACAAAGTTTGACTGGTAGTAACTGAGACGATAGAAATTCGACTGCTTCAGGTT 796  
| | | | |  
Db 661 AACAAAGTTTGACTGGTAGTAACTGAGACGATAGAAATTCGACTGCTTCAGGTT 720  
| | | | |  
QY 797 TTGGACTTTGTCTCAATCAGCTAACGTGTGAGATCCCTTTTGAATCGGCTTCTGCA 856  
| | | | |  
Db 721 TTGGACTTTGTCTCAATCAGCTAACGTGTGAGATCCCTTTTGAATCGGCTTCTGCA 780  
| | | | |  
QY 857 GTTGCAACATTTATGATGCAAGGCAATCACTCTGGGAAATTCCTCAGTATGAT 916  
| | | | |  
Db 781 GTTGCAACATTTATGATGCAAGGCAATCACTCTGGGAAATTCCTCAGTATGAT 840  
| | | | |  
QY 917 CTCAATGCAAGCCCTTGAGCTTGAATCTAAGTGGCACTTGTGAGTGAATCTATTCCT 976  
| | | | |  
Db 841 CTCAATGCAAGCCCTTGAGCTTGAATCTAAGTGGCACTTGTGAGTGAATCTATTCCT 900  
| | | | |  
QY 977 CCGAATTCGGAATCTTTAATCTTTCAACGAGAAATTTGATTTGCAAGTAACTGACT 1036  
| | | | |  
Db 901 CCGAATTCGGAATCTTTAATCTTTCAACGAGAAATTTGATTTGCAAGTAACTGACT 960  
| | | | |  
QY 1037 GGTTCAATTCACGCTGAGCTTGAAACATGCAAACTCCATTCCTGGAATCAATGAT 1096  
| | | | |  
Db 961 GGTTCAATTCACGCTGAGCTTGAAACATGCAAACTCCATTCCTGGAATCAATGAT 1020  
| | | | |  
QY 1097 AATCATCTCAGGGGTCAATATACCAACGAGCTTGGAAAGCTTACTGATTTGATCTG 1156  
| | | | |  
Db 1021 AATCATCTCAGGGGTCAATATACCAACGAGCTTGGAAAGCTTACTGATTTGATCTG 1080  
| | | | |  
QY 1157 AATGTGCGCAAGATGATCTGGAAGGACCTTACTGATCATCTGAGCTCTTGCAAAAT 1216  
| | | | |  
Db 1081 AATGTGCGCAAGATGATCTGGAAGGACCTTACTGATCATCTGAGCTCTTGCAAAAT 1140  
| | | | |  
QY 1217 CTAAACAGCTTAAATGTTTCATGGGAAAGTTTGTGCACTATACCCGAGCAATTCAA 1276  
| | | | |  
Db 1141 CTAAACAGCTTAAATGTTTCATGGGAAAGTTTGTGCACTATACCCGAGCAATTCAA 1200  
| | | | |  
QY 1277 AAGCTAGAAAGTATGACTTACCTTAATCTGTCCAGCAACAATATCAAGGTCCAAATCCG 1336  
| | | | |  
Db 1201 AAGCTAGAAAGTATGACTTACCTTAATCTGTCCAGCAACAATATCAAGGTCCAAATCCG 1260  
| | | | |  
QY 1337 GTTAGAGCTATCTCGTATGAGTAACTTAGATACTTTGATCTTTCCACAAACAATTAAT 1396  
| | | | |  
Db 1261 GTTAGAGCTATCTCGTATGAGTAACTTAGATACTTTGATCTTTCCACAAACAATTAAT 1320  
| | | | |  
QY 1397 GGAATCAATCTCTTCTCCCTGATGATTTGGAGCACTTCTCAAGATGAACTTGAGTAA 1456  
| | | | |  
Db 1321 GGAATCAATCTCTTCTCCCTGATGATTTGGAGCACTTCTCAAGATGAACTTGAGTAA 1380  
| | | | |  
QY 1457 AATCATATTAACCTGTGTAGTTCAGGCGACTTTGGAAATCTAAGAGCATGAGAAATA 1516  
| | | | |  
Db 1381 AATCATATTAACCTGTGTAGTTCAGGCGACTTTGGAAATCTAAGAGCATGAGAAATA 1440  
| | | | |  
QY 1517 GATCTTTCAATTAATGATATCTTGCGCCCAATTCAGAAAGCTTAAACCAATTACAGAAC 1576  
| | | | |  
Db 1441 GATCTTTCAATTAATGATATCTTGCGCCCAATTCAGAAAGCTTAAACCAATTACAGAAC 1500  
| | | | |  
QY 1577 AATAATTTTGCAGAGCTGGAATAATTAATACTGACTGTAATGTTGTTCTTTAGCCAAC 1636  
| | | | |  
Db 1501 AATAATTTTGCAGAGCTGGAATAATTAATACTGACTGTAATGTTGTTCTTTAGCCAAC 1560  
| | | | |  
QY 1637 TGTCTCAGTCTCAGTGTATGATGATATCTCATTAACCAACTCGTAGGTGATATCCCTAAG 1696  
| | | | |

Db 1561 TGTCTCAGTCTCAGTGTATGATGATATCTCATTAACCAACTCGTAGGTGATATCCCTAAG 1620  
| | | | |  
QY 1697 AACAAATACCTTCAGAAATTTTACACAGACAGCTTCATTTGGCAATCTGATCTTTGCGGT 1756  
| | | | |  
Db 1621 AACAAATACCTTCAGAAATTTTACACAGACAGCTTCATTTGGCAATCTGATCTTTGCGGT 1680  
| | | | |  
QY 1757 AGTTGGCTAAACTCACCGTGTCAATGATTCCTGTGCAACTGTACAGATGTCAATCTGTAGA 1816  
| | | | |  
Db 1681 AGTTGGCTAAACTCACCGTGTCAATGATTCCTGTGCAACTGTACAGATGTCAATCTGTAGA 1740  
| | | | |  
QY 1817 GCAGCTATTTTGGAAATAGTATTTGGGGACCTTGTGATCCTTCTCATGCTTAAATAGCA 1876  
| | | | |  
Db 1741 GCAGCTATTTTGGAAATAGTATTTGGGGACCTTGTGATCCTTCTCATGCTTAAATAGCA 1800  
| | | | |  
QY 1877 GCTTGGCCGACCGGATATACCTCCCTCTTTCTTATGATGATCACTTGACAAACAGTAACT 1936  
| | | | |  
Db 1801 GCTTGGCCGACCGGATATACCTCCCTCTTTCTTATGATGATCACTTGACAAACAGTAACT 1860  
| | | | |  
QY 1937 TATTCGACACCGAAGCTCGTCACTCTTCATATGAAACATGACCTGCACTTTACAGAGAT 1996  
| | | | |  
Db 1861 TATTCGACACCGAAGCTCGTCACTCTTCATATGAAACATGACCTGCACTTTACAGAGAT 1920  
| | | | |  
QY 1997 ATCATGGAATGACAGAGAACTTAAGTGAAGATATATCTTTGGGCAACGAGATCAAGC 2056  
| | | | |  
Db 1921 ATCATGGAATGACAGAGAACTTAAGTGAAGATATATCTTTGGGCAACGAGATCAAGC 1980  
| | | | |  
QY 2057 ACTGTATACAAATGTGTTTGAAGAAATGTAAACCGGTTGCGATTAAGCGGCTTTACTCT 2116  
| | | | |  
Db 1981 ACTGTATACAAATGTGTTTGAAGAAATGTAAACCGGTTGCGATTAAGCGGCTTTACTCT 2040  
| | | | |  
QY 2117 CACAAACCCACAGTCAATGAAACAGTTTGAACAGAACTCGAGATGCTAAGTATGATCAATCAAG 2176  
| | | | |  
Db 2041 CACAAACCCACAGTCAATGAAACAGTTTGAACAGAACTCGAGATGCTAAGTATGATCAATCAAG 2100  
| | | | |  
QY 2177 CACAGAAATCTTGTGAGCTTACAGACTTATTCCTCTCTCACTTTGGGAGTCTTCTGTTCC 2236  
| | | | |  
Db 2101 CACAGAAATCTTGTGAGCTTACAGACTTATTCCTCTCTCACTTTGGGAGTCTTCTGTTCC 2160  
| | | | |  
QY 2237 TATGACTATTTGGGAAATGAGTAGCCTCTGGGATCTTCTTCATGAGCCCTTACGAGAAATAAG 2296  
| | | | |  
Db 2161 TATGACTATTTGGGAAATGAGTAGCCTCTGGGATCTTCTTCATGAGCCCTTACGAGAAATAAG 2220  
| | | | |  
QY 2297 ACTCTTGATTTGGGACACACGCGCTTAAAGATGATGATGTGTCACACAGGTTTACCTTAT 2356  
| | | | |  
Db 2221 ACTCTTGATTTGGGACACACGCGCTTAAAGATGATGATGTGTCACACAGGTTTACCTTAT 2280  
| | | | |  
QY 2357 CTACACCATGACTGTAGTCTCAAGATTCATTCAGAGACGCTGAAGTCTGTCCAACTTCTC 2416  
| | | | |  
Db 2281 CTACACCATGACTGTAGTCTCAAGATTCATTCAGAGACGCTGAAGTCTGTCCAACTTCTC 2340  
| | | | |  
QY 2417 TTGGACAAAGACTTAGAGCTCGTTTGAACAGATTTTGGATTAACGAAATCTTGTGTGT 2476  
| | | | |  
Db 2341 TTGGACAAAGACTTAGAGCTCGTTTGAACAGATTTTGGATTAACGAAATCTTGTGTGT 2400  
| | | | |  
QY 2477 TCAAAGTCAATATCTTCAATCTTACGTGATGAGGACGATAGGTTTACATAGACCCCGAGTAT 2536  
| | | | |  
Db 2401 TCAAAGTCAATATCTTCAATCTTACGTGATGAGGACGATAGGTTTACATAGACCCCGAGTAT 2460  
| | | | |  
QY 2537 GCTGCGACTTCAGGCTCACTGAGAAATCCGATGTCTACAGTTATAGGAATATGTCCTTCTT 2596  
| | | | |  
Db 2461 GCTGCGACTTCAGGCTCACTGAGAAATCCGATGTCTACAGTTATAGGAATATGTCCTTCTT 2520  
| | | | |  
QY 2597 GAGTTGTTAACCCGAGAGAAAGCGTTGATGAGCAATCCATCTCCACATCTGATTAATG 2656  
| | | | |  
Db 2521 GAGTTGTTAACCCGAGAGAAAGCGTTGATGAGCAATCCATCTCCACATCTGATTAATG 2580  
| | | | |  
QY 2657 TCAAAGACGGGGAACATAGATGATGAGAAATGGACAGATCAGACATCAGACGTGT 2716  
| | | | |  
Db 2581 TCAAAGACGGGGAACATAGATGATGAGAAATGGACAGATCAGACATCAGACGTGT 2640  
| | | | |  
QY 2717 AAGATCTCGGTGTGTGAAAGAAATTTTCCAACTGGCACTCCTATGACACCAAAAGCAG 2776  
| | | | |

[illegible]

/product="putative\_receptor-like\_protein\_kinase"  
 /protein\_id="BAD94220.1"  
 /\_dd\_xref="GI: 62321114"  
 /translation="GDIPKNNNPSRPSPDSTIANPGLCGSWLNSPCDSRSTRYAVSIS  
 RAALIGALIGVILDMVLIAACRPNNPPEPFLDGSLDKPYTSTPTKVLHMMNAALHV  
 YEDIKMNTLSEKRYIIHGASSTVVCYKNGKAPVAKIKLTHNPQSMQCFEELME  
 LSIIRKNTLVLSQAVSIHSLGSLIPYDYLKNGLMPLDLHKKTKTDMPTRLIAAYG  
 TIOGIDPEYARTSRLEIKHRPVKSNLIDMLEDLRRALDYFIASLCYSKHTSTYWG  
 TCGIDPEYARTSRLEIKHRPVKSNLIDMLEDLRRALDYDESNLHLIMKTKNGNEM  
 EMADPDITSTCKDLGVYKKYFQALALCTKQPDNRPYMHQVTRYLUSFFMLSEQPPAII  
 DTATLAGSCYDEVANLKTPIHSVNCSSMSASDAQLFLRGGVIAQNSE"

Query Match	47.1%;	Score 1495.4;	DB 4;	Length 1508;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1499;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;
QY	1680	TAGGTGATATCCCTAAGAACAAATACTTCTCAAGATTTCACACAGACGCTTCATGGCA	1739	
DB	1	TAGGGGATATCCCTAAGAACAAATACTTCTCAAGATTTCACACAGACGCTTCATGGCA	60	
QY	1740	ATCTGTGCTTTTCCGGTAGTTGGCTAACTCAACCGTGTATGATTTCTCCGTGAACCTGAC	1799	
DB	61	ATCTGTGCTTTTCCGGTAGTTGGCTAAACACCGGTGTATGATTTCTCCGTGAACCTGAC	120	
QY	1800	GAGGTGCAATCCTTAGAGCAGCTATTCTTGGAAATAGCTATGGGGGACTGTGTATCTTC	1859	
DB	121	GAGGTGCAATCCTTAGAGCAGCTATTCTTGGAAATAGCTATGGGGGACTGTGTATCTTC	180	
QY	1860	TCAATGCTTTAATAGCAGCTTGGCCGACCGCATATCTCTCTCTTTCTTGATGGATCAC	1919	
DB	181	TCAATGCTTTAATAGCAGCTTGGCCGACCGCATATCTCTCTCTTTCTTGATGGATCAC	240	
QY	1920	TTGACAAACCGATTAATTTGACACCCGAAGCTGCTCATCTCTTCAATGAACATGGCAC	1979	
DB	241	TTGACAAACCGATTAATTTGACACCCGAAGCTGCTCATCTCTTCAATGAACATGGCAC	300	
QY	1980	TCCAGCTTTACGAGATATCATAGAAATGACACAGAACTTAATGTGAGAACTATATCATTTG	2039	
DB	301	TCCAGCTTTACGAGATATCATAGAAATGACACAGAACTTAATGTGAGAACTATATCATTTG	360	
QY	2040	GGCACGAGAGCATCAAGCACTGTATTAACAATGTGTTTGAAGAAATGTAAACCGGTGGCA	2099	
DB	361	GGCACGAGAGCATCAAGCACTGTATTAACAATGTGTTTGAAGAAATGTAAACCGGTGGCA	420	
QY	2100	TTTAAGGGGCTTTTACTCTCAACAACCCACAGTCATGAAACAGTTTGAACACGAACCTCGAGA	2159	
DB	421	TTTAAGGGGCTTTTACTCTCAACAACCCACAGTCATGAAACAGTTTGAACACGAACCTCGAGA	480	
QY	2160	TGCTAAGTAGCATCAAGCAACAGAAATCTGTGAGCTACACAGCTTATCCCTCTCTCACT	2219	
DB	481	TGCTAAGTAGCATCAAGCAACAGAAATCTGTGAGCTACACAGCTTATCCCTCTCTCACT	540	
QY	2220	TGGGAGTCTTCTGTCTATGACTAATTTGGAAATGGTAGCCCTCTGGGATCTTCTTCATG	2279	
DB	541	TGGGAGTCTTCTGTCTATGACTAATTTGGAAATGGTAGCCCTCTGGGATCTTCTTCATG	600	
QY	2280	GCCCTACGAAGAAAAGACTCTTGATTGGGACACAGGCTTAAGATATGCTATATGGTGCAG	2339	
DB	601	GCCCTACGAAGAAAAGACTCTTGATTGGGACACAGGCTTAAGATATGCTATATGGTGCAG	660	
QY	2340	CACAAAGTTAGCTTATATCAACATCATGCTGTAGTCGAAGGATCATTTCAAGAGACGTGA	2399	
DB	661	CACAAAGTTAGCTTATATCAACATCATGCTGTAGTCGAAGGATCATTTCAAGAGACGTGA	720	
QY	2400	AGTGTGCAACATTTCTTTGGAACAAAGACTTGAAGGCTGCTGTTGACAGATTTTGGAAATAG	2459	
DB	721	AGTGTGCAACATTTCTTTGGAACAAAGACTTGAAGGCTGCTGTTGACAGATTTTGGAAATAG	780	
QY	2460	CGAAAGCTGTGTGTGTGTCAAAAGTCAATATTTCAACTTAACGTGATGGGACAGATAGGTT	2519	
DB	781	CGAAAGCTGTGTGTGTGTCAAAAGTCAATATTTCAACTTAACGTGATGGGACAGATAGGTT	840	



QY 2520 ACATAGACCCCGATATGCTCGACATTCAAGGCTCACTGAGAAATCCGATGCTACAGTT 2579  
 DB 841 ACATAGACCCCGATATGCTCGACATTCAAGGCTCACTGAGAAATCCGATGCTACAGTT 900  
 QY 2580 ATGGAATATGCTCTTCTTGAAGTTGTTAAACCGAAGAAAGCCGTTGATGACGAATCCAACT 2639  
 DB 901 ATGGAATATGCTCTTCTTGAAGTTGTTAAACCGAAGAAAGCCGTTGATGACGAATCCAACT 960  
 QY 2640 TCCACCATCTGATTAATGCAAAAGCGGGGAAACATGAAAGCATGGAATGGCAATCCAG 2699  
 DB 961 TCCACCATCTGATTAATGCAAAAGCGGGGAAACATGAAAGCATGGAATGGCAATCCAG 1020  
 QY 2700 ACATCATGACGACGCTGTAAGATCTCGGTGTGTGAAGAAAGTTTCCAACTGCGACTCC 2759  
 DB 1021 ACATCATGACGACGCTGTAAGATCTCGGTGTGTGAAGAAAGTTTCCAACTGCGACTCC 1080  
 QY 2760 TATGACCAAAAGACAGCCGAAATGATGACCCCAATGACCAAGGTGATCTGTTCTCG 2819  
 DB 1081 TATGACCAAAAGACAGCCGAAATGATGACCCCAATGACCAAGGTGATCTGTTCTCG 1140  
 QY 2820 GCAGTTTATGCTATCGGAAACAACACCTGCTGCGATGACGACGTCAGCGACGCTGGCTG 2879  
 DB 1141 GCAGTTTATGCTATCGGAAACAACACCTGCTGCGATGACGACGTCAGCGACGCTGGCTG 1200  
 QY 2880 GTTCGCTGCTACGTCGATGATGATGATCAATCTCAAGACTCTCTTCTGCAATGCTCTT 2939  
 DB 1201 GTTCGCTGCTACGTCGATGATGATGATCAATCTCAAGACTCTCTTCTGCAATGCTCTT 1260  
 QY 2940 CCATGAGTCTTCTGATGCTCAACTGTTCTTCTGCTTGGACAAGTTATTTCTCAGACA 2999  
 DB 1261 CCATGAGTCTTCTGATGCTCAACTGTTCTTCTGCTTGGACAAGTTATTTCTCAGACA 1320  
 QY 3000 GTGAGTATTTTCTGATGAGGAGAGATCTTTAAAGGATCTTTGCTGCTGCTTAAAGC 3059  
 DB 1321 GTGAGTATTTTCTGATGAGGAGAGATCTTTAAAGGATCTTTGCTGCTGCTTAAAGC 1380  
 QY 3060 TGTAGAAAAATTAATGCTCATGATTAAGTATTAAGTATTAAGTATTAAGTATTAAGCAA 3119  
 DB 1381 TGTAGAAAAATTAATGCTCATGATTAAGTATTAAGTATTAAGTATTAAGTATTAAGCAA 1440  
 QY 3120 GTGTGCTGCTGATTAATGCTCTTCAAGCTGCACTTAAAGTATTAAGTATTAAGTATTAAGC 3176  
 DB 1441 GTGTGCTGCTGATTAATGCTCTTCAAGCTGCACTTAAAGTATTAAGTATTAAGTATTAAGC 1497  
 RESULT 6  
 AK073793 LOCUS 3673 bp mRNA linear PLN 24-JUL-2003  
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:J03070P05, full insert sequence.  
 ACCESSION AK073793  
 VERSION AK073793.1 GI:32983816  
 KEYWORDS FULL CDNA, CAP trapper.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP clade; Ehrhartoideae; Oryzaceae; Oryza.  
 1  
 The Rice Full-length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-length cDNA Project Team.  
 Kikuchi S., Sato K., Nagata T., Kawagashira N., Doi K., Kikuchi S., Yasaki J., Ishikawa M., Yamada H., Ooka H., Hotta I., Kojima K., Namiki T., Ohneda E., Yanagi W., Suzuki K., Li C., Lu M., Onitsuki K., Shishiki T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group, Otsu Y., Murakami K., Iida Y., Sugano S., Fujimura T., Suzuki Y., Tsunoda Y., Kurosaki T., Kodama T., Masuda H., Kobayashi M., Xie Q., Lu M., Narikawa R., Sugiyama A., Mizuno K., Yokomizo S., Nishikura J., Ikeda R., Ishibiki J., Kawamata M., Yoshimura A., Miura J., Kusumegi T., Oka M., Ryu R., Ueda M., Matsubara K., RIKEN, Kawai J., Carninci P., Adachi J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashidume W., Hayatsu N., Imotani K., Ishii Y., Itoh M.,

TITLE Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shitaki, T., Yoshino, M., and Hayashizaki, Y.  
 JOURNAL Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice  
 PUBLISHED Science 301 (5631), 376-379 (2003)  
 REFERENCE 2 (bases 1 to 3673)  
 AUTHORS Adachi J., Aizawa K., Akimura T., Arakawa T., Carninci P., Doi K., Fujimura T., Fukuda S., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayashizaki Y., Hayatsu N., Hiramoto K., Hiraoka T., Hori, F., Hotta I., Iida J., Iida Y., Ikeda R., Imamura K., Imotani K., Ishibiki J., Ishii Y., Ishikawa M., Itoh M., Kagawa I., Kanagawa S., Katoh H., Kawagashira N., Kawai J., Kawamata M., Kikuchi S., Kishikawa-Hirozane T., Kishimoto N., Kobayashi M., Kodama T., Kojima K., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Kurosaki T., Kusumegi T., Li C., Lu M., Masuda H., Matsubara K., Matsuyama T., Miura J., Miyazaki A., Mizuno K., Murakami K., Murata M., Nagata T., Nakamura M., Namiki T., Narikawa R., Nishikura J., Nishi K., Nomura K., Numasaki R., Ohneda E., Ohno M., Ohtsuki K., Oka M., Ooka H., Osato N., Ota Y., Otsu Y., Ryu R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Sato K., Sato K., Shibata K., Shinagawa A., Shiraki T., Shishiki T., Sogabe Y., Sugano S., Sugiyama A., Suzuki K., Suzuki Y., Tagami M., Tagami-Takeda Y., Tagawa A., Takahashi F., Takaku-Akahira S., Tanaka T., Tomaru A., Toya T., Tsunoda Y., Ueda M., Waki K., Xie Q., Yanagi W., Yamada H., Yamamoto M., Yasunishi A., Yasaki J., Yokomizo S., and Yoshimura A.  
 TITLE Direct Submission  
 JOURNAL Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agricultural Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)  
 COMMENT This clone is one of the 28k full-length cDNA clones from japonica rice.  
 URL: http://cdna01.dna.affrc.go.jp/cDNA/  
 NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Sato, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yasaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yanagi, W., Suzuki, K., Li, C., Onitsuki, K., Shishiki, T., and Yamamoto, M.  
 PAIS Genome Sequencing & Analysis Group: Otsu, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Nishikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K., and Murakami, K.  
 Genome Exploration Research Group in Riken: Adachi, J., Aizawa, K., and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A., and Hayashizaki, Y.  
 Location/Qualifiers  
 1..3673  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultiware="Nipponbare"  
 /db\_xref="taxon:39947"  
 /clone="J03070P05"  
 ORIGIN  
 Query Match 42.3%; Score 1343.8; DB 4; Length 3673;



Best Local Similarity 67.6%; Pred. No. 0;  
Matches 1969; Conservative 0; Mismatches 917; Indels 25; Gaps 5

Oy	112	TCCTCTTCGCTTGAGCTTAGTGTGACCTTCAAGAGGAGGGAGCAACCTTGCTGA	171
Oy	113	TCCTCTTCGCTTGAGCTTAGTGTGACCTTCAAGAGGAGGGAGCAACCTTGCTGA	172
Db	407	TCCTCTTCGCTTGAGCTTAGTGTGACCTTCAAGAGGAGGGAGCAACCTTGCTGA	466
Oy	172	GATTAAAGATCATTCAAAGATGTGAACATGTTCTTTATGACTGGACAACCTTCACTTC	231
Db	467	GATCAAGAAGTCTTCGCAATGTGGACAAACCTTACTGTACATTTGGGCGGGGGGCGG	521
Oy	232	TTGCGATTATGTGTCTGGAGAGGTGTGTCTTGTGAAAATGTACCTTCAATGTTGTTGC	291
Db	522	----GACTACTGCTGTGGCGGGGGGCGTCTCTGCGCAACAAGTCACTTCGCGGTGCGCG	577
Oy	232	TCCTTAATTTGTCAGATTTGAATCTTGAATGAGAAATATCACCTGTATTTGGAGATCTGAA	351
Db	578	GCTCAACCTATTCGGGGCTCAACCTTGAGGCGAGATCTTCGGGCGGTGGAGGTTGAA	637
Oy	352	GAGTCTCTTGTCAATTTGATCTGCGAGGTATCGCTGTCTGGACAATTCCTGATGAGAT	411
Db	638	GGGCACTGCTCGATTGACTTGAATGAGTCGAATGGGGGTCTGGGCGAGATCCGTATGAGAT	697
Oy	412	TGCTGACTGTTCTTCTTTGCAAACTTGAATTTATCTTCAATTAATGATGTGAT	471
Db	698	TGGCATTTGTTTCATCACTAAAAAATCTGTGATTTGTTTCAATTAACCTTGATGGGAGCAT	757
Oy	472	ACCGTTTTCGATTTGGAAGTTGAACCACTTGAGAGCGATTTGGAAGATTAACAAT	531
Db	758	TCCGTTCTCAGATGATGAAGCTGAAGCAATTTGAGAGCTTGATTTGAAGAACAAACCACT	817
Oy	532	GATAGAGCCGATCCCTTCAACCTTTCACAGATTCGAAACTGAAATTTCTGACTGGC	591
Db	818	GATCGAGATGATCCCATCAACGCTCTCAAGCTCCCAATTTGAAGATTTTGGACTGGC	877
Oy	592	ACAGATTAATCTCAGTGTGTGATATCAAGACTTATTTACTGAAATGAAGTTCTTCACTA	651
Db	878	ACAGAACAACTCAGTGTGTGAGATACCAAGACTGATATTTGGAACGAGTTCTTCAATA	937
Oy	652	TCTTGGGTTGGAGGAACCACTTATGTGCTGAACATTTCTCCAGATTTGTCTCACTGAC	711
Db	938	CTTGGGATTTAGCGGGTAAATTAATTTGAAAGGAGCATCTCCAGATATATGTCAAGTTGAC	997
Oy	712	TGCTTTTGGTATTTTGAAGTAAAGAACACAGTTTGACTGGTAGTATCTGAGACGAT	771
Db	998	TGGGCTTTGGTATTTTGAAGTAAAGAACACAGCTTGACTGGGCGGATTCAGAAACCAT	105
Oy	772	AGGAATTTGACACTGCTTCAGAGTTTGGACTTGTCTCAACATCAGCTAATCTGTGAGAT	831
Db	1058	TGGGAATCTGTAACAAGTTTCAAGGTCTTGGATTTGTCTTACATTAACCTTCTGATCAAT	111
Oy	832	CCCTTTTGAATTCGGCTTCCTGCAAGTTGCAACATTTATCTTGAAGGAAATCAACCTGC	891
Db	1118	TCCTTTCAACATTTGGTTTCTTCAACAAGTTGCTACCTATCTTGGCAAGGGAACATGTTTAC	1177
Oy	892	TGGGAAGATTCATCAGTATGTGTCTCATGGAAGCCCTTGACGCTTATGATCTTAAGTGG	951
Db	1178	TGGTCTTATTCATCAGTTATTTGGAACCTTATGGAAGGCTCTCGCTTACTGGAATCTGAGTTA	123
Oy	952	CAACTGTTGAGTGAATCTTATTTCTTCGATTTCTGGAATCTTACCTTTCACCGAGAAT	1011
Db	1238	CAACCAATTTGTGTCTTATTCATTCAGATTACTAGGCAATTTTAACTATCACTGAGAAGCT	129
Oy	1012	GTAATTTGACAGTAAACAGTGAATCTGTGTTCAATTTCACTGAGCTTGGAAACATGTCAA	1077
Db	1298	GTAATTTGACAGGCAATTAAGTTAAACAGGTTCAATTAACCACTGAGCTTGGAAATATGTCAAC	135
Oy	1072	ACTCATTAACCTGGAATCAATGATATCATCTCAAGGCTCATATACCAACCAAGACTTGG	1133
Db	1358	CCTTATTAATCTTGAACCTTAAAGATTAATCACTTGAAGGCTTCAATCTTCCAGAGTTGG	1411
Oy	1132	GAACTTACTGACTTGTGATCTGAATGTGCAACAAATGATCTGGAAGACCTATACC	119

Db	1418	AAAGCTAACAGGGTTATTGACTTAAACCTTGCAAAACAACACTTTGAAGTCCAAATCC	1477
OY	1192	TGATCATCTGAGCTCTTGACAACAACTCTAAACAGTTAAATGTTTCATGGGAACAAGTTTAC	1251
Db	1478	TGATTAACATAAGCTCATGTGTGAATCTCAATAGCTTCAATGGCTTAATGGCAACAATATAA	1537
OY	1252	TGGCACTATACCCCGAGACTTTCAAAGCTTAGAAAGTATGACTTAACTTAATCTGTCCAG	1311
Db	1538	TGGGACCAATCCCTCTTCATTTGCAATTAACCTTGAGAGCATACTTAATTTGTAATCTCATC	1597
OY	1312	CAACAATATCAAAAGTCCAAATCCCGGTTGAGCTATCTCGTATCGGTAACTTAGATCATTT	1371
Db	1598	AAATTTTCTATAGTGGTTCTATTTCTTATTAGACTATCGAGAAATCAACAATTTGGACACTT	1657
OY	1372	GGATCTTCTCCAAACAACAATAAATGGAATCATTTCTTCTCTCCCTGGTGAATTTGGAGA	1431
Db	1658	GGATTTATCTCGTAAACATGATTAATCTGGCCCAATTCATCAACCATTTGGAGATTTGGAGA	1717
OY	1432	TCTTCTCAAGATGAACCTTGAGTAAATTCATATPACTGTGTAGTTTCCAGGCCATTGG	1491
Db	1718	TCTATTAAGACTTAACTTGAGCAACAATGGCTTAGTAGAATTCATTTCTCGAGAAATTTGG	1777
OY	1492	AAATCTAAGAGCATCATGGAATAAGATCTTTCAATTAATGAATCTCTGGCCCAATTTCC	1551
Db	1778	CAACTGAGAGTATCATGAGATTGAATATGTCCAAACATCATTTGGCGGTTGATTTCC	1837
OY	1552	AGAAAGCTTAAACCAATTAACAGAACATATTTTGGCTGAGACTGGAAATATATAACCTGAC	1611
Db	1838	TCAAGAACTCGGAATGCTGGCAAAATCTGATGTTGTTAAATCTCAAAAACAACATATAC	1897
OY	1612	TGTATAATGTGGTTCAATTAGCCAACTGTCTCAGTCTCAGCTGATGTGAATGATTTCTATPA	1671
Db	1898	TGGGGAATGTCCTTCACTGATGAACCTGCTCAGGCTCAAAATCTTAATGATATCTCTATAA	1957
OY	1672	CAACCTGAGAGTATATCCCTAAGAACATATCTTCAAGATTTTCCACAGACACTT	1731
Db	1958	TAAATTTGGCTGTGTGTGATCTCTCATCTATPAACAACTTCTCAGGTTTTCGCTGACAGTT	2017
OY	1732	CATTGGCAATCTGTGCTTTGCGGTAGTTGGCTAACTCAACCGTGCATGATTTCTGCTCG	1791
Db	2018	TTTGGGTATTCAGAGACTTTGTGTGAATATGTGGCTTGTCTTCGTGCGGTTTCATGTGGCA	2077
OY	1792	AACGTACAGATGTCATTTCTTAGAGAGACTATTTCTGGAATAGCTATTTGGGGGAACTTGT	1851
Db	2078	TCAACAGAAACCAATATATCTCAAAAGGCTGCAATACTTGGAAATTCGCTGGGTGGCTGTGT	2137
OY	1852	GATCTCTTCTCATGCTCTTAATAGACGCTTGCACCGCATATATCTCTCTCTTTCTTTGA	1911
Db	2138	TATCTCTCTGTATGATCTTGAATGGGGTGTCTGAGGCTCATATGTCACCTGTGTTTCAAGA	2197
OY	1912	TGGAATCATCTTGACAAACAAGATCTTAATTTGGAACAACGAGTGTGTCATCTTCAATGAA	1971
Db	2198	TGTCTCTGTTAGCAAAACAGTAGAGCAATGTTCCTCCCAAGCTGTTATCTCTTCATATGA	2257
OY	1972	CATGGCACTCCACCTTTACAGAGATTCATGAGATGACAGAGATCTAAATGATGAAGTA	2031
Db	2258	CCTTTCCTCTTGTATATACAGATATATATGACGATGACGTGAAAACCTGAGTGAAGATGA	2317
OY	2032	TATCATTTGGGACGGAGATCTACAGCACTGTATACAAATGTGTTTTGAAGAAATTTGAACC	2091
Db	2318	CATCATTTGGGATCGAGACATCCACAGAGGT- TATTAATGTGTTTTGAAGAACCGCAAAC	2376
OY	2092	GGTTGCAATTAAGGGGCTTACTGTCAAAACCCACAGTCAATGAAACAGTTTGAACAGA	2151
Db	2377	AGTGGCAGTAAAAAGCTATATAGCCCATATCCACAGACTTCAAGGAATTTGAAAATGTA	2436
OY	2152	ACTCGAAGTGTAAAGATCAAGCAACAAGATCTTGTGAGCCTCAAGCTTAATTTCTT	2211
Db	2437	GCTTAGAGCTGTGTGATCAAAACACCGGAATCTAGTCAGTCTTCAAGATATTTCCCT	2496
OY	2212	CTCTCACTTGGGAGCTCTTCTGTCTATAGATATTTGAAAATGTATAGCTCTTGGGATCT	2271
Db	2497	ATCTCTGTGTGGAATCTTCTCTTCAAGATATCATGAAAATGGAAGCCTCTGGAATGT	2556

Oy	2272	TCTTCAT---	-GGCCCTACGAAAGAAAAGACTCTTGATTGGGACACAGCGCTTAAAGTAGC	2328
Db	2557	TTTTCATTAAGAAGTCCAACTAAGAAAAAATACTGATTGGGAACAATCCTCATACGAATTGC		2616
Oy	2329	ATATGGTACACACAAGGTATTAGCTTATCTACACCATGACTGTAGTCCAAAGATCAATTCA	2388	
Db	2617	TCTAGTGTCCGCCCCNAGGCTTGCTTATCTTATCATATACACTGTAGCCACGGAATATATCA	2676	
Oy	2389	CAGAGACGTGAAGTGTCTCAAATCTTCTTGAGACAAAGACTTAGAGCTCGTTTGACAGA	2448	
Db	2677	CAGGAGTGTGAATCAAAAAATAATACTCTTGATTAAGATTATAGGGCACATCTTACAGA	2736	
Oy	2449	TTTTGGATTAACGAAAAGCTTGTGTGTCAAAGTCACATATCTTCACTTACGTGATGGG	2508	
Db	2737	CTTTGGCACTTCTAAGATTGTGTGTTCAAAACTCACAGTCCACTGTGTGCATGGG	2796	
Oy	2509	CACAGTAGATTACATAGACCCTCGAGTATGTCGCACTTCACGGGCTCACTGAGAAATCCGA	2568	
Db	2797	AACATTTGGCTATATCATCTCTGAGTATGCTCGACCTCCCTCTCAATGAAAAATCTGA	2856	
Oy	2569	TGTCACAGTTATGGAATAGTCTTCTTGAGTTGTTAACCCGAAAGAAAGCGTTGATGA	2628	
Db	2857	TGTCACAGCTATGSCATTTGTTTCTTGACTGTGACCGGAAAAAGCCAGTGGACAA	2916	
Oy	2629	CGAATCCATCTCCACCATCTGATPATGTCAAAGACGGGGAACAATGAATGATGAGAAAT	2688	
Db	2917	CGAGTGCATCTCCATCACTTGATCTTGTCAAAGACGGCTTAACAATGCTGTCAATGAGAC	2976	
Oy	2689	GGCAGATCCACACATCAGATGAGAGCTGTAAAGATCTGGTGTGGGAAGAAAGTTTTCCA	2748	
Db	2977	AGTCGACCCGAGCATTGCGACACTTGGCAAGGATTTGTGTAGGTCAAGAAAGGTGTCCA	3036	
Oy	2749	ACTGGCACTCTCTATGACCAAAAGACAGCCGAATGATGAGACCCAAATGACACAGTGCAC	2808	
Db	3037	GCTGGCGCTCCTTTTGACACAAAGACAAACATCGATGGCGCGACAAATGACAGAGTTGT	3096	
Oy	2809	TCGTGTTCTCGGCAAGTTTATGCTATGGAACAACACACCTGCTGC-----GACTGA	2859	
Db	3097	GCGGCTCTTGACATGCTAGTTGTCGCCGACCCGACCGGAAGTCCGACAGCAGCTGGC	3156	
Oy	2860	CACGTACACGACGCTGGCTGTGTCSTGTAGCTGCATAGATATGCAATCTCAAGACTCC	2919	
Db	3157	CATGCGCAGCGGCTGCTGTGCCAGGTACATCAACAGATATGTCACCTTAAGAGGCAC	3216	
Oy	2920	TCATCTCTGCAATTGCTC---TTCCATAGAGCTCTGTATGCTCAACTGTTCTTCGGTT	2976	
Db	3217	CAGCGTGTCTTCCCTGCGCACTGCTCGTATCACTTCGATGCTAGCTGTTTTCAGATT	3276	
Oy	2977	TGACACAGTTATTTCTCAGAACAGTGAAGTATG	3007	
Db	3277	TGGCGAGGTCAATTTCTCAGAAACACAGAGTAG	3307	
RESULT 7				
AY244746		3089 bp	mRNA	linear
LOCUS				PLN 24-MAR-2004
DEFINITION			Arabidopsis thaliana ERECTA-like kinase 2 (ERL2) mRNA, ERL2-er12	
FEATURES			allele, complete cds.	
ACCESSION			AY244746	
VERSION			AY244746.1	GI:37954361
SOURCE			Arabidopsis thaliana (chale crees)	
ORGANISM			Arabidopsis thaliana	
			Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
			Spermatophytes; Magnoliophyta; eudicotyledons; core eudicotyledons;	
			rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsie.	
REFERENCE			Shpak,E.D., Berthiaume,C.T., Hill,J.E.J. and Torii,K.U.	
AUTHORS			Synergistic interaction of three ERECTA-family receptor-like	
TITLE			kinases controls Arabidopsis organ growth and flower development by	
			promoting cell proliferation	
JOURNAL			Development 131 (7), 1491-1501 (2004)	

PUBMED	14985254
REFERENCE	2 (bases 1 to 3089)
AUTHORS	Sapak, E.D., Berchtaume, C.T. and Torii, K.U.
TITLE	Direct Submission
JOURNAL	Submitted (27-FEB-2003) Biology, University of Washington, 1521 NE Pacific,
FEATURES	Seattle, WA 98195-1800, USA
source	location/Qualifiers
gene	1..3089
CDS	/organism="Arabidopsis thaliana"
	/mol_type="mRNA"
	/db_xref="taxon:3702"
	/chromosome="5"
	/map="BAC T28J14"
	/ecotype="Columbia"
	1..3089
	/gene="ERL2"
	/allele="erl2"
	186..3089
	/gene="ERL2"
	/allele="erl2"
	/note="putative leucine-rich repeat receptor-like kinase; redundant function with ERCTA, involved in inflorescence architecture"
	/codon_start=1
	/product="ERCTA-like kinase 2"
	/protein_id="AAE9764.1"
	/db_xref="gi:37954362"
	/translation="MRRIETWKGLPFCLGVVFMILGVSFPMNEGKALMAIKASFSN VANLLDMDDVHNDPCSRMGVPCDNLNVANSLNSLNIGESLSAGDLMLQS DLOENRKGGOI PDEIGLVAVYDFSPNISISXKOLEPRLNKOLGTG IPALTQIPNKITDILARNQVLTSIRPLLYNEVLYLGKGMLETLSPMDLTG LMYDVGRNNLTGTIPESIGCTSEILDVYNIOGTVPINIGFOVATISLOGKKI TGRPEVIYQLMQLAVLDLSNELTGPIPLILGMSFGKLIVHGKNLTQGI PELGA MSRIAYQLDNDELAVGKIPELIGKLEQLFELIANNNVWGI PENISGCALNPFWLA GNFLSGVAPELFERNIGSLTYLNTSSNPKGIPELGHII INLOTLDLGGNFSSGIP TLGDFELLILNTSRNHNGTLPAEPGNLRISQIIVDSFNLAGVIPRELGLONINS LIANNKHCKIPDQULTRCSLANLNTSNLSGILPPMKPTFRSPASFQNPBLCC NWSTICGPSLPKSQVFPRVAVICMVLAGFTILCMIFLAYVSKQOKVNLGSSKOPR GSTGLVILHMMAHTDPDIRVTENDLDEKXI IGYCASTVYKCTSKSRPARIKRI NOYSNFERFELETETGIS IHRNI VSHGVALSPFGNLFPDYMNENSIMDLHPGP KKVLDWEETRLKIAVGAAOGLAYLHDCTPRI IRDIKXSNI LIDGNEEARLSDGFI KSIPTATKYASTVIGTIGTVI DPEVARTSRNKESDIYSPGIVLEILLTGKKAADNEA NLHMWLISKADNTVMEDVDAEVSVTCMSDSHIKTQTOLALCTKRNDLERPTMOEVS RVLLSLVSPSPPKLPSPAKVQEGEERESHSDTTTPWFQVEDRIDSKSL"
ORIGIN	
Query Match	36.6%; Score 1161.8; DB 4; Length 3089;
Best Local Similarity	65.2%; Pred. No. 0;
Matches 1760; Conservative	0; Mismatches 927; Indels 12; Gaps 3;
Dn	150 AGAGAGGAGCAACGTTGCTGTGAGATTGAAGAAGTCATTCAAAGATGTGAACAATGTTCTT 209
Dn	274 ACGAAGGAAAAAGCGTTGATGCGAATAAAGCGTTTCATTGACGACGATGCGAATATGCTTC 333
Dn	210 ATGACTGACAACTTACACTTCTTGCGATTATGTGTCTGAGAGAGTGTCTTGTGA 269
Dn	334 TTGATTGGAGCAAGATGTTCATACCAACGACTTTTGTCTTGGAGAGTGTCTTGTGTGTA 393
Dn	270 ATGTCACCTTCAATGTTGTTGCTCTTAATTTGTGCAGATTGGAATTTGATGAGAGAACT 329
Dn	394 ACGTTAGCCTCAAGTGTCTCTCTTAATCTGTCAAACTGTAATCTTGTGAGAGATAT 453
Dn	330 CACCTGTATTGGAGATCTCAAGAGTCTCTTGTCAATTTGATCTGCGAGTATCGCTTGT 389
Dn	454 CATCTGCCCTTGGAGATTTGATGAAATCGCAATCAATGAACTGGAAGAAATAATTGG 513
Dn	390 CTGACCAAAATCCCTGATGAGATTGGTAGCTGTTCTTTTSCAAAATTGAAGCTTATCTT 449
Dn	514 GTGGCAAAATTCAGATGAGATGGAACTGTGTTCTCTTGCTATGTGATTTCTCCA 573
Dn	450 TCATATGAATTAAAGTGTACATACCCTTTTGGATTTGCAAGTTGAAGCACTTGACAGC 509
Dn	574 CCAATTGTGTGTGGAGACATACCCTTTTCAATCTTCAAACTCAACAGCTGGAGATTTC 633

QY	510	TGATTCTGAGAAATACCAATTGATGAGACCGATCCCTTCAACACTTTCAACAGATTCCAA	569
Db	634	TGAACCTTAAGAAATATATACGCTCAGCTGGCCAAATCCAGCAACCTTAATCTAGATTTCCAA	693
QY	570	AACCGAAATATCTGGACCTTGGCACGAAATMAACCTGAGTGGAGATACCAAGACTTATT	629
Db	694	ACCTTAAGACCCCTTGACCTCGCAAGAAACAGCTTACTGGTGAATACCAAGTTTACTCT	753
QY	630	ACTGGAATGAAGTTCTTCAGTATCTTGGGTTGCGAGAAACAATTAGTCGGTAACATT	689
Db	754	ACTGGAATGAAGTTTACAGTATCTCGGTTTACGGGAATATGTTAACTGGGAATGTT	813
QY	690	CTCCAGATTGTGTCACTGACTGCTGTGTGTAATTTGACGTAAAGAAACAACAGTTTGA	749
Db	814	CTCCGATATGTGTGAGCTGACGAGGGGTGTGTGGTACTTTGATGTGAGAGCAACAACCT	873
QY	750	CTGTGATGATACCTTGACAGACGATAGAAATTTGCACTGCTCTCCAGTTTGGACTTGTCT	809
Db	874	CTGGAACATATCCCAAGAGACATTGGCAATTGCAACAGCTTTGAGATCTTGGATGTATCT	933
QY	810	ACAATCAGCTAACCTGGTAGATCCCTTTTGA CATGGGCTCTCGCAAGTTGGAACATTAT	869
Db	934	ATATACAAATTAACCGAAGTTATACCTTCAATATTTGTTCTTCCAGATGACTATCTGT	993
QY	870	CATTGCAAGCAATCAACTCTCTGGGAAGATTTCACTCAGTATTTGTCATGCAAGCCC	929
Db	994	CACTTCAAGGAAACAAGTTGACTGCGCAAAATTCGGAAGTATTTGTCGATGCAAGCTC	1055
QY	930	TTGCAGCTTAGATCTAAAGTGCGCAACTTGTGATGATCTATTCCTCCGATTTCCGGA	989
Db	1054	TTGCTGTATGGATTTGAGTACCAATGAATTAACGGGCTTATTCACCAATATCTTGGGA	1133
QY	990	ATCTTACTTTTACCGAGAAATTTGATTTTGGCACAGTAAACACTGACCTGGTCAATCCAC	1049
Db	1114	ATCTGTCAATTAACGGAACCTGATCTCCATGCGAACAAGCTCACTGGAACAAATCCAC	1173
QY	1050	CTGAGCTTGGAAACATGTCMAAACCTCCATTAACCTGGAACCTAAGATATATCATCTCACG	1109
Db	1174	CCGAGCTAGGCAATATGTCAACGACTCAGCTATTGGCAACTMAATGATATATGAATGAGG	1233
QY	1110	GTCATATTAACAACAGAGCTTGGGAAGCTTACTGACTTGTGTGATCTGAATGTGCCAA	1165
Db	1234	GAAAGATCCCACTGAGCTTGGGAAGCTGGAACAATTTTGGAACTGGAATCTTGGGAACA	1293
QY	1170	ATGATCTGGAAGACCTTATACCTGATCATCTGAGCTCTTGACAAATCTTAAACAGCTTAA	1229
Db	1294	ACAATCTTGAAGGGGTGAATCCATCTAACATTAAATTAATGTTCTGTGCTGTGAATCAATT	1353
QY	1230	ATGTTTCATGGGAACAAGTTTATAGTGGCACTTATACCCGAGCAATTTCAAAAGCTAGAAGTA	1289
Db	1354	ATGTTTCATGGGAACCTTCTTGAGTGGAGCTGTACCACTTGAATTCGGGAATCTTGGAACT	1413
QY	1290	TGACTTACCTTATCTGTCTGACGACAACAATATCAAAAGTCCAATCCGCTTGAGCTATCTC	1349
Db	1414	TGACTTATCTAAATCTTCTCTCAAAAGATTTCAAGGGCAAAATATCTGCTAGCTGGCC	1473
QY	1350	GTAATCGGTAACCTTAGATCATTTGGATCTTTCCAAACACAGATTAATGGAATCATTCCT	1409
Db	1474	ATATCATCAATCTTGATCATTTGGATCTGTCTGGCAACAATTTCTCAGGCTCAATTCAT	1533
QY	1410	CTTCCCTTGGGATTTGGAGCATCTTCCAGATGAACTTGAGTAAGAAATCATATACTG	1469
Db	1594	GCAACTGCTCGAGAAATTCGGGAACCTCGAAGATTCAGATCATGATGTGTGATTTA	1653
QY	1470	GTTGATTTCCAGCGCACTTTGGAATCTTAAGAAGCATCATGGAATAGATCTTTCAATA	1529
Db	1594	GCAACTGCTCGAGAAATTCGGGAACCTCGAAGATTCAGATCATGATGTGTGATTTA	1653
QY	1530	ATGATATCTCTGGGCCAATTTCCAGAAGCTTAAACAAATTACAGACATTAATTTGCTGA	1589
Db	1654	ATTTTCTTGCCGGGTGTTATATTCCACTGGAATCTTGCGCAGATTCAGAACTTCTCTGGA	1713

OY	1590	GACGTGAAAATATATTAACCTGACTGCTATATG----	TGGTTCATTAGCCAACTGTCTCAGTC	1646
Db	1714	TATCGAAACAAACAAATTCATGGGAAAATCCCTGATCAGCTACCTAACTGGCTTCAGTC	1773	
OY	1647	TCACTGATTAATGAATGTAATCTCAATACAAACCTCGTAGGTGATATCCCTTAAGAACATTAAT	1706	
Db	1774	TTGGCAATCTGAACATCTCTTCAATATATCTTTTGGAATATATCCCACTATGAGAACT	1833	
OY	1707	TCTCAAGATTTTCCACGACAGACTTCATTGGCAATCCTGGTCTTTGGCGATAGTTGGCTAA	1766	
Db	1834	TTACACGTTTTTCCCGGCGAGCTTTTGGAAATTCATTTCTCTGGCGGAACTGGGTTG	1893	
OY	1767	ACTCAACGGTGCATGATTTCTGTGGAACGTGACAGTGTCAATCTTACAGACACTATTC	1826	
Db	1894	GATCAATCTGTGGCCCACTTTTACCTAAGTCAACAAGT----	ATTCAACAGAGTTGCCGTGA	1950
OY	1827	TTTGAATAGCATTTGGGGGAACTGTGATCCCTCTCAGGTCTTAATAGACCTTGGCCGAC	1886	
Db	1951	TTTTATAGTTCTCGGTTTCACTCACTCAATGCAATGATATTCATTGCGGTTTACAAGT	2010	
OY	1887	CGCATTAATCCCTCCTCTTTTCTTGATGATCACTTGAACAAACCGTAACCTTATTCGACAC	1946	
Db	2011	CAAGCAGCAGAAACAGTCTTGAAAGGCTCTTCAAAACA-----	CTGAAGGCTCA	2064
OY	1947	CGAAGCTGTCACTCTTCAATATGAAACATGGCACTCCACGTTTACGAGATATCATGAA	2006	
Db	2065	CGAAGCTGTGATCTTCACTGACATGGCTATTCACAGTTTGAATGATCATGAGAG	2124	
OY	2007	TGACAGAGAACTTAAGTGAAGAAATATCATTTGGGACCGAGCATCAAGCATGTATATCA	2066	
Db	2125	TTTACAGAAAACCTCGATGAGAAATACATATGGATACGGTGTCTTACGACACAAATTTACA	2184	
OY	2067	AATGTGTTTTGAGAATTTGTAAACCGGTGCGATTAAGCGGCTTATCTCACAACCCAC	2126	
Db	2185	AGTGCACCTCCAAACCTTCCCGACCTATTTGCCATTAAGCCAACTTACAATCAGTATCCCA	2244	
OY	2127	AGTCAATGAAAACAGTTTGAACACAGAACTCGAAGTGTCTAAGTATGATCAAGCACAGAAATC	2186	
Db	2245	GCAACTTCCGAGATTTGAAACAGAGCTCGAGACCATTTGGAGATCAGACACAGAAACA	2304	
OY	2187	TTTGAGACCTTACAAGCTTATTTCCCTCTCTCACTTTGGGAGTCTTCTGTCTTATGACTATTT	2246	
Db	2305	TAGTAACTTGGCAACGATGAGCTTATCTCCCTTTGGCAACCTCTCTTTACGACTTACA	2364	
OY	2247	TGGAATAATGAGAGCCTCTGGGATCTTTTTCATGGCCCTTACGAAAGAAAAGACTTTGATT	2306	
Db	2365	TGGAAAATGGCTCTCTTTGGGATCTTTCTCAATGGGCTTGGGAAAGAGTAAAGCTTAACT	2424	
OY	2307	GGGACACACGCTTTAAGATAGCATATGGTGCAGACACAGAGTTTAACTTATCTACACCATG	2366	
Db	2425	GGGAAAACAAAGCTGAATATAGCTGTGGAGCTGGCAAGGACCTTGCAATCTTCAACCATG	2484	
OY	2367	ACTGTACTCCAAAGATCATTCACAGAGACGTGAAGTGTCTCAACATTTCTTTGGACAAG	2426	
Db	2485	ACTGCACACCTAGGATATATCATCGAGACATCAAGTCATCAAAATATCTCTCTTGATGGGA	2544	
OY	2427	ACTTAGAGGCTCGTTTGAACAGATTTTGGATTTACGAAACACTGTGTGTCTCAAGTCAAC	2486	
Db	2545	ATTTTCGAAGCGCTTGTGTACGATTTTGGGATATGCGAAAGACATATCACAGCACCAAAAATT	2604	
OY	2487	ATACCTTAACCTTACGATATGGGACGATATGTTACATATAGACCCGAGATATCTCGACTT	2546	
Db	2605	ATGCTTCAACCTATGTTCTTTGGAACATTTGGATATATTTGACCAGAGTATGCTCGAATTT	2664	
OY	2547	CACGGCTCACTGAGAAATCCGATGTCTTACGTTATGGAATATGTCTTTGAGTTGTTAA	2606	
Db	2665	CGGCTGTGAACGAGAAAGTGTGATATCTACAGTTTCGGTATTTGTCTCTTGAACCTTCAA	2724	
OY	2607	CCGGAAGGAAAGCGCTTGAATGAGAAATCCAAATCTCCACCATCTGATTAATGTCAAAAGCG	2666	
Db	2725	CCGGCAAGAGAGGCTGTGGATTAACGAGGCCAACTTGCAATCAAAATGATTTATCAAAAGCGG	2784	
OY	2667	GGAACATGAAATGATGGAATGGCAGATCCAGACATCATCANTGAGGTGTAAGATCTCG	2726	

Db	2785	ATGATAACACAGTAATGAAGCTGTGATGACAGAGGCTCTAGTCACTTGATGATGACTGAC	2844
Qy	2727	GTGTGGTGAAGAAAGTTTCCAACTGGACATCCATGACCAAAAGACAGCCGAATGATC	2786
Db	2845	GACACATCAAGAAACATTTCAAGTACTCTTTGTGACCAACGAAATCTTTGGAGA	2904
Qy	2787	GACCCACAAATGACACAGGTGACTGTCTTCCGACAGTTTATTCGAACCAACCA	2845
Db	2905	GACCCACATGACAGAGAGTCTCTAGGGTTCTGCTCACTTGTCCTCGCTCCACTCTCA	2963
RESULT 8	AY244745	3100 bp mRNA linear	PLN 24-MAR-2004
LOCUS	AY244745	Arabidopsis thaliana ERECTA-like kinase 1 (ERL1) mRNA, ERL1-er11	
DEFINITION	AY244745	allele, complete cds.	
ACCESSION	AY244745		
VERSION	AY244745.1	GI:37954359	
KEYWORDS			
SOURCE		Arabidopsis thaliana (thale cress)	
ORGANISM		Arabidopsis thaliana	
REFERENCE		Bukatyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	
REFERENCE		1 (bases 1 to 3100)	
AUTHORS		Spak, E.D., Berchiaux, C.T., Hill, E.J. and Torii, K.U.	
TITLE		Synergistic interaction of three ERECTA-family receptor-like kinases controls Arabidopsis organ growth and flower development by promoting cell proliferation	
JOURNAL		Development 131 (7), 1491-1501 (2004)	
PUBMED		14985254	
REFERENCE		2 (bases 1 to 3100)	
AUTHORS		Spak, E.D., Berchiaux, C.T. and Torii, K.U.	
TITLE		Direct Submission	
JOURNAL		Submitted (27-FEB-2003) Biology, University of Washington, 1521 NE Pacific, Seattle, WA 98195-1800, USA	
FEATURES		Location/Qualifiers	
source		1..3100	
		/organism="Arabidopsis thaliana"	
		/mol_type="mRNA"	
		/db_xref="taxon:3702"	
		/chromosome="5"	
		/map="BAC MM19"	
		/ecotype="Columbia"	
gene		1..3100	
		/gene="ERL1"	
		/allele="er11"	
		/gene="ERL1"	
		/allele="er11"	
		/note="putative leucine-rich repeat receptor-like kinase; redundant function with ERECTA; involved in silique elongation"	
		/product="ERECTA-like kinase 1"	
		/protein_id="AA069763.1"	
		/db_xref="GI:37954360"	
CDS		/translation="MKERMQRMVSLAMVGFWFGVAMNNBEKALMAIKGFSNIV NMLDWDVHNSDLCWRGVFCNDVSVSVLNSLSNLGGEISPAIGDIRNQSIDL QGNLAQIDPEIGNCALSIVLDISENLVGDIPFSISKQJETTLLKNNOLGVPV ATLTOIPNLKRLDLAGNHLGELISRLYNNMVLQYGLRGNMLGVTLSMCOITGMY YFVDRGNMLGTIPESIGNCTSPQIILDSYNOITGEIPVNIQGLQVLTLSQGNRLTG RIEPVIGLMQALVLDLSNDELNGIPPIIGNSPFGKYLHGMLTGPIPSRLGNNS RLSTLQNDKLVGTIPPEIKLEQLFELNLSRLVGP1PSNISSCALANQVPHN LLSGSIPLARFNLSLTVLNLSNNFSGKLPELGH1INDKLDLSGNNSSG1PLTL GDSEHL1LNSLRNHLGOLPAEFGNRS1QMDIVSNLSLGSVPTLGLQONINS1L LNNKHLGKI1PDOLNCFITLVNLSNNSGIVPMPKNSRFAPASVFNVPY1CGM VGS1CGPLPKRSRGALICIVGVITLCMIPLAYKSOOKK1IGSKOABGT KVY1IGHDMA1HFDPMIDRMYENNEKFTIGYSS1VYCA1KSSP1AIK1XNYX PHN1REFTELEFTIGSTRHNRTVSLHGALSPTGNL1FYWENGSLMDLHSGKVV KLGWTR1K1AVGAQ1AYLHDCTPR11HRDIKSSN1LDENFEH1LDFGLAKS1 PASKTHAS1VLTIGT1YIDPEYARTSRINEXSDIYSGIYVL1ELLTKKAVDEAN1H	

Qy	131	GTAGCTACTGTGACCTTCAGAGAGAGAGCAACCTTCTCGAGATTAAAGTCAATCAAA	190
Db	263	GTTCCTTCGGCTATGAAACAACGAGGAAAGCTCTGATGCGCATTAAGGCTCTTTCACG	322
Qy	191	GATGTGAACAATGTTCTTTATGACCTGCAACTTCACTTCTTCGATTATGTCTGTG	250
Db	323	AACCTTAGTAATATGCTTTTGGATTGGACGATGTTCAACAACGATCACTGTCTTCTGG	382
Qy	251	AGAGGTGTCTTGTGAAAATGTCACCTTCAATGTTGTTCTTTAATTGTCAGATTG	310
Db	383	CGAGGTGTTTCTGCAACAACGTTAGCTACCTCGGTGTCTCTGAAATTTGTCCAGCTG	442
Qy	311	AATCTTGATGAGAAATCTCACTGCTATGAGATCTCAAGAGTCTCTGTCAATTGAT	370
Db	443	AATCTTGAGAGGAGATATCTCAGCTATTTGAGACTTACGAAATTTGCAATCAATAGAC	502
Qy	371	CTGCGAGTAATGCTTGTCTGCAACAATCCTGATGAGATTGTACTGTCTTCTTGG	430
Db	503	TTGCAAGGTATTAACATGACAGGTCAAAATCCAGATGAGATTGGAACATGTCTTCTCTT	562
Qy	431	CAAACTTACCTTATTCCTTCAATGAAATTAAGTGTGACATACGTTTTCGATTGGAAG	490
Db	563	GTTATCTGGAATTTGTCGGAATCTGTATATGAGACATACCTTCTCAATCTTAA	622
Qy	491	TTGAGCAACCTTGACGCTGATTTGGAAGATTAACCAATTGATAGGACCGATCCCTTCA	550
Db	623	CTCAGAGAGCTTGAACCTGATCTGAGAACATCAGCTCACAGCTCTGTACACAGCA	682
Qy	551	ACACTTTCACAGATTCGAAACCTGAAATTTCTGACTTGGCAGAGAAATTAACCTAGTGT	610
Db	683	ACCTTAACCCAGATTCGAAACCTTAAAGACATGATCTTCTGCAATCATCTTAACGGGT	742
Qy	611	GAGATACCAAGACTTATTTATCTGGAATGAAGTCTTCAATCTTGGTTCGAGAGAAAC	670
Db	743	GAGATATCGAGATTTGCTTATCTGGAATGAAGTCTTGGAGATTTGGAATTAACAGAGAAAT	802
Qy	671	AACCTAGCTGTAACATTTCTCAGATTGTGCAACTGCTGATCTTGTGATTTTTCAG	730
Db	803	ATGTTGACTGGAACGTTATCTTGTGATATGTGTCAGCTAACCGGTTTGTTGATCTTTGAT	862
Qy	731	GTAGAAACAACAGTTTGAATGATGATCTGAGACGATAGAGAAATTTGCACTGCTTC	790
Db	863	GTGAGAGAAATATATCACTGGAACCATCCGAGAGCATCGGAATTTGACACAGCTTT	922
Qy	791	CAGTTTTCAGCTTGTCTTCAATCAGCTAACCTGAGAGATCCCTTTTGCATCGGCTTC	850
Db	923	CAATCTCGACATCTTATTAATCAAGATTAACGAGAGATTCCTTAACAATATCGGCTTC	982
Qy	851	CTGGAAGTTGCAACATTAATCATGCAAGCAATCAACTCTCTGGAGAAATTTCCATCAGTG	910
Db	983	CTCAGAGTTCTACTCTGTACTTTCAGAGAAACAGATTTAGCGGTAGAAATTTCCAGAAAGTT	1042
Qy	911	ATTGCTCTCATGCAAGCCCTTGGAGTCTTAGATCTAAGTGGCAACTTGTGATGATCTT	970
Db	1043	ATTGCTCTAATGCAAGGCTTGTGCTTTTGGATTGAGTACAAATGAGCTTGTGTCCT	1102
Qy	971	ATTCTCTCGATTTCTGGAATCTTACTTTACCGAGAAATTTGATTTGGACAGTAACAG	1030
Db	1103	ATCCCAACCGATTTCTGCAATCTCTCAATTAACGGAAGTTGATCTCCATGCGCAATATG	1162
Qy	1031	CTGACCTGCTCAATTCACCTGAGCTTGGAAACATGTCAAAATCTCAATCTCTGAACTC	1090
Db	1163	CTCACTGCTCAATCTCCCTCTGAGCTTGGGAAATATGTACGCTTACAGCTATTTGGACCTA	1222
Qy	1091	AATGATATATCATCTCAAGGCTCATATACCAACAGAGCTTGGAAAGCTTACTGACTTGT	1150

Db 1223 AACGACATAAAGTAGGGAACTATTCACCTGAGCTTGGAAGGCTGGAGCAATGTTT 1282  
Qy 1151 GATTCGATGTCGGCCAAACATGATCTGGAGAGCCTATACCTGATCATCTGAGCTCTTC 1210  
Db 1283 GAACCTGATCTTGGCCAAAGCCGTTTAGTAGGGCCCATACCTCAACATTTAGTTCATGT 1342  
Qy 1211 ACAATCTAAACAGCTTAATAGTTCATGGGAAACAAGTTTAGTGACATATACCCCGACA 1270  
Db 1343 GCACCTTGATCAATTCATGATGAGGAACTCTTGAGTGATCTATTCACCTGCGC 1402  
Qy 1271 TTTCAAAAGCTAGAAATGATGACTTATCTGTCACAGCAAAATCAAGATCTCA 1330  
Db 1403 TTTCGCAATCTCGGAGCTTGAATCTATCTGATCTTTCGTCGAACATTTCCAGGAAAA 1462  
Qy 1331 ATCCCGGTGAGCTATCTCGATCGGTAATCTAGATCAATGATCTTTCACACAG 1390  
Db 1463 ATACCACTTGAGCTGGACATATATCAATCTTGACAACTAGATCTGTGCGCAATAC 1522  
Qy 1391 ATAAATGGAATCATCTCTCTCCCTTGATTTGGAGCATCTTCCAGATGAACTTG 1450  
Db 1523 TTCTCAGGGCTATACCATTTAACCTTGGCGATCTTGAAACCTTCTCATATTAATCTT 1582  
Qy 1451 AGTAGAATCATATTAATCTGTGATTCAGGCGACTTGGAAATCTAAGAGCATGATG 1510  
Db 1583 AGAGAAACCATCTTAATGAGCAATTAACCTGCAAGTTTGGAACTTCGAGCATTCAG 1642  
Qy 1511 GAAATGATCTTTGAAATTAATGATATCTGCGCCCAATTCGAGAGCTTAACCAATTA 1570  
Db 1643 ATGATGATGATCATTCATCAATCTGCTCCGAGTTATTCACATGAACTTGGCAATTG 1702  
Qy 1571 CAGAACATATTTTGTGAGCTGGAAATTAATTAACCTGAGCTGTATGTT---GATCA 1627  
Db 1703 CAGATTTAACTCTTTAATATGAAACAACAAGCTTCAATGGAAATTTCCAGATCAG 1762  
Qy 1628 TTAGCCAACTGTCTGACTGCTCACTGTATGTAATGATATCTCATAAACAATCTGATGAT 1687  
Db 1763 CTTAACGAATGCTTCACTCTTGTCAATCTGATATCTCTTCAACATCTCTCCGGATA 1822  
Qy 1688 ATCCCTAAGAACATTAATCTTCAAGATTTTACCAAGACAGCTTCATGGCAATCTGAT 1747  
Db 1823 GTCCCAACCAATGAAAACTTCTCAAGTTTGTCTCCAGCAGCTTGTGGAATTCATAT 1882  
Qy 1748 CTTTGGGTAGTGGCTAAACTCAACCTGTCAATCTGTGCAACTGTACAGATGTC 1807  
Db 1883 CTTTGTGGAACCTGGGTGATCTATTTGTGTCTTACCGAAATCTGCA-----GTA 1936  
Qy 1808 ATCTTAGACAGCTATTTCTGGAATGACTATTGGGGAGCTTGTGATCTTCTCATGTC 1867  
Db 1937 TTCTCCAGAGTGTCTTGAATCTGATCTGTGCTTGGCGTCACTCTCTATGATGAT 1996  
Qy 1868 TTAAATGACAGCTTGGCCGACGCAATATCTCTCTCTTCTTGTGATGATCACTTGACAA 1927  
Db 1997 TTCTTTCAGTTTAAACAATCAATGACAGCAAGAAATTTTACAAAGGCTC-----CTCA 2050  
Qy 1928 CCAGTAATTAATTCGACCGAGAGCTGTGATCTTATATGAAACAGGAGCTCCAGCTT 1987  
Db 2051 AAACAAAGCTGAAGGTTTAAACAAAGCTAGATTTCTCAATGACAGGCAATTCATACA 2110  
Qy 1988 TACAGAGATATCATGAGAAATGACAGAAATCTAAGTGAAGATATCATTTGGGACAG 2047  
Db 2111 TTTCATGATATCATGAGAGTGAAGTGAAGAACTTAAGCAAAAGTTTAAATTTGATAGT 2170  
Qy 2048 GCATCAAGACCTGTATTAACAATGTGTTTGAAGAATTTAAACCGGTTGAGATTAAGCG 2107  
Db 2171 GCTTCTAGACCGGTATTAACAATGTGCTTAAAGAGTTCCCGACCTATTTGCAATTAAGCG 2230  
Qy 2108 CTTTACTCTCAGAACCCAGAGTCAATGAAGAGTTTGAACAGAACTCGAGATGCTAAT 2167  
Db 2231 CTCTCAATATGATATCCGCAATTAATCTTGGGAAATTTGAGCAAGAACTTGAACATTTGG 2290  
Qy 2168 AGCATCAAGACAGAAATCTGTGAGCTTCAAGCTTATTCCTCTCTCACTTGGGAGT 2227

Db 2291 AGCATAGGACAGAAACATATGATGATGATGATGATGATGATGATGATGATGATGATG 2350  
Qy 2228 CTTCTGTTCTATGATATTTGAAATGATGATGATGATGATGATGATGATGATGATGATG 2287  
Db 2351 CTTCTTCTTATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2410  
Qy 2288 AAGAAAAAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2347  
Db 2411 AAGAAAGTGAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2470  
Qy 2348 TTAGCTTATCTACACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2407  
Db 2471 CTGAGCTATCTTACACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2530  
Qy 2408 AACATCTCTTGAACAAAGCTTGAAGCTGATGATGATGATGATGATGATGATGATGATGATG 2467  
Db 2531 AACATCTCTTGAAGCAATTTGCAAGCACTTATGATGATGATGATGATGATGATGATGATGATG 2590  
Qy 2468 TTGATG 2527  
Db 2591 ATACCACTGACAAACCAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2650  
Qy 2528 CCGAGATG 2587  
Db 2651 CCAAGATG 2710  
Qy 2588 GTCTTCTTGAATG 2647  
Db 2711 GTCTTCTTGAATG 2770  
Qy 2648 CTGATATG 2707  
Db 2771 CTGATATG 2830  
Qy 2708 TCGACGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2767  
Db 2831 GTGACCTGATG 2890  
Qy 2768 AAAAGACAGCGGATG 2827  
Db 2891 AAGCGAAACCTTGAAGAGAGACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2950  
Qy 2828 ATGCTATCGGAACACAC 2847  
Db 2951 GTCCCACTCTGCAAGTAC 2970

RESULT 9  
E12706  
LOCUS 9295 bp DNA linear PAT 27-APR-1998  
DEFINITION Arabidopsis thaliana gene involved in morphogenesis.  
ACCESSION E12706  
VERSION E12706.1 GI:3251538  
KEYWORDS JP 1997056382-A/2.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 9295)  
AUTHORS Mitsuoka,N. and Robato,E.U.  
TITLE GENE CODING FOR PROTEIN CONTROLLING MORPHOGENESIS OF PLANT  
JOURNAL Patent: JP 1997056382-A 2 04-MAR-1997;  
CHIKYU KANTYO SANJO GIUTTSU KENKYU KIKO, MITSURU GIOSAI SHOKUBUTSU  
BIO KENKYUSHO:KK  
OS Arabidopsis thaliana (chale cress)  
PN JP 1997056382-A/2  
PD 04-MAR-1997  
PT 24-AUG-1995 JP 1995216187  
PI MITSUKAWA NORIHIRO, ROBATO EFU UTSUTSURA  
PC C12N15/09,A01H5/00,C12N5/10;  
CC strandedness: Double;  
topology: linear;  
FH Key Location/Qualifiers

FT	source	1..9295	
FT	/organism='Arabidopsis thaliana'	FT	
FT	/strain='colombia'		
FT	intron	1882..2227	
FT	exon	2228..2366	
FT	intron	2367..2467	
FT	exon	2468..2539	
FT	intron	2540..2643	
FT	exon	2644..2715	
FT	intron	2716..2809	
FT	exon	2810..2878	
FT	intron	2879..2968	
FT	exon	2969..3040	
FT	intron	3041..3118	
FT	exon	3119..3190	
FT	intron	3191..3265	
FT	exon	3267..3328	
FT	intron	3339..3421	
FT	exon	3422..3493	
FT	intron	3494..3586	
FT	exon	3587..3655	
FT	intron	3656..3740	
FT	exon	3741..3812	
FT	intron	3813..3888	
FT	exon	3889..3960	
FT	intron	3961..4048	
FT	exon	4049..4120	
FT	intron	4121..4209	
FT	exon	4210..4281	
FT	intron	4282..4349	
FT	exon	4350..4421	
FT	intron	4422..4508	
FT	exon	4350..4421	
FT	intron	4581..4706	
FT	exon	4707..4778	
FT	intron	4779..4860	
FT	exon	4861..4932	
FT	intron	4933..5018	
FT	exon	5019..5090	
FT	intron	5091..5176	
FT	exon	5177..5248	
FT	intron	5249..5312	
FT	exon	5313..5481	
FT	intron	5482..5576	
FT	exon	5577..5648	
FT	intron	5649..5726	
FT	exon	5727..5800	
FT	intron	5801..5882	
FT	exon	5883..6011	
FT	intron	6012..6095	
FT	exon	6096..6443	
FT	intron	6444..6519	
FT	exon	6520..6890	
FT	intron	6891..6974	
FT	CDS		
FT	join(1830..1881,2228..2366,2468..2539,2644..2715, FT		

FT	2810..2878,2969..3040,3119..3190,3267..3328,3422..3493, FT		
FT	3587..3655,3741..3812,3889..3960,4049..4120,4210..4281, FT		
FT	4350..4421,4350..4421,4707..4778,4861..4932,5019..5090, FT		
FT	5177..5248,5413..5481,5577..5648,5727..5800,5883..6011, FT		
FT	/product='a protein involved in morphogenesis'		
FT	Location/Qualifiers		

	source	1..9295	
	/organism="unidentified"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:32644"		
ORIGIN			
Query Match	34.7%; Score 1102; DB 2; Length 9295;		
Best Local Similarity	84.9%; Pred. No. 0;		
Matches 1376; Conservative	0; Mismatches 0; Indels 244; Gaps 3;		
Qy	1801 AGTGTCAATCTTAGAGACAGTATTCTTGAATAGCATATGGGGGCTGTGATCCCTTC	1860	
Db	5881 AGTGTCAATCTTAGAGACAGTATTCTTGAATAGCATATGGGGGCTGTGATCCCTTC	5940	
Qy	1861 CATGCTTAAATAGACAGCTTGGCCGACATATCCCTCTTCTTCTTGATGATCACT	1920	
Db	5941 CATGCTTAAATAGACAGCTTGGCCGACATATCCCTCTTCTTCTTGATGATCACT	6000	
Qy	1921 TGACAAAC-----	1928	
Db	6001 TGACAAACAGGCTCTACTCTCAAAACACTTACGAATGTTCTTCACTTACAACTGATATC	6060	
Qy	1929 -----CAGTAACTTATGACACCCGAGCTCGT	1956	
Db	6061 CAATAGTAACTCTTAAATTTCTGCTGTGACATGATTAATTCACACCGAGCTCGT	6120	
Qy	1957 CATCCTTCATATGAACATGSCATCCACGTTTACGAGATATCATGAGATGACAGAA	2016	
Db	6121 CATCCTTCATATGAACATGSCATCCACGTTTACGAGATATCATGAGATGACAGAA	6180	
Qy	2017 TCTAAGTAGAAGATATATCTTGGGACGAGCATCAAGACTGTATCAATGTGTTTT	2076	
Db	6181 TCTAAGTAGAAGATATATCTTGGGACGAGCATCAAGACTGTATCAATGTGTTTT	6240	
Qy	2077 GAAGAATGTAAACCGGTTGCGATTAAACGGCTTCTCTCAAAACCAAGTCAATGAA	2136	
Db	6241 GAAGAATGTAAACCGGTTGCGATTAAACGGCTTCTCTCAAAACCAAGTCAATGAA	6300	
Qy	2137 ACAGTTTGAACAGAACTCGAGATGCTAAGTAGATCAACAGACAGAAATCTTGAGCCT	2196	
Db	6301 ACAGTTTGAACAGAACTCGAGATGCTAAGTAGATCAACAGACAGAAATCTTGAGCCT	6360	
Qy	2197 ACAAGCTTATCCCTCTCTCACTTGGGAGTCTTCTGTTTATAGCATATTTGGAAAAATGG	2256	
Db	6361 ACAAGCTTATCCCTCTCTCACTTGGGAGTCTTCTGTTTATAGCATATTTGGAAAAATGG	6420	
Qy	2257 TAGCCTCGGAGATCTTCTCAT-----	2278	
Db	6421 TAGCCTCGGAGATCTTCTCATAGTATCTCATCCCAAAACATAGAAAATTTTGAAT	6480	
Qy	2279 -----GGCCCTACGAGAAAAAGATC	2300	
Db	6481 CTTCTGTGACATTAACAACCTTGCTGTGTGTTTGTAAAGCCCTTACGAGAAAAAGATC	6540	
Qy	2301 TTGATTGGACACACGCGCTTAAGATAGCATATGCTGACACAAAGTTTGTATCTAC	2360	
Db	6541 TTGATTGGACACACGCGCTTAAGATAGCATATGCTGACACAAAGTTTGTATCTAC	6600	
Qy	2361 ACCATGACGTAGTCCAGAGATCATTCACAGACGGAAGTGTCCAAATCTCTGCG	2420	
Db	6601 ACCATGACGTAGTCCAGAGATCATTCACAGACGGAAGTGTCCAAATCTCTGCG	6660	
Qy	2421 ACAAGAAGCTTAGAGGCTCGTTTGAAGATTTTGGAAATAGCGAAAGCTTGTGTGTCAA	2480	
Db	6661 ACAAGAAGCTTAGAGGCTCGTTTGAAGATTTTGGAAATAGCGAAAGCTTGTGTGTCAA	6720	
Qy	2481 AGTCACATCTTCAACTTACGTATGGGACGATAGTTCATAGACCCGAGTATGCTC	2540	
Db	6721 AGTCACATCTTCAACTTACGTATGGGACGATAGTTCATAGACCCGAGTATGCTC	6780	
Qy	2541 GCACCTTACCGCTCACGAGAAATCCGATGTCTACAGTTATGGAAATAGTCTTGTAGT	2600	
Db	6781 GCACCTTACCGCTCACGAGAAATCCGATGTCTACAGTTATGGAAATAGTCTTGTAGT	6840	



OY	2601	TGTTAATACCCGAAGAAAGCGCTGTATGACGAATCCAATCCTCACACACTT-----	2649
Db	6841	 TGTTAACCCGAAGAAAGCGCTGTATGACGAATCCAATCCTCACACACTTGGTTGTTCTT	6900
OY	2650	-----	2649
Db	6901	TCTTGCCCATCTCTCTCTCAAGCTGCTCTGTTTAGTCGAATCCGTAATCTTGTGTTTCATTGA	6966
OY	2650	-----GATAATGTCAAAGACGGGGACAATGAAGTAGAGAAAATGGCAGATC	2696
Db	6961	 TTCACTTACATCAGATTAATGTCAAAGAAGGGGAAACAATGAAGTAGAGAAAATGGCAGATC	7020
OY	2697	CAGACATCAACATCCAGCTGTGTAAAGATCTTCGGTGTGTGAAGAAATTTTCCACTGGCAC	2756
Db	7021	CAGACATCAACATCCAGCTGTGTAAAGATCTTCGGTGTGTGAAGAAATTTTCCAACTGGCAC	7080
OY	2757	TCCTATGACACAAAGACAGCCGGAATGATTCGACCACCAATGCACAGGTTGACTGGTTC	2816
Db	7081	TCCTATGACACAAAGACAGCCGGAATGATTCGACCACCAATGCACAGGTTGACTGGTTC	7140
OY	2817	TCGGCAGTTTTATGTCTATCGGAACAACCACTGCTGCAGCTGACACGTCAAGCAGCTGG	2876
Db	7141	TCGGCAGTTTTATGTCTATCGGAACAACCACTGCTGCAGCTGACACGTCAAGCAGCTGG	7200
OY	2877	CTGGTTCGTCTACGTCGATGATGACAAATCTCAAGACTCTCTCAATCTGATTCCT	2938
Db	7201	CTGGTTCGTCTACGTCGATGATGACAAATCTCAAGACTCTCTCAATCTGATTCCT	7266
OY	2937	CTTCCATGAGTCTCTCTCATATGCTCAACTGTTTCTTCGGTTTGGACAAATATTCTCAGA	2996
Db	7261	CTTCCATGAGTCTCTCTCATATGCTCAACTGTTTCTTCGGTTTGGACAAATATTCTCAGA	7320
OY	2997	ACAGTAGATAGTTTTTCGTTAGAGAGAGAAATCTTAAACGGTAACTTTTGCGTGCCTTA	3056
Db	7321	ACAGTAGATAGTTTTTCGTTAGAGAGAGAAATCTTAAACGGTAACTTTTGCGTGCCTTA	7380
OY	3057	AGCTGTGAGAAAAATTAAATGCTCTCATGTGTAAGATTTATGACATGCTTATTATTATAGA	3116
Db	7381	AGCTGTGAGAAAAATTAAATGCTCTCATGTGTAAGATTTATGACATGCTTATTATTATAGA	7440
OY	3117	CAAGTGTGTGTGTGAATAATGTCTCAGATGTAAGATTTATGACATGCTTATTATTATAGA	3176
Db	7441	CAAGTGTGTGTGTGAATAATGTCTCAGATGTAAGATTTATGACATGCTTATTATTATAGA	7500
RESULT 10			
AUTHER		9295 bp DNA linear PLN 14-FEB-2004	
LOCUS		Arabidopsis thaliana DNA for receptor protein kinase, complete cds.	
DEFINITION		D83257	
ACCESSION		D83257.1 GI:1389565	
VERSION			
KEYWORDS		extra-cellular leucine-rich repeats; receptor protein kinase.	
SOURCE		Arabidopsis thaliana (chale cress)	
ORGANISM		Arabidopsis thaliana	
REFERENCE		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	
AUTHORS		1 Torii,K.U., Mitsuikawa,N., Oosumi,T., Matsunura,Y., Yokoyama,R., Whittier,R.F. and Komeda,Y. The Arabidopsis ERRECTA gene encodes a putative receptor protein kinase with extracellular leucine-rich repeats Plant Cell 8 (4), 735-746 (1996) 862444	
TITLE		2 (bases 1 to 9295) Mitsuikawa,N.	
JOURNAL		Direct Submission	
PUBMED		Submitted (29-Jan-1996) Norihito Mitsuikawa, Mitsun Plant Biotech.Res.Inst., Research Division, TCI-P21, Sengein 2-1-6, Teikuba, Ibaraki 305, JAPAN [E-mail:tsuoi129@korynu.statci.jp, Tel:0298-58-6252, Fax:0298-58-6234]	
REFERENCE		Location/Qualifiers	
AUTHORS			
JOURNAL			
TITLE			
FEATURES			

source	1. .9295 /organism="Arabidopsis thaliana" /mol_type="genomic DNA" /db_xref="taxon:3702" /clone="61H10" /clone_1b="Arabidopsis PI genomic library" /ecotype="Columbia" 1754. .7513 /gene="ER" exon /gene="ER" <1754. .1881 /number=1 /gene="ER" CDS join(1803. .1881,2228. .2366,2468. .2539,2644. .2715, 2807. .2878,2969. .3040,3119. .3199,3267. .3338,3442. .3493 3587. .3655,3741. .3812,3889. .3960,4049. .4120,4210. .4281 4350. .4421,4509. .4580,4707. .4778,4861. .4932,5019. .5090 5177. .5248,5413. .5481,5577. .5648,5727. .5800,5883. .6011 6096. .6443,6520. .6890,6975. .7331) /gene="ER" /note="leucine-rich repeats putative" /codon_start=1 /product="receptor protein kinase" /protein_id="BA111869.1" /db_xref="GI:1389566" /translation="MALFRDIVLGLFCLSLVATVTSSEGNLTLEIKSFQDVNVL YDMTSSPSYCWVRGSCENYTFNVNALNSDLNDEISPAIGDKLSLSDLRN RLSDQIDBEIGCSLONIDLSPNELSGDIPFSIKLQQLQLIKNNQLGIPSTL SOPINKLIDLAONKLSGEIPRLIYMWELQVIGLRGNLIGNISPDLCQLGLMYD VRNNSLTGSIPTETGCTAFQVLDSYNLTTEIEFPDGFQVATLSIQNQLSGKIP SVGLWMALVDLSNLSGSIPTLGNLTTEKLVLAHSNKLTSIPPELGNKSLH YLELNDMLGHIPELGLTDLFDLVANNDLEGPIDHLSGCTNINSLVNKNKS GTTIPRAOKSEMTYNLNSNNIKGPIVEISRIQNLDTLDSNNKINGIIPSLGDL EHLKMLSNHITGVVPGDFGNLSIMEIDLSNNDISGPIPEELNOLQNIILRLN NMLTGNVGSANCLSLTVLVNHNLDIPKNNSESPSPDFGNPGICGSLNRP CHSRPVRPSTISRAILICIAIGVILMLWILAACRPHNPPFLDLSLKPRTYSP KLVLVHNHMLHYEDIMWTEENLSKYITGHGASTYKCVLKNCKRVAIKRISHN POSQKQETELNLSIKHRNLVSLQAYSLSHLSGLAYDLLENGSLMDLHGPTKK TLMDDTLTAKYGAQGLAYLHSDSPRIHRDVSNNILDKLEARLIDFGJAKSL CVSHSHSTYMGVTIGYIDPEYARTSLTEKSDVYSYGVILELLETRKKAVDENSL HLIMSKGNENWEMADPDITSTCKDGVKKVQDLALLCTKROPNRPMTWQVTRL GSPRLSQPPAATDITSATLAGSCYDEYANLKTPIHSVNCSSMSADQALPLRFQVLS QNSE"
intron	1882. .2227 /gene="ER" /number=1
exon	2228. .2366 /gene="ER" /number=2
intron	2367. .2467 /gene="ER" /number=2
exon	2468. .2539 /gene="ER" /number=3
intron	2540. .2643 /gene="ER" /number=4
exon	2644. .2715 /gene="ER" /number=3
intron	2716. .2806 /gene="ER" /number=4
exon	2807. .2878 /gene="ER" /number=5
intron	2879. .2968 /gene="ER" /number=5
exon	2969. .3040 /gene="ER" /number=6

intron 3041..3118  
/gene="BR"  
/number=6  
exon 3119..3190  
/gene="BR"  
/number=7  
intron 3191..3266  
/gene="BR"  
/number=7  
exon 3267..3338  
/gene="BR"  
/number=8  
intron 3339..3421  
/gene="BR"  
/number=8  
exon 3422..3493  
/gene="BR"  
/number=9  
intron 3494..3586  
/gene="BR"  
/number=9  
exon 3587..3655  
/gene="BR"  
/number=10  
intron 3656..3740  
/gene="BR"  
/number=10  
exon 3741..3812  
/gene="BR"  
/number=11  
intron 3813..3888  
/gene="BR"  
/number=11  
exon 3889..3960  
/gene="BR"  
/number=12  
intron 3961..4048  
/gene="BR"  
/number=12  
exon 4049..4120  
/gene="BR"  
/number=13  
intron 4121..4209  
/gene="BR"  
/number=13  
exon 4210..4281  
/gene="BR"  
/number=14  
intron 4282..4349  
/gene="BR"  
/number=14  
exon 4350..4421  
/gene="BR"  
/number=15  
intron 4422..4508  
/gene="BR"  
/number=15  
exon 4509..4580  
/gene="BR"  
/number=16  
intron 4581..4706  
/gene="BR"  
/number=16  
exon 4707..4778  
/gene="BR"  
/number=17  
intron 4779..4860  
/gene="BR"  
/number=17  
exon 4861..4932  
/gene="BR"  
/number=18  
intron 4933..5018

/gene="BR"  
/number=18  
exon 5019..5090  
/gene="BR"  
/number=19  
intron 5091..5176  
/gene="BR"  
/number=19  
exon 5177..5248  
/gene="BR"  
/number=20  
intron 5249..5412  
/gene="BR"  
/number=20  
exon 5413..5481  
/gene="BR"  
/number=21  
intron 5482..5576  
/gene="BR"  
/number=22  
exon 5577..5648  
/gene="BR"  
/number=22  
intron 5649..5726  
/gene="BR"  
/number=22  
exon 5727..5800  
/gene="BR"  
/number=23

Query Match 34.7%; Score 1102; DB 4; Length 9295;  
Best Local Similarity 84.9%; Pred. No. 0;  
Matches 1376; Conservative 0; Mismatches 0; Indels 244; Gaps 3;

QY 1801 AGTGTCAATCTCTAGACAGACTATTCTTGAATAGCTATTGGGGAGCTTGATCCCTCT 1860  
DB 5881 AGTGTCAATCTCTAGACAGACTATTCTTGAATAGCTATTGGGGAGCTTGATCCCTCT 5940  
QY 1861 CATGCTCTTAATAGCAGCTTGCCGACCGCATTAATCCCTCTCTTTCTTGATGATCACT 1920  
DB 5941 CATGCTCTTAATAGCAGCTTGCCGACCGCATTAATCCCTCTCTTTCTTGATGATCACT 6000  
QY 1921 TGACAAAC----- 1928  
DB 6001 TGACAAACGAGTCTACTCTCAAAACCACTTACGAATGTTCTTCACTCAATGTAATC 6060  
QY 1929 -----CAGTAACCTTATTCGACCGAAGCTCGT 1956  
DB 6061 CAATAGTTAATCCTTAATTTCTGTCATCATGTAATTTTCGACCGAAGCTCGT 6120  
QY 1957 CATCCTTCATATGAACTAGGCACTCCACGTTTACGAGATATCATGAAATGACAGAA 2016  
DB 6121 CATCCTTCATATGAACTAGGCACTCCACGTTTACGAGATATCATGAAATGACAGAA 6180  
QY 2017 TCTAAGTGAAGATATATCATTTGGGACGAGACATCAAGCACTGTATCAAAATGTCTTT 2076  
DB 6181 TCTAAGTGAAGATATATCATTTGGGACGAGACATCAAGCACTGTATCAAAATGTCTTT 6240  
QY 2077 GAAGAATTGTAACCGGTGGGATTAAGCGGCTTATCTCAAAACCAAGTCAATGAA 2136  
DB 6241 GAAGAATTGTAACCGGTGGGATTAAGCGGCTTATCTCAAAACCAAGTCAATGAA 6300  
QY 2137 ACAGTTGAAACAGAACTAGATGCTTAAGATGATCAAGCAAGAAATCTTGACCT 2196  
DB 6301 ACAGTTGAAACAGAACTAGATGCTTAAGATGATCAAGCAAGAAATCTTGACCT 6360  
QY 2197 ACAAGCTTATTCCTCTCTCACTTGGGAGCTTTCTGTTCTATGACATATTTGGAAATGG 2256  
DB 6361 ACAAGCTTATTCCTCTCTCACTTGGGAGCTTTCTGTTCTATGACATATTTGGAAATGG 6420  
QY 2257 TAGCCTCGGATCTTCTCAT----- 2278  
DB 6421 TAGCCTCGGATCTTCTCATGTAAGTCTCATCGCAAAATGAAATATTGAAAT 6480

Qy	2279	-----GGCCCTACGAAAGAAAGCTC	2300
Db	6481	CTTCGTGACATACAACTTCGTCTGTGTTTGTGTAAGGCCCTACGAAAGAAAGACTC	6540
Qy	2301	TTGATTGGAGACACAGGCTTAAGATAGATAATGTGACGACACAAGGTTTACCTTATCTAC	2360
Db	6541	TTGATTGGGACACAGGCTTAAGATAGATAATGTGACGACACAAGGTTTACCTTATCTAC	6600
Qy	2381	ACCATGACTGTATGTCCAAAGATCATTCACAGACGTGAAGTCGTCCAACATCTCTTGG	2420
Db	6601	ACCATGACTGTATGTCCAAAGATCATTCACAGACGTGAAGTCGTCCAACATCTCTTGG	6660
Qy	2421	ACAAAGACTTAGAGGCTGTTTGAACAATTTTGGAAATAGCGAAAAGCTGTGTGTCTAA	2480
Db	6661	ACAAAGACTTAGAGGCTGTTTGAACAATTTTGGAAATAGCGAAAAGCTGTGTGTCTAA	6720
Qy	2481	AGTCACATCTACTCAACTTAACGTGATGGGACAGATAGTTATATAGACCCGAGATATGCTC	2540
Db	6721	AGTCACATCTACTCAACTTAACGTGATGGGACAGATAGTTATATAGACCCGAGATATGCTC	6780
Qy	2581	GCACCTTCACGGCTCACTGAGAAATCCGATGTCTACAGTTATAGAAATAGTCTCTTGGAGT	2600
Db	6781	GCACCTTCACGGCTCACTGAGAAATCCGATGTCTACAGTTATAGAAATAGTCTCTTGGAGT	6840
Qy	2601	TGTTAAACCCGAGGAAAGCCGTTGATGACGATCCATCTCCACCATCT-----	2649
Db	6841	TGTTAAACCCGAGGAAAGCCGTTGATGACGATCCATCTCCACCATCTGGTTGTTCTT	6900
Qy	2650	-----	2649
Db	6901	TCTTGCCATCTCTCTCAGCTGCTGTGTTTAGTCAAGTCCGTAATCTGTTTCATTGA	6960
Qy	2680	-----GATTAATGTCAAGACGGGGACAAATGAAGTATGGAATGGCAATC	2686
Db	6961	TTCACTTACATCAGATTAATGTCAAGACGGGGACAAATGAAGTATGGAATGGCAATC	7020
Qy	2697	CAGACATCACATCGACGTGTAAAGATCTCGGTGTGTAAAGAAAGTTTCCAACTGGCAC	2756
Db	7021	CAGACATCACATCGACGTGTAAAGATCTCGGTGTGTAAAGAAAGTTTCCAACTGGCAC	7080
Qy	2757	TCCTATGCAACAAAAGACCGGAATGATCGAACCCACATGCAACCCAGGTGACTCGTCTC	2816
Db	7081	TCCTATGCAACAAAAGACCGGAATGATCGAACCCACATGCAACCCAGGTGACTCGTCTC	7140
Qy	2817	TCGCGCAGTTTATGCTATCGGAACAACAACCTGCTGCGACTGACACGTCACGACGCTGG	2876
Db	7141	TCGCGCAGTTTATGCTATCGGAACAACAACCTGCTGCGACTGACACGTCACGACGCTGG	7200
Qy	2877	CTGGTGTGCTGACGTGATAGATATGCAAAATCTCAAGACTCTCATCTCTGCAATTGCT	2936
Db	7201	CTGGTGTGCTGACGTGATAGATATGCAAAATCTCAAGACTCTCATCTCTGCAATTGCT	7260
Qy	2937	CTTCCATGAGTGTCTTGATGATCTCAACTGTTCTTCGGTTTGGACAAAGTTATTTCTCAGA	2996
Db	7261	CTTCCATGAGTGTCTTGATGATCTCAACTGTTCTTCGGTTTGGACAAAGTTATTTCTCAGA	7320
Qy	2997	ACAGTGAATAGTTTTTTCGTAGAGAGAGAAATCTTTAAACGGTATCTTTTGCTGCGTTA	3056
Db	7321	ACAGTGAATAGTTTTTTCGTAGAGAGAGAAATCTTTAAACGGTATCTTTTGCTGCGTTA	7380
Qy	3057	AGCTGTATGAAAAAATTAATGTCTCATGTAAAGTATATGCACTGCGCTTAATATATTAGA	3116
Db	7381	AGCTGTATGAAAAAATTAATGTCTCATGTAAAGTATATGCACTGCGCTTAATATATTAGA	7440
Qy	3117	CAAGTGTGTGTGTGATATATGTCTTCAGACTGGCACTTGAATCTCTATAAGTTCTTGCC	3176
Db	7441	CAAGTGTGTGTGTGATATATGTCTTCAGACTGGCACTTGAATCTCTATAAGTTCTTGCC	7500

DEFINITION	Arabidopsis thaliana chromosome 2 clone T1D16 map B66, complete sequence.
ACCESSION	AC004484
VERSION	AC004484.3
KEYWORDS	HTG.
SOURCE	Arabidopsis thaliana (thale cress)
ORGANISM	Arabidopsis thaliana
REFERENCE	Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eutrosids II; Brassicales; Brassicaceae; Arabidopsis.
AUTHORS	1 (bases 1 to 82212) Rounsley,S.D., Lin,X., Kerchum,K.A., Crosby,M.L., Brandon,R.C., Sykes,S.M., Kaul,S., Mason,T.M., Kerlavage,A.R., Adams,M.D., Somerville,C.R. and Venter,J.C.
JOURNAL	Unpublished
REFERENCE	1. 82212 2 (bases 1 to 82212) Lin,X.
AUTHORS	Submitted
JOURNAL	Submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
REFERENCE	3 (bases 1 to 82212) Town,C.D. and Kaul,S.
AUTHORS	Direct Submission
JOURNAL	Submitted (27-FEB-2002) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA, cdwmeig:c.org
COMMENT	On Apr 18, 2002 this sequence version replaced gi:6598423.
FEATURES	Location/Qualifiers
SOURCE	1. 82212 /organism="Arabidopsis thaliana" /mol_type="genomic DNA" /db_xref="taxon:3702" /chromosome="2" /map="B66" /clone="T1D16" /ecotype="Columbia" complement(1..5932) /note=Overlap with BAC clone T9022 (AC002505:1..5932)." 1. 2862 /gene="At2g26350" /note="synonym: T1D16.1" join(1..33132..328411..505585..774869..9381009..10871177..13101562..16562076..21522399..2862) /gene="At2g26350" join(239..328411..505585..774869..9381009..10871177..13101562..16562076..21522399..2501) /gene="At2g26350" /codon_start=1 /product="putative peroxisome assembly protein PER8" /protein_id="AA14959.1" /db_xref="GI:20197181" /translation="MKLIGMLYYVLVTGSGOOTLGEYCDIIQVAGPYGSPPARALITLQDAVPIYAERISTRATQAVTFPDSDFGSGHLSHSPMDLPSSEVSTSVSRILDRMRSMHRAIQRPVYLPRARVLDLVRANMLYFEPFYYIKSRAGVRVVFQKQDNQRPYQITGVFLITQICIIAAGLRNLSSTSSIQQASIGSYQTSGGGLPVCNIEGNLITSEAKGWSYDSYSTAVGKCTLCSTRHPIATPCGHVFCWSCIMVCKNECKECPICRPTNHTSSIVCLYHSPF" complement(3661..4993) /gene="At2g26340" /note="synonym: T1D16.2; supported by cDNA: gi_13899086_gb_AP370538_1_AF370538" complement(join<3661..4037,4109..4176,4255..4349,4439..4509,4611..4659,4786..>4993) /gene="At2g26340" complement(join(3788..4037,4109..4176,4255..4349,4439..4509,4611..4659,4786..4945)) /gene="At2g26340" /codon_start=1 /product="expressed protein" /protein_id="AA14958.1" /db_xref="GI:20197179" /translation="MSSIHATVSLPLFNSNHKKLTCAATLSPPPKQSRVSVSFLSLRLPNDAMAGLNDIKYVKKRQDPLFAYPPVLAQIQIDDEGLFLAVKPEFACRQLNSGPASSLRIVRAVAYASDGFSKTADVDVDCRLRLFELDSIFLKA

repeat_region	SRKDSNATVYLVKMSQLRALTALRDLSDLTQTPSQUIDKRGKAVEVYRSASEEDAGSDDL ESSEIKQLQSDIL"
gene	complement(6064..6110) /rpt_family="(GA)n" 6297..12070 /gene="Ac2g26330"
mRNA	/note="synonym: T1D16.3; identical to GB-U47029 and GB-D83257; contains a protein kinase domain profile (PDOC0100); contains IRR Leucine Rich Repeat domain; supported by cDNA: gi 14334873.gb AY035110.1" join(6297..6451,6798..6936,7038..7109,7214..7285, 7377..7448,7539..7610,7689..7760,7837..7908,7992, 8157..8225,8311..8382,8459..8530,8619..8690,8780.. 8820..8891,9079..9150,9277..9348,9431..9502,9589.. 9747..9818,9983..10051,10147..10218,10297..10370, 10453..10581,10666..11013,11090..11460,11545..12070) /gene="Ac2g26330"
CDS	join(6373..6451,6798..6936,7038..7109,7214..7285, 7377..7448,7539..7610,7689..7760,7837..7908,7992.. 8157..8225,8311..8382,8459..8530,8619..8690,8780.. 8820..8891,9079..9150,9277..9348,9431..9502,9589.. 9747..9818,9983..10051,10147..10218,10297..10370, 10453..10581,10666..11013,11090..11460,11545..11901) /gene="Ac2g26330"
	/codon_start=1 /product="putative receptor-1-like protein kinase, ERECTA"
	/protein_id="AAC14518.1"
	/db_xref="GI:3075386"
	/translation="MALPRDIYLGFLRCLSAVATVSEBAGTILEIKSPKDNVNL YDPTISDDYCVWRGVCSEVTFNVVALNLSDLNDEISPAIGDLKSLISLDRGNG RLSGQIPDIDGCCSLQNIIDLSEFNLSGDIPSPISKLQQLBQLIKNNQILGPIPSITL SOPINKIKIDLAQNKLSGEIPRLIYVNEVLYGLGRGNLVGNISPLDCLQTGLMYPD VYNSLSTGSIPTETIGCTAFGLVDLSYNOLTEIPEDIGFLVAVTSLIQNQLSGKIFP SVYGLMQLAAVLIDSGNLGSLIPILGNLTPEELYHNSKLTGSIPEELGNLSKILH YLEANDNHITGHPPELGLTDLFDLANANDBEPIPDHSSCTNLNSLVHNSKTS GITPRAPFQLESSTYLNSSNNIKGPIPELSRINCLDNLDSNKNIGIIPSLGSDI EHLKNLISRNHITGVVPDGFGNLRISMEIDLSNNDISGPIPEELNQILNILLRLEN NMINTGVVSLANCLSTVLVANSNNLVGDIPIKNNFSRSPDSFIGNGLCGSWLNRP CHDSRTVAVSISRAILIGIAGVILMLVAILACRPNHPFLDGLDKPVTYSFSP KLIYLMNNALHYVEDIMKMTNLESEKYLIGGASSTYKCVLKNCKRVAIKRLYSKHK POSMQRFETLEMSISIKRNVISLQNSISHLGSLPYVDLEMSLQVATLHGTFRKK TLDMDRLKIAFGAAGLAVYLDHSDSPRIHNDVSNVYLDKDLKALTDIFGAKSL CVSKSTGTSYVNGTIGYIDPEYATSRSLTEKSDVYSYGIVLLELTRKAVDANSNLH HILMSGTGNNVEWEMADPDITESTKCDLGAVKCFQALALCTKRGPNRPFMHQVTRVY GESFMLEQPPAATDTSATLACGYDEVANLKTSPHNSVCSMSASDAQLFRLFQGVIS QNSE"
misc_feature	7205..7710 /gene="Ac2g26330"
repeat_region	/note="molecular marker er" complement(12313..12357) /rpt_family="AT_rich" 12862..12895
repeat_region	/rpt_family="AT_rich" complement(13276..13296) /rpt_family="(TAAAAA)n" complement(13645..13665) /rpt_family="AT_rich" complement(13681..13708)
repeat_region	/rpt_family="AT_rich" 13981..14879 /gene="Ac2g26330"
gene	/note="synonym: T1D16.4" join(<13981..14213,14783..>14879) /gene="Ac2g26330"
mRNA	join(13981..14213,14783..14879) /gene="Ac2g26330"
CDS	/codon_start=1 /product="MADS-box protein (AGL33)" /protein_id="AAC14519.1" /db_xref="GI:3075387"
	/translation="MRTIKNNKQKIVENNGRKKLKLKRIEKLKRSKFSKRRKGL PKAAEVALLCSDIMLIVVSPTEKPTVNTSRSFHTILRFQMLSLQREEBECDSL VFIIIT"

repeat_region	complement (14242, .14263) /rpt_family="AT_rich"	
repeat_region	complement (14300, .14321) /rpt_family="AT_rich"	
repeat_region	complement (15117, .15151) /rpt_family="AT_rich"	
repeat_region	15228, .15248 /rpt_family="AT_rich"	
repeat_region	complement (15506, .15528) /rpt_family="AT_rich"	
repeat_region	complement (15865, .15941) /rpt_family="AT_rich"	
repeat_region	complement (16091, .16121) /rpt_family="AT_rich"	
gene	complement (16528, .17826) /rpt_family="AT_rich" /gene="AT2926310" /note="synonym: T1D16.5; predicted by genScan and gtrial"	
mRNA	complement (join<16528, .16577,16654, .16705,16956, .16992, 17194, .17266,17397, .17473,17788, .>17826)	
CDS	/gene="AT2926310" complement (join<16528, .16577,16654, .16705,16956, .16992, 17194, .17266,17397, .17473,17788, .17826)	
	/codon_start=1 /product="hypothetical protein"	
	/protein_id="AAC14521.1"	
	/db_xref="GI:3075389"	
	/translation="MLKENASRSNSEKGRKYASVPASKDKCDLYKLLREDIYM SVLVVNYNGDKNTNYRDVPEKSLRRLRYKGIIDPRRDEQQLTEIGCNIGAVRS KDLCS"	
misc_feature	15166, .23272 /note="molecular marker GPAL"	
gene	complement (19279, .22971) /gene="AT2926300"	
mRNA	/note="synonym: T1D16.6; identical to GB_M32887; supported by cDNA: gi_14326501.gb_AF385704.1.AF385704, .19926, 20018, .20111,20194, .20328,20704, .20759,21001, .21102, 21185, .21292,21395, .21472,21648, .21737,21828, .21865, 21961, .22033,22122, .22310,22800, .22971)	
CDS	/gene="AT2926300" complement (join<19446, .19623,19701, .19780,19867, .19926, 20018, .20111,20194, .20328,20704, .20759,21001, .21102, 21185, .21292,21395, .21472,21648, .21737,21828, .21865, 21961, .22033,22122, .22181)	
	/gene="AT2926300"	
	/codon_start=1 /product="G protein alpha subunit 1 (GPAL)"	
	/protein_id="AAC14520.1"	
	/db_xref="GI:3075388"	
	/translation="MGLCSRSRHHTEDENTQAAEIERIEGPAKAEKIRKLLL GAESKSTFIPOIKLLPOTGDEGLSKYVIVHANYOTIKLHDGKEPANEETD SAKYMSSEISAIIGELKSTIGRLDIPRLTKDIAIEGILMDPAIOETCARGNELQV	
Query Match	34.7%; Score 1102; DB 4; Length 82212;	
Best Local Similarity	84.9%; Pred. No. 0;	
Matches 1376; Conservative	0; Mismatches 0; Indels 244; Gaps 3;	
OY	1801 AGTGTCAATCTTCAAGACAGACTTTCTTGGAAATAGTATTGGGGACCTGTGATCTTCT	1860
Db	10451 AGTGTCAATCTTCAAGACAGACTTTCTTGGAAATAGTATTGGGGGACCTGTGATCTTCT	10510
OY	1861 CATGGCTTAAATAGCAGCTTGGCGACGGATATCTCTCCCTTTCTTGATGAGTACT	1920
Db	10511 CATGGCTTAAATAGCAGCTTGGCGACGGATATCTCTCTTCTTGATGAGTACT	10570
OY	1921 TGACCAAC-----	1928
Db	10571 TGACCAACGAGCTACTCTCCAAACACCTTTAAGCATGTCTTCACTCAACATGTAAATC	10630
OY	1929 -----CAGTACTTAATTGACACCGAAGCTCGT	1956
Db	10631 CAATAGTTAATCTTAAATTTCTGTGTGACATCAGTAACTTAATTGACACCGAAGCTCGT	10690



QY	465	CATACCGTTTTCCGATTTTCGAAGTTGAAGCACTTGACAGAGCTGATCTCGAAGATTAACCA	528
Db	387	GATCCCTCGATGAGATTGGCCGATTTGTTCATCACTCTAAAACTCTGATATTGAAGAACCAACA	446
QY	529	ATTGATAGSAGCCGATCCCTTCAACACTTTTCACAGATTTCCAAACCTGAAAAATTCTGACACTT	588
Db	447	ACTGATCGGAGTGTATCCCATTCAGGCTCTCACACTCCCAAAATTGGAAGATTTTGGACCTT	506
QY	589	GGCACAAGATTAACCTCAGTGTGTGAGATACCAAGACTTAATTTACTGGAATGAGATTCTTCA	648
Db	507	GGCACAAGAACCAACTGAGTGGAGAGATPCCAAAGCTGATATATTGGAACGAGGTTCTTCA	566
QY	649	GTACTCTGGGTTGGAGAGAAACAATTAGTGTGATACATTTTCTCAGATTTGTGTCAACT	708
Db	567	ATACCTGGGATTACGGCGGTAAATTAATGAAGGACGACATCTCCCAAGATATATGCCAGTT	626
QY	709	GACTGCTTTTGGTATTTTGAAGTAAAGAACACAGATTGACTGTGATATACCTGAGAC	768
Db	627	GACTGGGCTTTGGTA-----	641
QY	769	GATAGAAATTCACCTGCTTCCAGGTTTGGACTTGTCTCAATCAGCTAACCTGTGTA	828
Db	642	-----CTTGATTTTGTCTTAACAATTAACCTTGTGATC	674
QY	829	GATCCCTTTTGAACATCGGCTCTCGGAAAGTTGGCAACATTATCATTTGCAAGGCATCAACT	888
Db	675	AATTCCTTCAACATTTGGTTCTTCAAGATGTCTACACTATCTTTGCAAGGAAACATGTT	734
QY	889	CTCTGGGAAGATTCATCAGTGAATTGGTCTCATGCCAAGCCCTTCAGCTTATGATCTTAG	948
Db	735	TACTGTGCTATTCATCAGTTATTTGACCTTATCAGGCTCTGCTGTACTGATCTGAG	794
QY	949	TGGCAACTTTGAGTGTGATTTATTTCTCCGATTTCTGGAATCTTACTTTACCGGAA	1008
Db	795	TTACAACCAATTTGTCTGGTCTTATTCATCGATCTAGGCAATTTTAACTATCACTGAGAA	854
QY	1009	ATTGTATTGGACAGTAAACAGCTGACCTGGTTCAATTCACCTGAGCTGGAAACATGTC	1068
Db	855	GCTGTATATGGAAGGCAATTAAGTTTAAACAGGTCCAATACACACTTACGCTTGGAAATATGTC	914
QY	1069	AAAATCCATTAACCTGGAACCTCAATGATATATCATCTCCGGGTGATATACGACAGAGCT	1128
Db	915	AACTCTTATTAATCTTAAGACTTAACGATATATCAACTTAGCGGTTCAATCTCCAGAGTT	974
QY	1129	TGGAAAGCTTACTGAATTGTTTGAATCTGAATGTGGCCAACAATGATCTGAGAGACTTAT	1188
Db	975	CGGAAGCTTAACAGGTTATTTGACTTAAACCTTGCAAAACAACCTTGAAGGCTCAAT	1034
QY	1189	ACCTGATATCTGAGCTCTTGCACAAATCTTAAACAGCTTAAATGTATCAGTGGACAGATT	1248
Db	1035	CCCTGATTAACAATAGCTCATGTGTGAATCTCAATATGCTTAATCTTAATGGCAACAGATT	1094
QY	1249	TAGTGGCACTATACCCCGAGACTTTCAAAAGCTAGAAAGTATGACTTAACCTTAATCTGTC	1308
Db	1095	AAATGGGACATTTCTCTCTCATTTGSCAATACTTAGAGCATGACTTAATTTGAATTTGTC	1154
QY	1309	CAGCAACAATATCAAAAGTCCAAATCCGGTTGAGCTATCTGTATCCGTTAACTTAGATAC	1368
Db	1155	ATCAAAATTTTCTAAGTGTGTCTAATTTCCATTTGAGGCTATCGAATATCAAAATTTGACAC	1214
QY	1369	ATTGAGATTTTCCAACAACAGATTAATGGAATCATTTCTTCCCTTGGTATTTGGA	1428
Db	1215	CTTT-----	1218
QY	1429	GCATCTTCTCAAGATGAACTTGAGTAGAATCATATATACGTGTAGTTCCAGGCGACTT	1488
Db	1219	-----AACTTAGGAACAATGGTCTAGTAGATTCAATCTCTGCAGAAAT	1262
QY	1489	TGGAATCTTAAGAACCATGAGAAATGATCTTTCAATATATGATATCTTGGCCCAAT	1548
Db	1263	TGGCAACTTGGAGGATATCATGAGATTTGATATGTCCAACAATCATCTTGGCGGTTTGTAT	1322

QY	1549	TTCCAGNAGAGCTTAAACCAATTTCACAAACATATTTTGTGAGCATCGGAAAAATATAACT	1608
Dp	1323	TCTTCAGAACTCGGAGATCGCAAAAATCTGATGTTGTTAAATCTCAAAAACAACACAT	1382
QY	1609	GACTGGTAATGTTGGTTCATTAGCCAACTGTCTCAGTCTCATCTGATTTGAATGATCTCA	1668
Dp	1383	AACTGGGGAGATGTCTTTCACGTAGAACGTGCTTACGCTCAATATCTTAAATGATCTTA	1442
QY	1669	TAAACAACCTGTAAGTGATATATCCCTTAAGAACATTAATCTTCMAAGATTTTTCACAGACAG	1728
Dp	1443	TAAATAATTTGGCTGGGTGTGACCTACATGATTAACAACTTTCACGCGTTTTCGCTGCAG	1502
QY	1729	CTTCATTTGGCAATCCGTGCTTTTGGCGATAGTGGCTAAACTCACCGTGTCAATGATTCG	1788
Dp	1503	CTTTTTCGGTAATCCAGACATTTGTGGAATATGGCTTGCGTTCTTGTGTCCGTTCAATCGG	1562
QY	1789	TCGAACGTACGAGTGTCAATCTTAAGACAGCTATTTCTTGAAATAGCTATTTGGGGACT	1848
Dp	1563	CCATCAACAGAAAACCAATATCTCAAAAGCTGCATACTTGGAATTCGCGTGGGTGGCT	1622
QY	1849	TGATATCCCTTCATAGGTCTTAATAGCAGCTTGCCGACCGGATATCCCTCCCTTTCT	1908
Dp	1623	TGTAATCTCTCGATGATCTTAAGTACCGGTCTGCAGGCTCTAATGTCCACTCTTTTCAA	1682
QY	1909	TGATGATCACTTGACMAACAGTAATCTATTCGACACCGAAGCTCGTCACTCTTCATAT	1968
Dp	1683	AGATGTCTCTGTAGCAAAACAGTAGACATGTTCCCCCAAGCTGGTTATCTTTCATAT	1742
QY	1969	GAACATGCACTCCACGTTTACGAAGATATCATAGAAATGACACAGAACTTAACATGAGAA	2028
Dp	1743	GAACCTTTCCTTCTGTATACGAGATTAATATGACATGACTGAATAACCTGAATGAGAA	1802
QY	2029	GTAATATCATTTGGGACAGGACATCAAGCACTGTATACAAATGTGTTTGAAGATTTGAA	2088
Dp	1803	GTAATATCATTTGGGTACGAGACATCCAGACCGTTTATTAATGTGTTTGAAGAACCGAA	1862
QY	2089	ACCGGTTCGATTAAGCGGCTTTACTCTCAACCCACAGTCAATGAACAGTTTGAAC	2148
Dp	1863	ACAGATGCGAGTAAAAAAACCTATATAGCCCACTATCAACAGAGCTTCAAGGAATTTGAAAC	1922
QY	2149	AGAACTCGAGATGCTAAGATGATCAAGACAGAAATCTTGAGCCTAACAAGCTTATTC	2208
Dp	1923	TGAGCTTGAACACTGTGTGATCATACACCGGAATCTAGTCACTTTCAGAGATATTC	1982
QY	2209	CCTCTCTCATTTGGGAGATCTTCTGTCTATGACTATTTGGAAAATGCTAGCCCTTGGGA	2268
Dp	1983	CTATCTCCGTGTGAAATCTTCTCTTACGATTAACATGAAAAATGGAACCTCTGGGA	2042
QY	2269	TCTTCTTCAT--GGCCCTACGAAGAAAAAGACTTTGATTTGGGACACACGGCTTAAGAT	2325
Dp	2043	TGTTTTCGATGAAGGTCTCAACTPAAGAAAGAAAACTTATTTGGGAAATCTGTACGAAT	2102
QY	2326	AGCATATGTCGACGACAAAGTTTAGCTTATCTACACATGACTGTAGTCCMAAGATCAT	2385
Dp	2103	TGCTCTAAGGTGGCGCCAAAGGCTTGCTTATCTTATCATAGCTGTAGCCACGAGATAT	2162
QY	2386	TCACAGAGACGTGAAGTGGTCCACATTTCTTTGGACAAAGACTTAAGAGGCTCGTTGAC	2445
Dp	2163	ACAACAGGATGTGAATAATCAAAAAATATATCTCTTGATTAAGATTAATGAGGACATCTTAC	2222
QY	2446	AGATTTTGAATAGCAAAAAGCTGTGTGTCGAAGTCAATCACTTCAATTCAGTAT	2505
Dp	2223	AGACTTTTGGCATGTCTAAGAGTTTGTGTGTTTCAAAAACTCAACGTCCACTATGTCTAT	2282
QY	2506	GGGACGATAGGTTACATAGACCCGAGTATGCTGCACCTTCAAGGCTCACTGAGAAATC	2565
Dp	2283	GGGAACATATGGCTATATGATCTGAGATATCTCGCACCTCCGCTCAATGAAAAATC	2342
QY	2566	CGATGTCTACAGTTATAGAAATAGTCTTCTTGAAGTTTAAACCGGAAGGAAGCGGTGGA	2625
Dp	2343	TGATGTCTAACGTATAGGGAATTTGTCTGTAGCTGTGACCGGAAAAAAGCCAGTGGGA	2402
QY	2626	TGACGAATCCAATCTCCACATCTGATATGTCAAAGAAGGGGAAACATATGAATGATGGA	2685



Db	Accession	Source	Gene	CDS
Db	2403	CACGAGTGCATCTTCATCACTTGATCTTGTCAAAAGACGGCTAAACAATGCTGTCATGGA		
Oy	2686	AATGCGACATCCAGACATCAATCAGCCTGTAAAGATCTCGGTGGTGGAAGAAAGTTT		
Db	2463	GACAGTGCACCCCGACATTCGACAGACACTTGCAGAGATCTTGGTAGAGTCAAGAAAGTGT		
Oy	2746	CCAACTGCGACTCTTATGCACCCAAAAGAAGCCGATGATGCACCCACATGCACAGGT		
Db	2523	CCAGCTGGCGCTCTTGTGACCAAGAGACAACCATCGGATCGGCCGACATATGCAGAGGT		
Oy	2806	GACTCGTGTCTTCGGCAGTTTATGCTATCGGAACAACCACTGCTGC-----GAC		
Db	2583	TGTGGCGCTCTTGACATCCCTAGTTCGTCGCCGACCCGACACGAAGTCCGACAGCACT		
Oy	2857	TGACACGTGCACGACGCTGGCTGGTTCGTGCTACGTGATGATGATGCAATTCACAGAC		
Db	2643	GGCATTGCCGACGAGCGGCTGCTGTCGCCAGTCAATCAACAGATATGCACCTTAAGAG		
Oy	2917	TCCCTCATTTCTGTCAATTCCTC---TTCCATGAGTCTTCTGATGCTCACTGTTCTTCG		
Db	2703	CACCAAGCGTCTCTTCCTCGCCCAACGTGTCGTACTTCGATGCTGAGCTGTTCTCAA		
Oy	2974	GTTTGACACATGTTATTTCTGCAACACGTAGTAG 3007		
Db	2763	GTTTGGCAGGTCAATTTCTCAGAACACAGAGTAG 2796		
RESULT_13	AY332474			
LOCUS	AY332474			
DEFINITION	Oryza sativa (japonica cultivar-group) transmembrane protein kinase			
ACCESSION	AY332474			
VERSION	AY332474			
KEYWORDS	PK3			
SOURCE	Oryza sativa (japonica cultivar-group)			
ORGANISM	Oryza sativa (japonica cultivar-group)			
REFERENCE	1 (bases 1 to 3184)			
AUTHORS	Yao, Q., Peng, R. and Xiong, A.			
JOURNAL	Isolation of a transmembrane protein kinase from rice			
REFERENCE	2 (bases 1 to 3184)			
AUTHORS	Yao, Q., Peng, R. and Xiong, A.			
JOURNAL	Direct Submission			
REFERENCE	Submitted (30-JUN-2003) Bio-Tech Center, Shanghai Academy of			
AUTHORS	Agricultural Science, Beid Road 2901, Shanghai 021-201106, China			
JOURNAL	Location/Qualifiers			
FEATURES	1..3184			
SOURCE	/organism="Oryza sativa (japonica cultivar-group)"			
	/mol_type="mRNA"			
	/db_xref="taxon:39947"			
	1..3184			
	/gene="PK3"			
	57..3056			
	/gene="PK3"			
	/note="protein kinase; PK3"			
	/codon_start=1			
	/product="transmembrane protein kinase"			
	/protein_id="AA001160.1"			
	/db_xref="GI:33242913"			
	/translation="MAAARAPLWMVVVVVAVVAEASGGGGGGDGGSKALMGVKA			
	GFPGAAALVDMWDGADHCAMRWGTCNFAFAVALALNSLNLGGLSPALIKLKLQ			
	FVLDIKSKLTGQIPLDEIGDCISLKYIDLSGLILVGLIPFISIKQLEBILKNNOLT			
	GPISITSOIPLNLITLDAQNLQGLDIPRLIYMWVQVGLKRNLSLTGLSPDMCO			
	TGLVYFVGRNLNGTIPESIGNSITPEIILDISYNOISGIPVNIQGLVATISLGN			
	RLTKITPDVIGLMQALVALVLDSENEIVGIPSLIGNISYTGKYLHKNKLTGYIP			
	GNMSKLSYQLQNDRELVTGTPAELGKLEBPELILANNILQGLPANISSCTALNKN			
	VYGNKGLNGSLPAGFQKLESILYVNLSSNFKNGIPSELGHIINDLTLDLSYNFSGV			
	PATIGDHEHLELNLSTKNHLDGVPAPFGNLRVQVLDMSNNNLGSLPEELQQLNL			

Query Match	32.6%	Score 1035.2	DB 4	Length 3184
Best Local Similarity	63.8%	Pred. No. 0		
Matches 1687	Conservative 0	Mismatches 888	Indels 69	Gaps 5
234	CGGATTTATTTGTCGTGGAGAGGTGTGTCCTTGTAATAATGACCTTCATGTTGTGTC	293		
235	CCGACCACTGGCGGTGGCGGGCGCTCACTCGCAACAAGCCTCTTGTGGCGCTCGCC	294		
294	TTAATTTGTCAGATTTGATCTTATGAGAAATCTCACCTGCTATGAGATCTCAGA	353		
295	TGAATCTGTCAAATCTAAACCTAGAGAGTGAATCTCGCGGCATCGAGAGCTCAGA	354		
354	GTCTCTTGTCATTTGATCTGGAGATATCGCTTGTCTGCACAAAATCCCTGATGATGG	413		
355	ATCTACAGTTGCTGATCTCAAGGGGAAACAAGCTCACTGGCCAAATCCCAAGATGAGATTG	414		
414	GTGACTGTCTCTTTTGCAAAAATCTAACCTATTCCTCAATGAAATTAAGTGGACATAC	473		
415	GGGACTGCATCTCTTAAATATTTGGATTGTCTGGCAACTTGCTGTATGGAGACATCC	474		
474	CGTTTGCATTTTCAAGTGAAGCACTTGAGCAGCTGATTTGAGAAATACCAATTTGA	533		
475	CTTCTCTCATCTCAACTCAAGAGCTTGAAGAGCTGATTTTGAAGAAACAACGACTCA	534		
534	TAGGACCGATCTCCTTCAACACTTTGACAGATTCGAAACCTGAAATTTCTGACTTGGCAC	593		
535	CGGACCCATTCCTCTTCAATTTGTCACAAATTCGAAATTCAGACACTTGAACCTGGCAC	594		
594	AGATTAATCTCAGTGTGAGATATCCAAAGACTTTTATCTGGAATGAAATTTCTTCAGATATC	653		
595	AGAACCGAGCTTACAGGGGAATATCCCAAGGCTCATATCTGGAATGAAATTTCTCAATATCC	654		
654	TTGGCTTGCAGAGGAAACAATTTAGTGGTAAACATTTCTCAGATTTGTGTCAACTGACTG	713		
655	TAGCTTTGAGGGGTAACTCACTGACTGAACTTTGTACCTGACATGTGCAACTGACTG	714		
714	GTCTTTGGTATTTTGAAGTAAGAAACAACGATTGACTGTGATATATACCTGAGACGATAG	773		
715	GCCTGTGTACTTTGATGATGAAGGGAACAATCTCAACAGGACCATTTCCAGAGACGATAG	774		
774	GAAATTCAGCTGCCCTTCAGGTTTGGACTTGTCTCAATCACTACGTAAGTGTGAGATCC	833		
775	GGAAGTCAACAGGCTTTGAGATTTCTGGAACATTTCTGATATACCAAACTCTGTGGAAATAC	894		
834	CTTTTGACATCGGCTTCCTGCAAGTTGCAACATTTATCTGCAAGGAATCAACTCTCTG	893		
835	CTTACACATAGGCTTTCTTCAAGTATGACCACTGTCACTTCAAGGAATTAAGTCACTG	894		
894	GGAAGATTCATCAGTATGATGTCTCATGCAAGCCCTTGCAGCTTTAGATCTTAAGTGGCA	953		
895	GGAATATTCAGATGTGATTTGGCTGTATGCAACCTGTGCTGTCTTACAGCTGAGTGA	954		
954	ACTTGTGAGTGAATCTATTTCTCCGATTTCTGGAAATCTTACTTTTCCAGGAAATTTGT	1013		
955	ACGAGCTGTAGGGGCCATTTCTTCAATCTGAGCAATCTATCTTACTGGAATAATCTAT	1014		
1014	ATTGACACAGTAAACAAGCTGACTGTTCAATTCACATGAGCTTGGAAACATGTCAAAAC	1073		
1015	ATTTACATGGGAACAACTTACTGAGTCAATACCGCGGAGCTTGGGAACATGATGAAC	1074		
1074	TTCATTACTGGAATCAATGATATATCTCAACGGGTCAATATACCAACAGACTTGGGA	1133		

1075 TTAGTACTACCACTGAAATGATATGAAATTTGGTGGCAGCAATTCAGCAGAGCTTGGA 1134  
1134 AGCTTACTGACTTGTGATCTGAAATGGGCAACATGATGAGAGGACTTATCTG 1193  
1135 AACTGGAAGACTTTTGAACATATCTGCAACAAACATCTTCAAGGCTATCTCG 1194  
1194 ATCATCTGAGCTTTGCAACATCTAAACAGCTTAAATGTTCAATGAGGAAACAGTTTATG 1253  
1195 CAACATCACTTCTGCACTGCTTAAACAATTCATATGTTTATGGCAATAGCTAATG 1254  
1254 GCACATTAACCCGAGCAATTCAAAAGCTAGAAATGATGACTTACTTATCTGTCAGCA 1313  
1255 GTTCTATCTCTGCTGCTTCCAGAAAGTTGAGAGCTGACTTACTTGAACCTATCTTCAA 1314  
1314 ACAATATCAAGGCAATCCCGGTGAGCTATCTCGATCGTAACTGATGATCATTTGG 1373  
1315 ACAATTTCAAGGCAATTTCTTCTGAGCTTGATGATCATATGATGAGCAATTTGG 1374  
1374 ATCTTTCCAAACACAGATTAATGAAATCAATTCCTTCTTCCCTTGGTATTTGGAGCATC 1433  
1375 ATCTTTCTCAATGAAATCTCTGAGCAAGTTCTGCTACCATTTGGTATCTAGAGCAC 1434  
1434 TTCTCAAGATGAATCTGATGAAATATATATATCTGATGATTCAGAGGCACTTTGAA 1493  
1435 TTCTTGAAGTGAATTTGATGAAAGCAATCTTGAATGGGCCAGTTCTGCTGAGTTTGA 1494  
1494 ATCTAAGAGATGATGAAATATGATCTTCAATTAATGATCTGAGGCCAATTCAG 1553  
1495 ACTTGAAGAGGCTCAAGATATGATATGTCACAAACAACTTATCTGATGATCTGCGC 1554  
1554 AAGAGCTTAAACCAATTAACAGAACTAAATTTTGTGAGAGCTGAGAAATATATCTGCTG 1613  
1555 AGGAACTTTGAGCAATCTTCAAAACCTTGAATGCTGATTTCTTAACAACAATTTGGT 1614  
1614 GTAATGT--TGTCTATTAAGCACTGCTCACTGCTCA-----CTGATTTGAAT 1660  
1615 GGGAGATCCCTGCTCAATGGCCCACTGCTTCACTTAAATATACCTTGAATTCAGAAAT 1674  
1661 GATCTCATATCAACATCTGATGATGATATCCCTAAGAAACAAATTAATCTTCAAGATTTTCA 1720  
1675 TTGCTATCAACAATTTATCTGAGATGCTCCGATGGCAAGAACTTCTGAAATTTCCCA 1734  
1721 CCAGA-----CAGCTTCA 1733  
1735 ATGGAAGGCAATCTTCTAATTTCTGATGCAACAGTACATTAATCATTAATGCAAGCTTCT 1794  
1734 TTGGCAATCTGCTGCTTTGGCGTATGGCTAACTCACTGCTGATGATTTCTGCGAA 1793  
1795 TTGGTAAATCCATTAATCTGATGCTGCTCCAAAGATTCACAGCTGCGACACTCTCATGGA- 1853  
1794 CTGTAAGAGTCAATCTCTAAGAGCACTTCTTGAATGATGATGAGGGAATTTGGA 1853  
1854 --CAAGAGTTAATATTTCAAGAGCAAGATGCTTGCATTAATCTTGAAGCTTATAT 1911  
1854 TCCCTTCTCATGCTTATATAGCACTTGGCCAGCGCAATCTCTCTTCTTCTGATG 1913  
1912 TGCTCTGCGTTCTGCTGTTGCTATATATAAACAATCAACAGCACTGCTTCAAG 1971  
1914 GATCATCTTGAACAACAGTAACTTATTCGACACCGAAGCTGCTCATCTTCAATGACA 1973  
1972 GATCCGATTAAGCCAGTCAAGGAC-----CTCCAAAGCTATGTTCTCCAGATGAGCA 2025  
1974 TTGGACCTCCAGCTTATGAGAGATTCATGAAATGACAGAAATCTAAGTGAAGATTA 2033  
2026 TTGGTATTCATCTTACGAGGACATCATGAGGCTGACAGAAATTTTGGCAGAAATACA 2085  
2034 TCATTGGGCAACGAGATCAAGCACTGTATCAATGTTTGAAGATTTGTAACCGG 2093  
2086 TCATTGGCTAATGGGCTCAAGCACTGTCTAACAATGTAACCTAAGAGCGGCAAGGCA 2145  
2094 TTGGGATTAAGCGGCTTACTCTCAACAACCAAGTCAATGAACAGTTTGAACAGAAC 2153  
2146 TTGCTGTCAAGCGGCTTTACAGTCAATTAACATTAAGCTCCGAGAGTTTGAACAGAAC 2205

2154 TCGAGATGCTAAGTACATCAAGCAAGAAATCTTGTGAGCCTACAGAGCTTATTCCTCT 2213  
2206 TAGAGCAATTTGGCAGCATATCGGCACAGAAATCTTGTAGSCTCCATAGGCTTCTCGTAT 2265  
2214 CTCACTTGGGAGTCTTCTGTTCTATGATCTATTTGAAAAATGTTAGCTCTGGATCTTC 2273  
2266 CTCACATGGAATCTGCTCTTCTATGATATGAGAAATGTTCTTGTGGGATCTTC 2325  
2274 TTGATGGCCCTAGAGAAAGAAAGACTTGTATGTTGGGACACAGGCTTAAGATGATGAT 2333  
2334 GTGAGACAGAGGTTTATGTTATCTACACCATGACTGATAGTCCAGAGATCATTCAGAG 2393  
2386 GAGCTGCAAGAGGCTGCGCTATATCTCCACATATAGTCAACCTCGATATATCCAGAG 2445  
2394 ACGTGAATGCTCCAAATCTCTTGGACAAAGACTTGAAGGCTCGTTGACAGATTTTG 2453  
2446 ATGTCAGTCTCCAAATCTCTGCTGACGAGAACTTCGAAGGCGCACCTCTCAGATTTG 2505  
2454 GAATAGGAAAGCTTGTGTGTGTCAAAAGTCAATCTTCACTTACGTGATGGGACGA 2513  
2506 GCAATAGCAATATGCTCCCTCTGCAAGTCCCATGCTCACTTATGCTGAGAAACA 2565  
2514 TAGATTACATAGACCCGAGATGCTGCACTTCAAGGCTCACTGAGAAATCCGATGCT 2573  
2566 TCGCTATCATTTGATCCGAGATATGCAAGACTTCCAGGCTCAATGAGAAATCTGATGT 2625  
2574 ACAATTAAGAAATGCTCTTCTTGAATTTTAAACCGAAGAAAGCCGTTGATGAGCAAT 2633  
2626 ACAGCTTCCGACATGCTCTTCTGAAATTTGCTCAAGGAAAGAGCCGCTGCAACAAGAT 2685  
2634 CCAATCTCCACATGATATATGTCAAAGAGGAGAAACAATGATGAGAAATGAGCAG 2693  
2686 CGAATCTGCAATTAATTAATCTTCCAAAGCTATGCAACAGATCATGAGAGCAGTGG 2745  
2694 ATCCAGACATCATGAGCTGATTAAGATCTCGGTGCTGTAAGAAATTTTCCAACTGG 2753  
2746 ACTGAGAGTGTAGTACGATGACGACGAGCAATGAGACTGTCAAGAAAGCCCTTCAAGT 2805  
2754 CACTCTATGACCCAAAGACAGCCGATGATGAGCCCAATGACACAGTGAATCTGCT 2813  
2806 CCTTCTGTGACCAAGAGGACCTTTCAGACCGGCGCACCATGACAGAGTTGCAAGG 2865  
2814 TTCT 2817  
2866 TGCT 2869

RESULT 14  
AX654770 2895 bp DNA linear PAT 22-MAR-2003  
DEFINITION Sequence 4640 from Patent W003000898.  
ACCESSION AX654770  
VERSION AX654770.1 GI:29157584  
KEYWORDS

ORGANISM  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP  
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
1 Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M.,  
Katzagiri, F., Quan, S., Tao, Y., Whitam, S., Xie, Z., Zhu, T. and Zou, G.  
Plant genes involved in defense against pathogens  
Patent: WO 03000898-A 4640 03-JAN-2003;  
Syngenta Participations AG (CH)  
Location/Qualifiers

FEATURES  
source  
1..2895  
/organism="Oryza sativa"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:4530"



QY 2489 ACTTCACTTACGTGATGGGACGATAGTTACATAGACCCCGAGTATGCTCGCACTTCA 2548  
| | | | |  
Db 2368 GCCTCCACTTATGTCAGAGAACATCGGCTACATTTGATCCGGAGTATGCGAGGACTTCC 2427  
| | | | |  
QY 2549 CGGCTCACTGAGAAATCCGATGTTCTACAGTTATGGAATAGTCTTCTTGAATTCTTAAC 2608  
| | | | |  
Db 2428 AGGCTCATATGAGAAATCTGATGTGTACAGCTTCGGCATCTGCTTCTGGAATTCCTACA 2487  
| | | | |  
QY 2609 CGAAGGAAGCCGTTGATGAGCAATCTCCACCATCTGATATATGTCAGAAACGGGG 2668  
| | | | |  
Db 2488 GGGAGAGAGGCGCTGCAAGAGAAATCGAATCTTGATCATATGATTAATCTCCAAAGCTGAT 2547  
| | | | |  
QY 2669 AACATGATGATGAGAAATGCGATCGACATCAATCGACGCTGTAAGATCTCGCT 2728  
| | | | |  
Db 2548 GACAAACAGTCATGAGAGGCGAGTGGAGCTCGAGGTGTACGTGACGTGACGGAATGAGGA 2607  
| | | | |  
QY 2729 GTGCTGAAGAAAGTTTCCACTGCGACTCTTATGACCAAAAGACGCGGAATGATGCA 2788  
| | | | |  
Db 2608 CTGCTCAGGAAGGCGCTTCAGCTCGCCCTTCTGTGACCAAGAGGCAACCTTCAGACGG 2667  
| | | | |  
QY 2789 CCCACATGACCGAGTGTCTGTTCT 2817  
| | | | |  
Db 2668 CCGACATGACGAGGTTGCAAGGCTCT 2696  
| | | | |

RESULT 15  
AY182166 2450 bp mRNA linear PLN 30-JAN-2003  
LOCUS Elaeis guineensis clone Rik-OPmf receptor-like protein kinase mRNA,  
DEFINITION partial cds.  
ACCESSION AY182166  
VERSION AY182166.1 GI:28140042  
KEYWORDS

SOURCE Elaeis guineensis (African oil palm)

ORGANISM Elaeis guineensis  
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Arecales; Arecaceae; Arecoidae;  
Coccolae; Elaeidinae; Elaeis.

REFERENCE 1 (bases 1 to 2450)  
See, P.T., Harikrishna, K., Ho, C.L. and Ong Abdullah, M.  
An examination of gene expression in somatic embryogenesis of oil  
palm (Elaeis guineensis)

JOURNAL Unpublished  
AUTHORS 2 (bases 1 to 2450)  
REFERENCE See, P.T., Harikrishna, K., Ho, C.L. and Ong Abdullah, M.  
AUTHORS Direct Submission  
TITLE Submitted (18-NOV-2002) Biotechnology, University Putra Malaysia,  
JOURNAL Serdang, Selangor 43400, Malaysia  
LOCATION/Qualifiers

FEATURES  
source  
1. 2450  
/organism="Elaeis guineensis"  
/mol\_type="mRNA"  
/db\_xref="taxon:51953"  
/clone="Rik-OPmf"  
<1. 2160  
/codon\_start=1  
/product="receptor-like protein kinase"  
/protein\_id="AA026312.1"  
/db\_xref="GI:28140042"  
/translation="EIPNIGFLOVATLSLOGNRLTGKIPVIGLMOALAVLDSENE  
LVGTIPILNLSTYKLYLHGNKLTGP1PELGNMTKLSTLQNDKLVLT1PAELG  
KLBELEFNLANNLBEPIPONTSLCTALNLFVNGHNLNGSLPLQKLESLTYLNF  
SSNFKGVNPELRI INLDTLDSNNHSGP1DPSIGDLEHLLEMLNNLNGPLP  
TERENLNSGOTIDSYNKLSGP1PELIGOVOTIDTLINNDLVLGELPVOLNCFSLP  
SLNLSFNNFSGDVLSPKFSRFPESFLGNMCGMLGSSCCGDLHGSKYITISRAV  
VCTLGCITLSSMLVAIYKSSOPKFTKSNRTVQPPKLVLRMDMAIHTEDIR  
ITEMLSERYIIIGVASSTVYKCVLKNKPLAIKRLYQYPNLHEFELETTGSIH  
RNLVSLHGYSLSPHGNLIFYDMENGLLMDLHGPSKRVKLVDMTRKILVGAAGIA  
YLHDDCNPRIIHRDVSSNILLDENFEHLSDFIACIPAKTHASTYVLVGTGYD  
PEYKARTRLNEKSDVVSFGTIVLELLTGKXAVDNDNLHOLIISKADNTVMEAVDE  
VRSPTAMTCCCKAQALAIACORSRPTMHEVATVLSLLPSPSLKPLVLPQKPMYAH  
YLAAGPVKIKRTHDNNSSDGWFLRFEVTSKTL"

CDS  
1. 2450  
/organism="Elaeis guineensis"  
/mol\_type="mRNA"  
/db\_xref="taxon:51953"  
/clone="Rik-OPmf"  
<1. 2160  
/codon\_start=1  
/product="receptor-like protein kinase"  
/protein\_id="AA026312.1"  
/db\_xref="GI:28140042"

ORIGIN

Query Match 25.2%; Score 800.6; DB 4; Length 2450;  
Best Local Similarity 64.2%; Pred. No. 2, 7e-256;  
Matches 1219; Conservative 0; Mismatches 649; Indels 9; Gaps 2;

QY 827 GAGATCCCTTTTGAACATCGGCTTCTGCAAGTTGCAACATTAATTCAGAGCAATCA 886  
| | | | |  
Db 1 GAGATTCCTTACAAATATGCGTTCTGCAAGTGGTCAACATGCTCCCTTCAAGGAAATAGA 60  
| | | | |  
QY 887 CTCTCGGGAAGATTCATCAGTATGATGTCATGCAAGCCCTTGCAAGTCTTATGATCTTA 946  
| | | | |  
Db 61 CTCACAGGGAAGATTCAGAGGTATGCGCTTATGCAAGCTCTTGCAATATGATTTTA 120  
| | | | |  
QY 947 AGTGGCAACTGTTGATGATCTATTCCTCGATTCGGAATCTTACTTTCACCGAG 1006  
| | | | |  
Db 121 AGTGAATAATGACGTGTGGAACCAATTCCTCGATTCGGAATCTTACTTTCACCGAG 180  
| | | | |  
QY 1007 AATTTGATTTGCAAGTAACAAGCTGATGTTCAATTCACCTGAGCTTGGAAACATG 1066  
| | | | |  
Db 181 AAGCTATATCTTACATGAGAAACAAGCTTACTGCAACATCCCTCAGAGTGGGAACATG 240  
| | | | |  
QY 1067 TCAAAATCCATTAACCTGGAACCTCAATGATATCATCTCAGGGTCAATACCCAGAG 1126  
| | | | |  
Db 241 ACAAACTTACCTATCTGCACTAATGACACAAGCTTATGATCTTATTCACAGCTGAG 300  
| | | | |  
QY 1127 CTGGGAAGCTTACTGACTGTTTGTATCTGATATGCGCAACATGATCTGGAAGACCT 1186  
| | | | |  
Db 301 CTGGGAAGCTTACTGAGAGCTGTTTGTATGATGATGATCTTGCACATTAACAACCTGAGGGTCT 360  
| | | | |  
QY 1187 ATACCTGATATCTGAGCTCTTGCAACAATCTTAAACGCTTAAATGTTCTATGGAACAAG 1246  
| | | | |  
Db 361 ATTCCCAAGATATACAGCTTGTGCACTGCAATTAATTAATTAATGTCATGATTAAGG 420  
| | | | |  
QY 1247 TTTAGTGCACTTATACCCGAGCATTTCAAAAGCTAAGTAAGTATGACTTACTTAATCTG 1306  
| | | | |  
Db 421 TTGATATGCTTATCCCATTCAGCTTCCAGAAAGTGAAGCTGACCTATCTGAACTTC 480  
| | | | |  
QY 1307 TCCAGCAACAATATCAAAAGTCCCAATCCCGTTGAGCTATCTGATCGGTAACTTAAT 1366  
| | | | |  
Db 481 TCATCAACAACAATTAAGGCAAAAGTCCCTGGGAATTAAGCGGAATTAATCAATCTGAT 540  
| | | | |  
QY 1367 ACATTGATCTTTCCAACAACAAGATTAATGATATCTTCTTCTTCTTCTGATGATTTG 1426  
| | | | |  
Db 541 ACCCTGATCTCTCGAACAATCAATTTTCTGATCCCAATCTTATCTATTTGGGAGCTG 600  
| | | | |  
QY 1427 GAGCATCTTCAAGATGAAGCTTGAAGTAATCATTAATCTGATGATTTCCAGGCGAC 1486  
| | | | |  
Db 601 GAGCATCTTCTGAGCTGAACCTTAAGTAATTAATCTCAATGAGCCCTTCCAACTGAA 660  
| | | | |  
QY 1487 TTTGGAATCTAAGAGCATCATGGAATGATCTTCAATATGATATCTTGCGCCA 1546  
| | | | |  
Db 661 TTTGGGAATCTGGGTATGTCAAACCATGATATATCTTAACAACAAGCTGTGCTGCA 720  
| | | | |  
QY 1547 ATTCCAGAAGCTTAAACAATTAACAACAATATTTTGTGAGACTGGAATAATTAAC 1606  
| | | | |  
Db 721 ATTCTGGAAGAAGCTGGAAGAGTGAACAATGATTAATTTGATTTCAACAACAAGAT 780  
| | | | |  
QY 1607 CTGACTGTATATG- - -TGCTTCAATGACCACTGTCTCAGTCTCACTGATTTAGATGTA 1663  
| | | | |  
Db 781 CTATATGATGATGATCAAGTTCATTAATGACCAATGCTTCAAGCTTATCTTGAATCTT 840  
| | | | |  
QY 1664 TCTCATTAACAACCTCGTAGGTGATATCCCTAAGAACATTAATCTTCAAGATTTTCACA 1723  
| | | | |  
Db 841 TCATTTAATAAATCTTCTGGAAGATGTTCTCTCCAAAGAACTTTTCAAGGTTTCCCA 900  
| | | | |  
QY 1724 GACAGCTTCAATGGAATCTCTGCTCTTGGGGATGATTTGGCTAAACCTACCGTCTGATGAT 1783  
| | | | |  
Db 901 GAAAGTTTCTAGGAATTAATATGTTGTGTGGAACAAGCTGTGGGATCTCTTGTGACAA 960  
| | | | |  
QY 1784 TCTGCTGAAGCTGAGAGTGAATCTCTAGAGAGCTATTTCTTGAATAGCTATTTGGG 1843  
| | | | |  
Db 961 GATCTTATGATGATGAAGATGATATTTCTGAGCTGCTGTTGTCTGCAATTAACATGAGC 1020  
| | | | |



**THIS PAGE IS BLANK**



GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: September 2, 2006, 06:51:05 ; Search time 48 Seconds  
(without alignments)  
1956.408 Million cell updates/sec

Title: US-10-519-135-2

Perfect score: 5043  
Sequence: 1 MALFRDIVLIGFLCISLVA.....SASDAQLFIRFGVIGVQNSSE 976

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5043	100.0	976	2	B84659
2	3059	60.7	932	2	T48489
3	1504.5	29.8	1124	2	B84742
4	1446	28.7	1109	2	T18536
5	1412.5	28.0	1133	2	T05322
6	1410.5	28.0	1003	2	T05898
7	1397	27.7	1123	2	D96756
8	1368.5	27.1	1002	2	T46033
9	1367.5	27.1	1192	2	T48499
10	1365.5	27.1	1192	2	T50850
11	1343	26.6	987	2	T50850
12	1335.5	26.5	1068	2	B86312
13	1334.5	26.5	1064	2	B86465
14	1331	26.4	1013	2	T10659
15	1319	26.2	996	2	F86410
16	1310	26.0	1027	2	B86089
17	1301	25.8	981	2	T50851
18	1296.5	25.7	978	2	B96787
19	1293	25.6	999	1	S27756
20	1280	25.4	1029	2	T00712
21	1280	25.4	1143	2	B84431
22	1267.5	25.1	1196	2	T09356
23	1262	25.0	1029	2	T05050
24	1253	24.8	1130	2	B86479
25	1242	24.6	1166	2	F96598
26	1227.5	24.3	976	2	T05897
27	1216	24.1	991	2	T52400
28	1205	23.9	977	2	C96745

## ALIGNMENTS

30	1204	23.9	1079	2	C96772	probable receptor
31	1192.5	23.6	1114	2	T04587	hypothetical prote
32	1183	23.5	1095	2	G96746	probable receptor
33	1175.5	23.3	1008	2	D84434	probable receptor
34	1149	22.8	996	2	T10725	protein kinase Xa2
35	1147.5	22.8	890	2	E84846	probable receptor
36	1147	22.7	990	2	T03784	probable receptor
37	1144	22.7	988	2	T45717	receptor-kinase 11
38	1142	22.6	967	2	T48210	hypothetical prote
39	1141.5	22.6	1009	2	T45645	receptor kinase-11
40	1141	22.6	960	2	H84632	probable receptor
41	1133	22.5	1025	1	A57676	protein kinase Xa2
42	1126	22.3	1025	2	T45647	receptor protein k
43	1122.5	22.3	890	2	C96654	hypothetical prote
44	1120	22.2	921	2	B86234	hypothetical prote
45	1120	22.2	964	2	T49038	hypothetical prote

## RESULT 1

probable receptor-like protein kinase, ERECTA [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 31-Dec-2004  
C/Accession: B84659  
R/lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.T.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayer, L.; Tallon, L.; Euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999  
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A/Reference number: A84420; MUID:20083487; PMID:10617197  
A/Accession: B84659  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-976 <STO>  
A/Cross-references: UNIPROT:Q42371; UNIPARC:UPI0000048588; GB:AE02093; NID:G3075386; PIR C/Gene: A8262330  
A/Map position: 2  
C/Superfamily: Receptor-like protein kinase

Query Match	Score	DB 2	Length	976
Best Local Similarity	100.0%	Pred. No. 2.9e-219		
Matches	976	Conservative	0	Mismatches 0; Indels 0; Gaps 0;
QY	1	MALFRDIVLIGFLCISLVA	1	1
DB	1	MALFRDIVLIGFLCISLVA	1	1
QY	61	VSCENVTFFNVVALNLS	61	61
DB	61	VSCENVTFFNVVALNLS	61	61
QY	121	LDLSFNEISGDI	121	121
DB	121	LDLSFNEISGDI	121	121
QY	181	PRLIYNEVLQYGLRGN	181	181
DB	181	PRLIYNEVLQYGLRGN	181	181
QY	241	LDLSYNQLGEL	241	241
DB	241	LDLSYNQLGEL	241	241
QY	301	PIIGNLTFFKLYLH	301	301
DB	301	PIIGNLTFFKLYLH	301	301
QY	361	NVANDLEGPIDHLS	361	361
DB	361	NVANDLEGPIDHLS	361	361

```

Db      361 NVANNDEGEP1PDHLSSCTNLNLSLNVHGNKFSGTIPPAFOKLESMTYLNLSNNIKGP1P 420
Qy      421 VELSRIGNLTLDLSNNKINGIIIPSSIGDLFHLKMLSRNHTIGVPGFGNRSIMEI 480
Db      421 VELSRIGNLTLDLSNNKINGIIIPSSIGDLFHLKMLSRNHTIGVPGFGNRSIMEI 480
Qy      481 DLSNNDISGPIPEBLNQLQNIILRLBNMNLTVNGVSLANCLSLTVLVNSHNLVGDIPK 540
Db      481 DLSNNDISGPIPEBLNQLQNIILRLBNMNLTVNGVSLANCLSLTVLVNSHNLVGDIPK 540
Qy      541 NNNFRRSPSPSFGICNPGELCSGMLNSPCHDSRRTRYVSIIRAAIIGIAGIIVILLMLIA 600
Db      541 NNNFRRSPSFGICNPGELCSGMLNSPCHDSRRTRYVSIIRAAIIGIAGIIVILLMLIA 600
Qy      601 ACPHPNPPFLDGLDKPVYTPSTPKLVIILHNMALHYVEDIMRMTENLSEKYLIIHGQASS 660
Db      601 ACPHPNPPFLDGLDKPVYTPSTPKLVIILHNMALHYVEDIMRMTENLSEKYLIIHGQASS 660
Qy      661 TVYKCVLKNCKPVAIKRLYSHNPQSMKQFETELMSSLIKHRLVSLQAVSLSHLSLFLF 720
Db      661 TVYKCVLKNCKPVAIKRLYSHNPQSMKQFETELMSSLIKHRLVSLQAVSLSHLSLFLF 720
Qy      721 YDYLENGSLMDLHGPTKKKTLDMDTRLKIAYGAAQGLAYLHDCSPRIIHRDYKSSNII 780
Db      721 YDYLENGSLMDLHGPTKKKTLDMDTRLKIAYGAAQGLAYLHDCSPRIIHRDYKSSNII 780
Qy      781 LDKDLRLDLDFGIAKSLCVSKSHSTYVNGTIGYIDPEVARTSRLTEKSDVSYGIVLL 840
Db      781 LDKDLRLDLDFGIAKSLCVSKSHSTYVNGTIGYIDPEVARTSRLTEKSDVSYGIVLL 840
Qy      841 ELLTRRAVNDDESNIHLHLSKTKGNNEVEMADBDITSTCKDLGVKKVFPQALLCTKRQ 900
Db      841 ELLTRRAVNDDESNIHLHLSKTKGNNEVEMADBDITSTCKDLGVKKVFPQALLCTKRQ 900
Qy      901 PNDPRTHQOTRVYLGSMLEQPPAATDTSAITLASCYVDEYANLKPHTSNCSSMSASD 960
Db      901 PNDPRTHQOTRVYLGSMLEQPPAATDTSAITLASCYVDEYANLKPHTSNCSSMSASD 960
Qy      961 AQLFRFGOVISONSE 976
Db      961 AQLFRFGOVISONSE 976

```

## RESULT 2

```

T48489
Receptor-like protein kinase - Arabidopsis thaliana
N,Alternate names: protein T28J14.120
C,Species: Arabidopsis thaliana (mouse-ear cress)
C,Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 31-Dec-2004
C,Accession: T48489
R,Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Le
submitted to the Protein Sequence Database, April 2000
A,Reference number: Z24493
A,Accession: T48489
A,Status: preliminary
A,Molecule type: DNA
A,Cross-references: UNIPROT:Q9LYP7; UNIPARC:UPI0000048A86; EMBL:AL163652
A,Experimental source: cultivar Columbia; BAC clone T28J14
C,Genetics:
A,Map position: 5
A,Intons: 43/2; 91/2; 115/2; 139/2; 163/2; 187/2; 211/2; 234/2; 258/2; 282/2; 306
A,Note: T28J14.120
C,Superfamily: Receptor-like protein kinase

```

## Query Match

```

Best Local Similarity 60.7%; Score 3059; DB 2; Length 932;
Matches 597; Conservative 131; Mismatches 202; Indels 16; Gaps 5;

```

```

Qy      31 LEIKKSKDVNNVLYDMTTSFSSDYCVWRGVSCENYTFNVVALMLSDNLNDSIPAGID 90
Db      1 MAIKASFNVANNMLLMDVDVHNDPFCWGRVFCNVSLNVSLNLNLGGEISALGD 60

```

```

Qy      91 LKSLISIDLRGNRLSGQIPDEIGDCSSLOMLDLSFNEISGDIIPFSISKQLQELIKNN 150
Db      61 LMLQSIDLQGNLGGQIPPEIGNCVSLAVVDPSTNLLFPDIPFSISKQLQELIKNN 120
Qy      151 QILGPIPTSLSQIPNLKILDLAONKLSGEIPRLIYNNEVQYIGLGNLNVGINSPDLCQ 210
Db      121 QLTGPPIPATLTQIPNKTLDLARNQLTGEIPRLIYNNEVQYIGLGNLNVGINSPDLCQ 160
Qy      211 LTGLMFPDVNNSLTGSIPEITGNCTAFQVLDLSYNQLTGEIPDFDIFGLQVATLSLQNG 270
Db      181 LTGLMFPDVNNSLTGSIPEITGNCTAFQVLDLSYNQLTGEIPDFDIFGLQVATLSLQNG 240
Qy      271 LSGKIPSVIGLQALAVLADLSGNLGSIPPIGNLTFTFKLYLHNSKLTGSIPPELGNM 330
Db      241 LTGRIPFVIGLQALAVLADLSNDELTPPIPIGNLSTFKLYLHNSKLTGSIPPELGNM 300
Qy      331 SKLHYLELNNLHGTIPPELGLTDLFDLVANNDEGEP1PDHLSSCTNLNLSLVHGNK 390
Db      301 SRLSYQLQNDNELVGKIPPELGLTDLFDLVANNDEGEP1PDHLSSCTNLNLSLVHGNK 360
Qy      391 FSGTIPPAFOKLESMTYLNLSNNIKGP1PELSRIGNLDTLDLSNNKINGIIIPSSIGDL 450
Db      361 LSGAVPEFKNLSLTLYLNLSNFSKGIPEALGHIINLDTLDLSGNNSGSIPLTGLD 420
Qy      451 EHLKMLSRNHTIGVPGFGNLSRIMEIDLNNDISGPIPELNQLONIILRLBNMNL 510
Db      421 EHLKMLSRNHTIGVPGFGNLSRIMEIDLNNDISGPIPELNQLONIILRLBNMNL 480
Qy      511 LTGNV-GSLANCLSLTVLVNSHNLVGDIPKNNNFSFSFSDSTGNPGLCGSMNLNSPCHD 569
Db      481 IHGRIPOQLNCSLANLNTSFNNLSGIIIPMKNFRFSFASFFGPFGLCGMNVGSI 540
Qy      570 SRRTRVSRRAIIGIAGIIVILLMLVLAACRPHNPPFLDGLDKPVYTPSTPKLVL 629
Db      541 SLRPSQV-FTRVAVICNVDFITLCHIFAYVKKSKQOKVLGSSKQP--ESTLTVL 597
Qy      630 HNMALHYVEDIMRMTENLSEKYLIIHGQASSYKCVLKNCKPVAIKRLYSHNPQSMKQ 669
Db      598 HMDAHTFDIMRVTEENLDEKYLIIHGQASSYKCVLKNCKPVAIKRLYSHNPQSMKQ 657
Qy      690 ETELEMLSSIKHRLVSLQAVSLSHLSLFLYDYLENGSLMDLHGPTKKKTLDMDTRLK 749
Db      658 ETELETTGISIRHNRIVSLHGYALSPEGNLLFYDMENGSLMDLHGPTKKKTLDMDTRLK 717
Qy      750 IAYGAQGLAYLHDCSPRIIHRDYKSSNIIILDKDLRLDLDFGIAKSLCVSKSHSTYV 809
Db      718 IAYGAQGLAYLHDCSPRIIHRDYKSSNIIILDKDLRLDLDFGIAKSLCVSKSHSTYV 777
Qy      810 MGTIGYIDPEVARTSRLTEKSDVSYGIVLLLELTRKAVDNDESNIHLHLSKTKGNNEV 869
Db      778 LGTIGYIDPEVARTSRLTEKSDIYSFGIVLLELTRKAVDNDEANLQMLISKADDDVTM 837
Qy      870 EMADPDITSTCKDLGVKKVFPQALLCTKRQPPDRPMHGVTVLGSFMLEQPPAATDT 929
Db      838 EAVDAEVSIVTCOMSGHRTKTFQALLCTKKNPLERPMQVSRVLSLVSPPP----- 891
Qy      930 SATLAGSCYVDEYANLKPHTSNCSSMSASDAOLFLRFGOVISONS 975
Db      892 -KLLPSPAKVQGBERRESHSDTT-----PQMFVQFREDIKSS 931

```

## RESULT 3

```

B84742
probable receptor-like protein kinase [imported] - Arabidopsis thaliana
C,Species: Arabidopsis thaliana (mouse-ear cress)
C,Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 31-Dec-2004
C,Accession: B84742

```

```

R,Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Varakan, S.E.; Umayam, L.; Tallon, L.;
euser, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402: 761-768, 1999
A,Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A,Reference number: A84420; MUID:20083487; PMID:10617197

```



Db 426 ANSSLEVLDTIRNMFTGHIPIPNLCOSQKRLKLLGVNVLGSSVSDLGCSSTLERLLEE 485  
352 -----GKLTID-----LFDLVANNNDLEGPDPHLSCTNLNLANVGNKFGSTIPRAF 399  
Db 486 NNLRGGIPDVEKONLFFDL--SGNNFTGPIPSLGNLKNVTAIYSSNOLSSIPPEL 543  
Qy 400 QKLESMTYLLSSNNIKGPIPELISRGNTLPTDLSNNKNGIIPSSLGDEHLLKNLS 459  
Db 544 GSIYKLEHLNLSHILKGIIPSELNCHKLSELDASHNLNGISIPSTGISTELTCLKSLG 603  
Qy 460 RNHTITGV-----GDF---GNLRSMEDIDLSNNDISGIPPELN 496  
Db 604 ENSESGGIPISLFGSNKLLMLQLGGLNLAGDIPVGLQALRSNLSSNKLNGQLPDLG 663  
Qy 497 OLQNIILRLNENNLTVGNVSLANCLSLTVNVSHNLVGDIPKQ--NNFSRFPDSPTGN 555  
Db 664 KLMLELDVSHNLSGLRLSTIQSITFINISHNLPSCGVPVPSLTKFLNLSPTSSGN 723  
Qy 556 PGLC-----GWLNSPCHDSRRTVRSISRALLGIALIGLVILMLVLAACRP 604  
Db 724 SDLCINCPADGLACPESSILRPCMOSNTGKGSLTGIALIVGLALLFTICLFLPSA-- 781  
Qy 605 HNPPEFLDGLDKVVTYTPKLVILHNNMLHYEDIMRMTENISEKTIIGHGASSTVYK 664  
Db 782 -----FLFLHCKK---SVEOIAISAQEGDGLNKLVEATENLNDKRYVIGKGAHGTIYK 832  
Qy 665 CVLKNCKPVAIKRL-YSHNPQSMKQFETELMELSIKHRNLVSLQAVSLSHGLSLFPDY 723  
Db 833 ATLSPDKYAVKLVFPGIKNGSVSMREITIGKVRHRLIKLEEWLKRREYLIITY 892  
Qy 724 LENSGLWDLHGPTKKTLTDWDTLKIAYGAQGLAYLHDSBPRIIHRDVKSSNILLDK 783  
Db 893 MENSGLHDILHETNPKPLDWTSTHNIAYGTAHGLAYLHFDQPAIVHRDIKPMNILLDS 952  
Qy 784 DLEKRLDPEGLAKSLCS-KSHSTYVWGTYIDPEYARTSLTEKSDPYVYVILEL 842  
Db 953 DLEPHISDFGIKLLDQSAFISPSNTVQGTGYAPENAFITTVKRSRSDYVIVILEL 1012  
Qy 843 LTRKKAUDDSSNLH-----HLMSKYGNEVEMADPDTITSTCKLGVVKV---FOL 892  
Db 1013 ITRKKAIDPEFNGSTDIIVGWRSVWTOGT--EICKIYDPSLDELILSSVMEQVTEALSL 1070  
Qy 893 ALLCTKROPNDRPTMHQVTRVL 914  
Db 1071 ALRCAKEVDKRPTRMDVVKOL 1092

RESULT 5  
T05322  
hypothetical protein F18F4.240 - Arabidopsis thaliana  
N:Alternate names: hypothetical protein F1C12.60  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 31-Dec-2004  
C/Accession: T05322; T04898  
R/Bevan, M.; Teeriy, N.; Arctiles, W.; Buyschaert, C.; Daseville, R.; De  
ewes, H.M.; Mayer, K.F.X.; Scheller, C.  
submitted to the Protein Sequence Database, April 1998  
A/Reference number: Z15408  
A/Accession: T05322  
A/Molecule type: DNA  
A/Residues: 1-1232 <BEV>  
A/Cross-references: UNIPROT:Q9SN91; UNIPARC:UPI0000A00ED; EMBL:AL022224  
A/Experimental source: cultivar Columbia; BAC clone F1C12  
R/Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft,  
submitted to the Protein Sequence Database, February 1998  
A/Reference number: Z15388  
A/Accession: T04898  
A/Molecule type: DNA  
A/Residues: 1-305 <BEW>  
A/Cross-references: UNIPARC:UPI0000175657; EMBL:AL021637  
A/Experimental source: cultivar Columbia; BAC clone F18F4  
C/Genetics:  
A/Map position: 4

A/Introns: 863/1; 116/1  
A/Note: F1C12.60; F18F4.240  
C/Superfamily: Receptor-like protein kinase; leucine-rich alpha-2-glycoprotein repeat hom  
Query Match 28.7%; Score 1446; DB 2; Length 1232;  
Best Local Similarity 31.4%; Pred. No. 1.3e-57;  
Matches 389; Conservative 163; Mismatches 321; Indels 366; Gaps 30;  
Qy 7 IVHLGFLCFLSVAT--VTSEBQATLLEIKKSF---KDVNNVLVDWTTSPSSDYCVWRCV 61  
Db 5 VLLHLFLCFSGGCGQRIINNDIQTLLEVKKSLVTRPQEDBPLRQM--NSDNNYCWGTG 63  
Qy 62 SCENV-TFNVAALNLSLDLNGEISPAIGDKLSLIDRGNR----- 103  
Db 64 TCDNTGFRVIALNTGLGTGSIISPMFGRFDNLHLDLSNNLVGPPIPALSNLTSLES 123  
Qy 104 ----- 103  
Db 124 LPLFNSQLTGEIPSQGLSVNIRSLRIGDNLVGDIPETLGNLVNLQMLALASCLRTGPI 183  
Qy 104 -----LSQIIPDEIGDCS-----SLQN 120  
Db 184 PSQGLRIVRQSLIDQNYEGEIPALGNCSDLYFTAAEMNLNGTIPALGRLENLEI 243  
Qy 121 LDISFNEISGDIPFSISKQLBQILIKNNQLGPIPTLSQIPNLKIIDLAKNLSGET 180  
Db 244 LNLANNLSLGEIPSQGEMSQLQYLSIMANQGLIPKSLADLGNLQTLDSLANNLTGEI 303  
Qy 181 PRLIY-----NEWQYLGRRNNLVGNISPLQQTGL 214  
Db 304 PE-EFMMNSQLDLVLANNHLSGLPKSICSNNTNLEQLVLSQTQSGEIPVELSKQSL 362  
Qy 215 WYFDVRRNNSLTGSIPT----- 231  
Db 363 KQDLDSNLSLAGSIPALFELVELTDLYLHNNLTGTLSPSISNLNLQMLVLYHNNLEG 422  
Qy 232 -----IGCTAPQVLDLSLNQLTGEIPPIGFL-QY 261  
Db 423 KLPKEISALRKLVELFLYENRFGEIPQEIIGNCTSLKMDIMFNNHREGELIPSIGRKL 482  
Qy 262 ATLSLQGNQSLGKIPSVIGMQALAVLDLSGNLSGSIPIPLNLFTTEKLYHNSKLTG 321  
Db 483 NLHLRQNELVGGPASPGLNGCHQNLIDLDNLQSGSISSPFLKGLBQELMLYNSLQ 542  
Qy 322 S-----IPPELGNSKHL 334  
Db 543 NLPSLSLSLNLRLINLSHRLNGTIRPLCGSSSYLSFDVNNGFDEIPLGLNGQNL 602  
Qy 335 YLELNDNHLTGHIPEELGKLTDLFDLVANNNDLEGPDPHLSCTNLNLANVGNKFPST 394  
Db 603 RLRLGKQQLTGKIPWTLGKIRELSLDMSSNALTGTPLOLVCKKLTIDLNPNFLSGP 662  
Qy 395 IPRAFQLEEMTYLNLS-----NNIKGPIPELISRGINDL 430  
Db 663 IPPWGLTSQLGEBKSSNOFVSLPTELFNCTKLVLSDGNSLNGSIPOEIGNIGALN 722  
Qy 431 TLDSLNNKINGIIPSSLGDEHLLKNLSRNHITGVVPGDFGNLRIME-IDLSNNDISG 489  
Db 723 VLNLDKQFSGSLPQMGKLSKLYELRSNLSLTGEIPVEIGLODQSLADLSYNNFTG 782  
Qy 490 PIPELNQNLNILLRLNENNLTVGNV-GSLANCLSLTVLVNSHNLVGDIPKNNNSRFS 548  
Db 783 DISITIGTSLKLETLDSLHQLTGEBVGSQDMKSLQYLVNVSFNNNGKTKK--QFSRP 840  
Qy 549 PDSFIGNPGCGSWLNSPCHDSRRTVRSISRALLGIALIGLVILMLVLAACR----- 603  
Db 841 ADSFLGNTGLCGSPL-SRCN-----RVRTTIALTRI-----GLMILVIALFFQKRDHFFK 889  
Qy 604 --PHNPPEFLDGLDKVVTYTPKLVILHNNMLHV---YEDIMRMTENLSEKTIIGHGA 658  
Db 890 KVGHGSAIYSSSSSSGATHKP-----LFRNGASKSDIRIMEDIMETHNLSSEFMIGSGG 944  
Qy 659 SSTYVKCVLCKKCPVAIKR-LYSHNPQSMKQFETELMELSIKHRNLVSLQAV--SLSHL 715

```

Db      945 SGKYYKAELENGEFTVAVKKILIMKODLMSNKSFSREVKTLGRIRRHRLVVKLMGVCSSSEG 1004
QY      716 GSLLFPDYLENGSLMDLHG-----PRKKTLMDMTDLTKAYGAAGLAVLHDCSRIT 770
Db      1005 LNLITIEYMGNGSTMDLHEDKPVLEKKKLLDMEALRIAVGAQVEYLHDCVPIV 1064
QY      771 HRDVKSNLILDDLEARLTDPFGIAKSL---CVSKSTSTYVMGTIGYIDPEVARTSRLT 827
Db      1065 HRIIKSNVLLDSNMEHLDFGLAKVLTENCNTNTSNTWCFACSYGIIAPEYASLKAT 1124
QY      828 EKSDVYSYGVILLELTRRAVD---ESNL-----HHLIMSKTYGNNEVEMADPDI-- 876
Db      1125 EKSDVYSYGVILLELTRRAVD---ESNL-----HHLIMSKTYGNNEVEMADPDI-- 876
QY      877 -----TSTCKDLGVKKVYFQALALCTKROPNDPRTMHQ 909
Db      1182 LHPFEDDAC-----QVLEIALQCTKTSPQERPSRQ 1213

```

## RESULT 6

```

E86308
hypothetical protein F20D23.7 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2004
C:Accession: E86308
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Comu, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
aneen, N.P.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maltli, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E86308
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1133 <STO>
A:Cross-references: UNIPROT:Q9SH12; UNIPARC:UP10000048275; GB:AE005172; NID:95734762; PI
C:Genetics:
A:Map position: 1
C:Superfamily: Receptor-like protein kinase

```

```

Query Match      28.0%; Score 1412.5; DB 2; length 1133;
Best Local Similarity 32.6%; Pred. No. 3,7e-56;
Matches 371; Conservative 169; Mismatches 392; Indels 207; Gaps 23;
QY      7 IVVLGFLFCLSLAVATYTSSEGAFLLEIKSKFKDVNNVLYVMTTSPSSDYCVWNGVSCENV 66
Db      11 VILCSFSF---ILVRSINERGVLEFKAFPLANDSNGYLAWSNOLDSPN-CNMWGIACTHL 66
QY      67 TENVVALNLSIDLDEISPAIGDL-----KSLISDLRGN 102
Db      67 R-TVTSVDLNGMNLSTGLSPICKLHGLKLTANSTNFISPIQDLSLCSLEVLDTCTN 125
QY      103 R-----LSGQIDPEIGDCSSLQNLIDLEFNLSGDIPISISK 138
Db      126 RFHGVPIPIQLTMTITLTKLCLCENYLFSGIPROIGNLSIQELVIVSNNTLGVIPPSMAK 185
QY      139 LKQLEDLILKNNOLIGPIPTLSQIPRLKTLDAONKLTSEIRLLIYMEVLOYLGLRGN 198
Db      186 LKRLRIIRGRNFSGVIPSEISGCSLKVLAENLESLPKOLEKQNTLDTLIMON 245
QY      199 NLVGNISPDLCQTLGLWYFVRNNSLTGSIPTIGCTAFOVDLSYNOLTGEPIDIG- 257
Db      246 RLSGEIPPSVGNISRLLEVALAHENYFTGSIPIREIGLTKTKKRLVLYTNOLTGEPREIGN 305
QY      258 FLQVATLSLOGNOLSGKIPSVIGLMOALAVLDSGNLSSGSPILLIGNLTFTEKLYAHN 317
Db      306 LIDAAEIDFSENGTGFIPKEFGHILNLKHLHFENILGPIPREIGELTLLEKDLSTIN 365

```

```

QY      318 KLNGSTIPPELGNNSKLHYLELNDNHLTGHTPEPIGLTDLFDLVANNDLEGP1PDLSS 377
Db      366 KLNGSTIPPELGNNSKLHYLELNDNHLTGHTPEPIGLTDLFDLVANNDLEGP1PDLSS 377
QY      378 CTNLSNLSNMGNGSGTIPPAFOKLESMYVNLSSNNIKGPIVEL----- 423
Db      426 FQTLILSLSGNLSGNIPRDLCTCKSLTKMLGDQNLGSLTEL.FNLQNLALAEHQN 485
QY      424 -----SRIGNL----- 429
Db      486 WLSGNISADGLKLNLERLANNFTGEIPEIIGNLTKIVGNISSNOLTGHIPELGS 545
QY      430 -----DTLIDLSNNKINGITPSIGDLEHLKMLSRNHTGVNPGDGNLSIEIDL--- 482
Db      546 CVTIQRLDSGNKFSYIAOELQVLYLETLRLSDRLTGEIPIHSGFDLRLMELQGN 605
QY      483 -----SNNDISGPIPEELNOLQNIILLRLNNNLGTNV-GLSLA 519
Db      606 LLSENIPVELGKLTSLQISLNTSHNNLSGTPPSLGNLQWLELYLNDNLSGEIPASIG 665
QY      520 NCLSLTLVNLVSHNLVGDIPKNNFSRFPDSFTGNPGICGSWLN-----PCHDSRRTV 574
Db      666 NLMSLIICNISNNNLVGTVPDIAVFORMDSNFGNMGHGLCNSORSHCOPLVPHSDSKLNW 725
QY      575 RVGIS-RAAILGIA--IGGLVILMLV-----IAACRPNPPFLDGSIDKPV 619
Db      726 LINGSGRQKILITTCVIGSVFLITGLCWTIKRBPFAVLAEDOTKPDVMD----- 778
QY      620 TVSTPKLVILHMMALHVEDIMRMENTSEKYLIGHGASSTYVKCVLKNCKEPAIKRLV 679
Db      779 SYVFPKKGK-----TGGLVDAIRNSEDVVLDRGACGTIYKMGSGEVIAVKLN 830
QY      680 S--HNPQMKQFTELEMLSSITGRNLVLSIQAVSLHSLGSLFYDYLENGSLMDLHGPT 737
Db      831 SRGEGASSNSFPAEISTIGKIRHRNIVKLYGFCYHQNSNLLEYEYMSKSLGEOLQGE 890
QY      738 KKKTLMDRLKAYAGAAGLALHDCSPRIIHRVKSNNILDDLEARLDPFIAS 797
Db      891 KNCLLDMNARYRALDAAGSLCYLHDCPPQIVHRDKSNINLIDDRFQHLVGDPIAKL 950
QY      798 LCVSKSTSTYVMGTIGYIDPEVARTSRLTEKSDVSYGIVLELTRRAV---DDESN 854
Db      951 IDLSYSKMSNAVAGSYIAPEYATYMKTEKCDIYSPGVILLELTRKRPVPLEGGD 1010
QY      855 LHHLMSTKGN--EVNEMADPDI-TSTCKDLGVKKVYFQALALCTKROPNDPRTMHQVTR 912
Db      1011 LVWVVRISIRNMIPTEMFDAFLDNDKRTVHMSLVLIKALFCTSNSPASRPTMREVA 1070
QY      913 VLGSFMLSQPPAATTSATLACVYDE-----YANLKT-PHSVNCSSMSASDAQ 963
Db      1071 ----MTERGSSSLSSSISITSETPLEANSKGMVLIHHTHTTLTLCNFRTECDSHM 1124

```

## RESULT 7

```

T05898
hypothetical protein F6H11.170 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 31-Dec-2004
C:Accession: T05898
R:Bevan, M.; Brandt, P.; Dose, S.; Jarke, D.; Scharfe, M.; Schon, O.; Bancroft, I.; Mewe,
submitted to the Protein Sequence Database, April 1998
A:Reference number: Z15456
A:Accession: T05898
A:Molecule type: DNA
A:Residues: 1-1003 <BEV>
A:Cross-references: UNIPROT:Q49545; UNIPARC:UP10000042341; EMBL:AL021684; GSPDB:GN00063;
A:Experimental source: cultivar Columbia; BAC clone F6H11
A:Gene: ATSP.F6H11.170
A:Map position: 5
A:Intons: 867/1
C:Superfamily: Receptor-like protein kinase; leucine-rich alpha-2-glycoprotein repeat hom

```









Db 419 EDLWKLPLMALDLDSDNNFTGEIPKSLWKSNTIMEFTASVYNRLSEGYLPALIGNAASLRLV 478  
QY 338 LNDNHLTGHPPELGLKTLDFDLNVANNDEGPIPDHLSSTCTNLSLVN----- 386  
Db 479 LSNQNLGELPREIGKLTSLVNLNANMFQGIPELGDCTSLTTLTDLGNNLQGIIPD 538  
QY 387 -----HG-----NKPSGTIPR 397  
Db 539 KITRALQQLCVLSYNNLSGSIPEKPSAYFHQIEMPDLSFLQHGIIPDLSYNNLSGPIPE 598  
QY 398 AFQKLESMYTLNLSNNIKGPIPEVLSRIGNLTLDIS----- 435  
Db 599 ELGECVLVYSLSNHLSGSEIPASLSRLTNLTLLDSNALTSGISPREMGNLSKLQGLN 658  
QY 436 --NNKINGIIPSSIGDLEHLKNNLSRNHTGVPGPGNLRSLMEIDLSNNDISGPIPE 493  
Db 659 LANNQNLGHPPESGLLGSLVKNTLTKNKLDPVPASLGNLKELTNHDLSFNLSGELSS 718  
QY 494 ELNQLQNIILRLNENNLTVGNVGS-LANCLSLTVLVNLSHNNLVGDIPE----- 539  
Db 719 ELSTMETVGLVYIEQKFTGEIPBELGNLTQLETLVDSENLISGEIYTKICGLPNEFLN 778  
QY 540 --KNNFSRSPDS-----FIGNPGLCGSMWNSPCHDSRRTVVSIISRAIIGIAI 588  
Db 779 LAKNNLRGEVPSDGVCDPSPKALLSGNKELCGRVVGSDCKIEGFKLR---SAMGIAGLML 835  
QY 589 GGLVILLMLVLAACR-----PHNPP-----FLDGLDKVTYVSTP 624  
Db 836 GFTIIVFVFSLRMMATKRVKQKORDPERMESRLGFVDNLVFLSGSRSP----- 890  
QY 625 KLVILHNMMALHYE-----DIMRMTENLSEKVIIGHGASSTYKCVLKCKEPAI 675  
Db 891 ----LSINIM--FEQPLKVRGLDYEATDHPKSKNIIIDGGGTYVYKALPEKVVAV 944  
QY 676 KRLVSHNPQSMKQFETELMLSSIKHNNVSLQVSLSHGSLFYDLENGSLMDLHG 735  
Db 945 KKLSEAKTQGNREPMAMETLGVKHPNVLVLGYSFSEKLLVYEVWNGSLDHMLRN 1004  
QY 736 PT-KKKTLDMDTRKLYGAAQGLAYLHDCSPRIHRDYKSSNIIIDKLEARLTDFGI 794  
Db 1005 QTMLEVLVDMSKRLKIVAGARGLAFHGHGFIPIHRIIDIKASNIIIDGDFEPFVADPGL 1064  
QY 795 AKSLCYSKSHSTFVMGTGIYIDPEYARTSRLTEKSDVSYGVILLELTRKAV----- 849  
Db 1065 ARLISACSESVSYIAGTFGIIPPEYGASABATTKGVYSFVGLLELVGKEGTGDFK 1124  
QY 850 -DDESNIHLHMSKTGNNVEWEMADPDITSTCKDLGVVKKVFOQLALCTKROPNDREPTM 908  
Db 1125 ESEGGNLVGAIAIKINGKAVDIVIDLVSVALKNQL-RLDQIAMLCLAETPAKRNML 1183  
QY 909 QVTRVL 914  
Db 1184 DVLKAL 1189

RESULT 12  
T50850  
receptor protein kinase homolog [imported] - soybean  
C/Species: Glycine max (soybean)  
C/Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 31-Dec-2004  
C/Accession: T50850  
R/Yamamoto, E.; Karakava, H. C.; Knad, H. T.  
Biochim. Biophys. Acta 1491, 333-340, 2000  
A/Title: Molecular characterization of two soybean homologs of Arabidopsis thaliana CLAV  
A/Reference number: Z25262  
A/Accession: T50850  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-987 <YAM>  
A/Cross-references: UNIPROT:Q9M6A7, UNIPARC:UPI00000AC3C7, EMBL:AF197947, PIDN:AAF59906,  
C/Genetics:  
A/Gene: CLAVB  
C/Superfamily: Receptor-like protein kinase; leucine-rich alpha-2-glycoprotein repeat hd

Query Match 26.6%; Score 1343; DB 2; Length 987;  
Best Local Similarity 34.1%; Pred. No. 4.1e-53;  
Matches 346; Conservative 175; Mismatches 358; Indels 136; Gaps 24;  
QY 9 LIGFLFCLSL-VATVTS-BEGATLLEIKKSPKD---VNNVLYDMTSPS-SDYCVWNGVS 62  
Db 9 LLEFIPFIMRVATCSFTDMESLTKLQKSMKDDKADALHDMKFFPSLSAHCFSGG 68  
QY 63 CENVTFVVALNLSDLNDEGISPAIGDKSLSIDRGRSLSGQIPDEIGDCSSLQNL 122  
Db 69 CDR-ELRVAVINVSFVPLFCHLPEEIGQLDKLENTLVSQNNLTVSGVPEKLEAALTSLKLN 127  
QY 123 LSFNELS-----GDIPFSIKLQLEBOLIKNNQLGPI 157  
Db 128 ISHNVSGHPFGQIILPMYKLEVLVDYDNNFTPLPELVYKLEKLYLKLDGNYFSGSIP 187  
QY 158 STLQIPLNLKILDLAONKLSGEIPRLIYWNVEVLQYGLRGNNLV-GNISPDLCQLTGLMY 216  
Db 188 ESYSEPKSLFSLSTNSLSGKIPKSLSKLTKRLYKLGYNNAVEGIPPEFGSMKSLRY 247  
QY 217 FVVRNNSLTGSIPEITGCTAFQVLDLSYNQLTGEIIPFDI-GFLQVATSLQGNLSGKI 275  
Db 248 LDISSCNLSGEIIPSLANLTNLTDLFLQINNLTGTPSELASAVWSIMSLDLSINDLTGEI 307  
QY 276 PSVIGLMQALAVDLGNNLSGSIPTLIGNLTETKLYHSNKLTSIPBELGNMSKLYH 335  
Db 308 PMGFSQLRNLTLNPFQNNLRGVSFVSGELPYLETLQLMDNPSFVLPNLDQNGKLF 367  
QY 336 LELNDNHLTGHPPELGLKTLDFDLNVANNDEGPIPDHLSSTCTNLSLVNHNKSGGTI 395  
Db 368 FDIYKHHFTGLIRDLCKSRLOTIMTDNFFRGPPIPEINGNCKSLTKIRASNNVYLVNGV 427  
QY 396 PRAPQKLESMYTLNLSNNIKGPIPEVLSRIGNLTLTDLSDNNKINGIIPSSIGDLEHLK 455  
Db 428 PSGIFKLPSVTYIIELANNFENGLPEISG-ESLGLITLSSNNLFSGKIPALNKLRLAQT 486  
QY 456 MNLNRNHTGVPGDGNLSIMEIDLSNNDISGPIPELNLQNIILRLNENNLTVGNV 515  
Db 487 LSLDANPEVGEIAGEVFDLPMLVNINSGNNLGPITTLTRCVSLAVALSRNMLBGI 546  
QY 516 G-----SLAN-----CLSLTVLVNLSHNNLVGDIPEKNNFSRSPD 550  
Db 547 PKGIKULTDLSINVSINOQSPVPEIRFMLSITLTLDSNNNFICKVPPVGGGFAYSEK 606  
QY 551 SFTGNPGLCGSWNSPCHDS-----RRTVVSISRAIILGAIIGLVLLMVL 599  
Db 607 SFGNPNLCTS--HSCPNSSLYPDALKKRGPMSLKSTRVIVIALGTAALLVAVTV 663  
QY 600 AACRPHNPPFDGSDIKPVYVSTPKVLILHNMMA---LHYV-----EDIMRMTENL 648  
Db 664 YMMRRRK-----MILAKTWKLTAFORLNFKAEDV---ECL 696  
QY 649 SEKYIIGHGASSTYKCVLKNCCKPAIAIKRLY-SHNPSMKQFETELMLSSIKHNNLVSL 707  
Db 697 KEENITIGKGAGIVYGGSMNGTDVAIKRLVAGSGSRNDYGFALLETLOKIHNNIMRL 756  
QY 708 QAVSLSHLGLFYDYLENGSLMDLHGPTKKKTLDMTRKLYGAAQGLAYLHDCSP 767  
Db 757 LGVSNKETVLLIYEVMPNGSLGEMLHG-AKGHLLKMEMYKIAVBAKGLCYLHDCSP 815  
QY 768 RIHRPVSNNIILDDLEARLTPDGLASLC-VSKSHSTYVMGTGIYIDPEYARTSRL 826  
Db 816 LIHRDRKSNVNIILDDLEHVAVDLPGALFVDPGASQSSISAGSIVYAPETVAITLKV 875  
QY 827 TEKSDVSYGVILLLELTRKAVDESNLHLI--MSKTGNNVEWEMADP----- 874  
Db 876 DEKSDVYSRGVVLLEILIGRKPVGGEFGDGVIDYGNVKNKR---LELAQPSDAALVAVY 931  
QY 875 DITSCKDLGVVKKVFOQLALCTKROPNDREPTMHQVTRVLGSMLESEOPPAATDT 929  
Db 932 DPLSGVPLTSLVIMFNIAMCVKEMGPARPTWREVVH-----MSEPPHSATHT 981

RESULT 13  
B86312  
F11A6.9 protein - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear crease)  
C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Dec-2004  
C/Accession: E86312  
R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; anen, N.F.; Hughes, B.; Huizart, L.  
Nature 408, 816-820, 2000  
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maltl, R.; Marzalli, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A/Reference number: A86141; MUID:21016719; PMID:11130712  
A/Accession: E86312  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 11088 <STO>  
A/Cross-references: UNIPROT:Q9FZ59; UNIPARC:UPI000004827B; GB:AEO05172; NID:910802748; P1  
C/Genetics:  
A/Map position: 1  
C/Superfamily: Receptor-like protein kinase

Query Match 26.5%; Score 1335.5; DB 2; Length 1088;  
Best Local Similarity 33.4%; Pred. No. 1e-52;  
Matches 353; Conservative 176; Mismatches 358; Indels 201; Gaps 25;

6 DIVLGEFLCISLVAATVS--EEGATLEIKSEKFDVA-NVLYDW-----TTSFSDYCV 57  
8 EITLCLFLFYFRDYSLSNSDGLALLSLKHFDKPLEVASTWKMTSETTPCANN-- 65

58 WRGVSCNVTNNV-ALNSDLNDGEISPAIGDKSLSLDGRNLSGQIPDEIDCS 116  
66 WFGVTCI-DLSGNVETNLSASGSLGSEIGELKLVTLDSLNSFSGILPESTLCNCT 124

117 SLQNLDSFPELSDGIDPFISISKQLBQLIKNNQLIGPISLTSLQPNKIITDLAONKL 176  
125 SLETLDSLNDPSEGVDPDIFGSLONLTFLYIDRNLSGLIPASGGLIELVLRMSTNNL 184

177 SGEIPRLIYNNEVQVYGLRGNNLVGNISPDLCOTGLWFDVYNNLSLTGSIPEITGNC 236  
185 SGITPELGNCSKLEYALANNKNGSLPASYLLENLGEIPVSNNSLGGRIHFGSSNCK 244

237 AFOVLDLSYNQLTGEIPFDIG-FLQVATLSLQNSGSKIPSVTGLMQLAVLDLGNL 295  
245 KLVSLDLSFNDPQGVPEIGNCSSLSHSLVWVKCNLTGTIPSSMGMLRKVSVIDLSNRL 304

296 SGIPIPLIGLUTFEKLYLNSNKLTGSIPELGMKSLHYELMDNHLTGHIPELGLKT 355  
305 SGNIPQELGNCSSLETIKLNDNQGEIPALSKLKLQSLLEFNNKLSGIEIPGIKTIQ 364

356 DLFDLANNNDLEGPID-----DHLSSCT-----NINSLNVHGNKF 391  
365 SLTGMLVYNNLTIGELPEVETQKLKKLTLPNNGFPGDIPMSGLNRSLEEVLDGNRF 424

392 SGITP-----RAFOKLE-----S 404

425 TGEIPPHLCHGQKRLFLTGSNQLHGKIPASIROCKTLERVLREDNKLGLVPEFPELS 484

405 MYTINLSSNNIKGPIPELISIGLDTLDSNNKINGIPESGLDEHLKMNLSRHIT 464  
485 LSYVNLDSNFSFEGIPSLSGCKNLTLTIDISQNKLTGLIPELGNLQSLGLNLSHNYLE 544

465 ----- 464

545 GPLPSQLSGCARLLYFDVGSNLSNGSIPSPFRWKSSTLVLDNNFLGAIPOFLAELD 604  
465 -----GVVPGDFGNLRSI-MEIDLSNNDISGPIPEELNQONITLARLENNNL 511

Db 605 LSDLRIARNAFGKIPSSVGLKSLRYGLDLSANVFTEGIPPTLGLINLERLINSNKL 664

Qy 512 TGNVGSIANCLSTVLNVSHNNLVGDI PKN--NNFSRFPDSFIGNPGJC-----GSM 562  
Db 665 TGPLASVLSQSLKSNQVDVSNQFTGPI PNVLSNSSKFS-----GNPDLCIQASVSAI 719

Qy 563 LNSPCHDSRRRTVVSISRAAIL--GIAIGLVILLVLIACRPHNPPLDGLDKPV 620  
Db 720 IRREFKSCQGVKLTWTKIALIAAGSSLVYALLFALFVLCR-----CKRG 767

Qy 621 YSPFKVILHMNAALVYEDIMTENTLSEKYIIGGASVTYKCVLKNCKPVAIKRL-Y 679  
Db 768 KTDADANILAEESL-LINKVLATNDLDKTYIGGAGCVVRASLGSQEEYAVKCLIF 826

Qy 680 SHNPQSKQFETELMSSIKHNLVSLQVSYSHLSGLFLFYDLNGLSLMDLH-GPTK 738  
Db 827 AEHIRANQNMKRIETIIGVVRHNNLRLEFRFMKXEDGLMYGMNGSLHDVLRHNGG 886

Qy 739 KKTLDWDTRIKIAVGAAGLAVYHDCSPRIHRDYKSNILDKLEARLDPFGIAKSL 798  
Db 887 EAVLDWSARFENIALGISHGLAVLHDCHPPIIRHDIKPENILMDSMEPHIGDFGLARLI 946

Qy 799 CVSKSHSTYVMGTIGIYDPEVARTSLTEKSPVSYGVYLELRRRAYD---DESN 854  
Db 947 DDSVTSTAT-VTGTGYIAEENAYKTVRSKESDVSYGVVLELVGKRLDLSFPEDIN 1005

Qy 855 LHHILMSKTGNNEVME-----MADPDITSYCKDLGVKKVQF--DALCTKRPNDRPT 906  
Db 1006 IYVWVSYSVSSYDEDDTAGPIVDPKLVDELDTKAREQAIOVTDLALACTDGRPNRPS 1065

Qy 907 MHQVTRVL 914  
Db 1066 MRDVVKDL 1073

RESULT 14  
B86465  
probable protein kinase [imported] - Arabidopsis thaliana  
C/Species: Arabidopsis thaliana (mouse-ear crease)  
C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Dec-2004  
C/Accession: B86465  
R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; anen, N.F.; Hughes, B.; Huizart, L.  
Nature 408, 816-820, 2000  
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maltl, R.; Marzalli, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A/Reference number: A86141; MUID:21016719; PMID:11130712  
A/Accession: B86465  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-1064 <STO>  
A/Cross-references: UNIPROT:Q9FX19; UNIPARC:UPI000004980A; GB:AEO05172; NID:910086466; P1  
C/Genetics:  
A/Map position: 1  
C/Superfamily: Receptor-like protein kinase

Query Match 26.5%; Score 1334.5; DB 2; Length 1064;  
Best Local Similarity 33.4%; Pred. No. 1.e-52;  
Matches 354; Conservative 155; Mismatches 364; Indels 187; Gaps 26;

Qy 12 FLTC-----LSVATYTSSEGATLEIKSPKDVNNVLYDWTSPESDVCWVRGVS 62  
Db 12 FLFCSSWVMAQPTLSL-----SSDQALLSLKKRSP--SLFSSWPDQDTP-CSWYGIT 62

Qy 63 C--ENVTFNVVA-----LNTSDNLNDEISPAIGDKSLSLIDL 99  
Db 63 CSADNRVIVSIVDPTFLNLSISIDLSLSLQGLNLSSTNLSSPIRPPSFGKLTHTLALDL 122



